Preventing foot and mouth disease - how are the costs divided between the public authorities and the pig and cattle industries in Denmark?

Christensen, Tove; Denver, Sigrid; Alban, Lis; Boklund, Anette ; Houe, Hans; Leth Hougaard, Jens ; Mortensen, Sten; Rasmussen, Susanne D.; Tamstorf, Trine V.; Toft, Nils

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001

Occurrence of a conflictive species as assessed by modeling and evaluated by use of multi-source citizen science data

Lis Alban[1], Astrid Molkte Jordt[2], Martin Lange[3], Stephanie Kramer-Schadt[4], Lisbeth Harm Nielsen[1], Søren Saxmose Nielsen[5], Hans-Hermann Thulke[6], Henrik Vejre[7], [1]Danish Agriculture & Food Council, Copenhagen V, Denmark; [2]Department of Geosciences and Natural Resource Management, Frederiksberg, Denmark; [3]Helmholtz Centre for Environmental Research UFZ, Leipzig, Germany; [4]Leibniz Institute for Zoo and Wildlife Research IZW, Berlin, Germany; [5]Department of Large Animal Sciences, Frederiksberg, Denmark; [6]Helmholtz Centre for Environmental Research Leipzig - UFZ, Leipzig, Germany; [7]Department of Geosciences and Natural Resource Management, Frederiksberg, Denmark. Contact: lia@lf.dk

Denmark was considered without an established population
of free-ranging wild boar. Today, sporadic observations of wild boar challenge that view. Due to its reservoir role for economic devastating swine diseases, wild boar represents a potential threat for Denmark's position as a large pig- and pork-exporting country. This study assessed the prospects of wild boar invasion in Denmark. Multi-source citizen science data of wild boar observations were integrated into a multi-modelling approach linking habitat suitability models with agent-based, spatially-explicit simulations. We tested whether the currently observed presence of wild boar is due to natural immigration across the Danish-German border, or whether it is more likely that wild boar escaped fenced premises. Five observational data sources served as evaluation data: 1) questionnaire sent to all 1,625 registered owners of Danish farm land,
located in the 60 parishes closest to the border, 2) online questionnaire, 3) mobile web-based GPS application, 4) reports in media or by governmental agencies, and 5) geo-referenced locations of fenced wild boar populations. Data covering 2008 to 2013 included 195 observations of wild boar, including 16 observations of breeding sows. The data from the Danish Nature Agency and the mailed questionnaires confirmed each other regarding the location of wild observations, while data from the Danish Veterinary and Food Administration, the media and the electronic questionnaires documented individual scattered observations in the rest of Jutland. Most observations were obtained in the region bordering Germany. It is uncertain whether the relatively few observations represent an established population. Model outcomes suggested that the origin of about half of the area with sporadic observations of wild boar could be attributed to spatial expansions from a local Danish population near the border. However, the other half, located distant to the border were likely a result of animals escaping fenced premises inside the country. The approach serves as a template to assess the status of an invading species and improve the knowledge base for risk assessment and management decision.

002

Agent-based modeling as an innovative tool to simulate dynamics of disease transmission at the wildlife-livestock interface

Karin Orsel[1], Omar Charif[2], Danielle Marceau[2], Mathieu Pruvot[3], Alessandro Massolo[4], Marco Musiani[5], [1]University of Calgary, Calgary, AB, Canada; [2]University of Calgary, Calgary, AB, Canada; [3]Wildlife Conservation Society, Phnom Penh, Cambodia; [4]University of Calgary, Calgary, AB, Canada; [5]University of Calgary, Calgary, AB, Canada. Contact: karin.orsel@ucalgary.ca

Background:Most epidemiological models have limitations for studying disease transmission in multi-host systems, such as the wildlife-livestock interface. Agent-based modeling (ABM) offers a spatially-explicit framework to simulate the behaviour of individuals (represented as agents) and pathogens, and their interactions with the environment. The objective of our study was to use ABM to investigate dynamics of infectious disease transmission between cattle and elk. Methods: The ABM included four main interrelated modules: pasture, cattle, elk, and pathogens. Pasture represented the geographic environment in which cattle move; it incorporated a model to simulate seasonal grass growth and depletion through grazing. Cattle and elk were described by attributes such as age, body weight, sex, infection status, and physiological status (i.e. pregnancy), which govern their nutritional needs. The use of the same environment by cattle and elk, guided by habitat selection functions, creates pathways for disease transmission. Infection of cattle and elk by the pathogen, or contamination of the environment were modeled as changes of the 'infection status' attribute. Pathogens were simulated by specifying different incubation periods, intra- and inter-species probabilities of infection, recovery times, persistence in the environment etc. The ABM was calibrated with extensive field data and modules were validated using the pattern-oriented modeling approach. Scenarios of intra- and inter-species pathogens transmission were simulated over one year. Results: The model will allow us to quantify the risk of pathogen transmission under current management practices based on pathogen characteristics, and evaluate alternative management scenarios to mitigate this risk. Conclusions: Through modeling the complexity of hosts' interactions with their environment, we can better understand the risks and drivers of disease transmission for different pathogens and cattle management strategies. Relevance: ABM provides an excellent tool for veterinary epidemiologists to simulate scenarios in a complex multi host system supporting decisions on livestock and pasture management.

003

Investigating koala declines with online tools

Joerg Henning[1], Matt Taylor[2], Allan McKinnon[3], Rachel Allavena[1], [1]University of Queensland, Gatton, Qld, Australia; [2]Identic Pty Ltd - Identification Tools and Software Development, Brisbane, Qld, Australia; [3]Moggill Koala Hospital, Department of Environment and Heritage Protection, Moggill, Qld, Australia. Contact: j.henning@uq.edu.au

South East Queensland koalas (Phascolarctos cinereus) are currently experiencing a drastic population decline, with increasing numbers of dead or ill animals being found. The aim of this research project is to design online tools for members of the public to capture information on distressed wild koalas, to store this information in an online database on sightings of koalas and to develop a database for koalas submitted to wildlife hospitals. KoalaBASE, a web-based database for diagnostic, clinical, pathological and epidemiological data on koalas has been already created (http://www.uq.edu.au/vetschool/koalabase). KoalaBASE facilitates data input at multiple veterinary centres, as well as the use of the data by multiple stakeholders such as government departments and researchers. KoalaBASE uses standardised fields, terminology, and drop down menus for epidemiological and pathological data, including standardised case definitions - all of these facilitating rapid data analysis. A mobile app will be designed to run on smartphones, tablet computers and other mobile devices. It can be used by members of the public to collect detailed information and photographs on sick, injured or at risk koalas. This data is then submitted to wildlife rescuers who can instantly respond to the calls to ensure that koalas are immediately submitted to the hospitals. Sightings data will be stored in an online database application, called KoalaSAFE and records will be validated and cross-checked and linked to the clinical online database KoalaBASE. The development of these software products will allow an identification of trends in disease patterns and the construction of threat maps for subpopulations. This provides an early alert system and enables government bodies to deliver rapid targeted and efficacious interventions and to set-up active surveillance if necessary and it allows researchers to formulate specific research questions to new koala threats that might arise. Overall, the research will provide a simple and economical approach for data collection and surveillance to help to understand and ultimately prevent further losses of this already imperiled and iconic Australian animal species.

004

APHAEA: Towards a harmonized wildlife health and population monitoring in Europe

Christoph Staubach[1], Christian Gortazar[2], Ezio Ferroglio[3], Marie-Pierre Ryser-Degiorgis[4], Thijs Kuiken[5], Marc Artois[6], Dolores Gavier-Widen[7], Franz Conraths[1], [1]Friedrich-Loeffler-Institut, Greifswald - Insel Riems, Germany; [2]Universidad de Castilla - La Mancha, Ciudad real, Spain; [3]Università degli Studi di Torino, Grugliasco, Italy; [4]Centre for Fish and Wildlife Health - Vetsuisse Faculty, Bern, Switzerland; [5]Erasmus University Medical Centre, Rotterdam, Netherlands; [6]VetAgro Sup - Campus Veterinaire, Lyon, France; [7]National Veterinary Institute, Uppsala, Sweden. Contact: christoph.staubach@fli.bund.de

Purpose: Europe is increasingly concerned about infections of humans or domestic livestock that are shared with wildlife. Recent examples include the emergence of African Swine Fever in Poland and the Baltic countries in relation with wild boar; the re-emergence of tuberculosis in many countries in relation with different wildlife hosts including ungulates and badgers; and the lagomorph-related increase of leishmaniosis in human in Spain. However, Europe's characteristic diversity makes it difficult to monitor both the disease agents and their wildlife host populations in a harmonized and coordinated way.

Methods: The EU consortium APHAEA (EMIDA ERA-NET) has set up tools that aim to overcome these limitations. First, "Disease Cards" including recommended sampling and diagnostic protocols are now available for the most relevant diseases shared between wildlife and livestock or humans. Second, host "Species Cards"include reviews on abundance estimation methods and recommendations of the most suitable methods at different spatial scales. Additionally, APHAEA also aims at strengthening a European Wildlife Health Network that will continue beyond the end of the project and contribute to sustained and improved wildlife health surveillance in Europe. A specific website (www.APHAEA.eu) and annual meetings as well as consultation workshops with external partners and stakeholders facilitate participation and information exchange.

Results: In collaboration with an extended network of collaborating partners, APHAEA performed a questionnaire and trans-national surveys using standardized methods on selected pathogen and host binomial including Aujeszky's disease virus in wild boar, *Francisella tularensis* in rodents and *Echinococcus multilocularis* in foxes. This exercise revealed the strengths and weaknesses of this incipient European monitoring scheme.

Conclusions and relevance: One goal of this wildlife health surveillance network is to complement longer established international health surveillance programs for domestic animals and people, and in this way to contribute to early warning of emergence and re-emergence of wildlife-related diseases.

005

Spatial analysis of risks for the transmission of bovine Tuberculosis at the wildlife-domestic interface in Spain

Nathaniel LaHue[1], Joaquin Vicente[2], Christian Gortazar[2], Pelayo Acevedo[2], Beatriz Martinez-Lopez[1], [1]UC Davis, Davis, CA, [2]IREC (UCLM-CSIC-JCLM), Cuidad Real, Spain. Contact: nplahue@ucdavis.edu

Eurasian wild boar (WB) and Red deer (RD) have been proven to be the most important wildlife reservoirs for livestock tuberculosis (TB) in Spain. Some areas of south-central Spain (SCS) have mean TB prevalences ranging from 20% in RD to 70% in WB. These high prevalences in wildlife have been also associated with high incidence of TB in cattle, in part due to transmission at the wildlife-domestic interface. The aim of this study was to identify areas at high risk of wildlife-livestock interaction and characterize the risk factors contributing to the potential transmission of TB at this interface. Detailed longitudinal data from the TB eradication program (i.e., farm location, demographics, number of sampled and positive animals, farm TB status, type of farm, etc.) was collected from 2007 to 2014. Information about the location (polygons) and estimates of the wild population and TB status by hunting estate was also utilized. First we spatially described the abundance and dynamics of wildlife reservoirs nearby livestock premises. We then used cluster analysis to evaluate significant aggregation of TB cases in livestock, wildlife and both. Second, we used generalized estimated equations (GEE) to evaluate the environmental and climatic factors at the wildlife-domestic interface contributing to TB occurrence on livestock premises while accounting for the dependence structure of the data (spatial autocorrelation and repeated measures). Resultant maps and outputs identified high risk areas (and risk factors) where TB is likely to be transmitted at the wildlife-domestic interface. These should advise the implementation of risk-based interventions to better prevent and control TB at the wildlife-domestic interface, a step needed for the successful eradication of TB in cattle in Spain.

006

Diagnosis animals received at the wildlife rehabilitation center of Belo Horizonte, Minas Gerais State, Brazil, from 2003 to 2012.

Sara C. P. F. Silva[1], Ana Cláudia P. Freitas[2], Pedro L. L. Pereira[1], João Paulo A. Haddad[1], Misael E. Oviedo-Pastrana[1], Daniel A. R. Vilela[3], Danielle F. M. Soares[1], [1]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil; [2]Prefeitura de Belo Horizonte, Belo Horizonte, Brazil; [3]Instituto Brasileiro do Meio Ambiente e dos Recursos Naturais Renováveis, Belo Horizonte, Brazil. Contact: sarinhapaulino@hotmail.com

Purpose:
The wildlife rehabilitation center in Belo Horizonte (CETAS - BH) is one of the responsible organs for the receipt of wild animals in Minas Gerais (MG). The knowledge of the animal traffic is an important instrument of wild species conservation, because it allows the improvement of environmental education and the enforcement actions. This study aimed to diagnose the species of wildlife seized or voluntarily surrendered in CETAS-BH and analyze their spatial distribution, from 2003 to 2012.
Methods:
The species were identified and classified according to the taxonomic key and the risk of extinction. Descriptive spatial analysis identified the geographic coordinates of the cities where the animals were found to make maps showing their spatial distribution.
Results:
In the analyzed period, 74.008 live animals were received, being 95,6% birds, 2,6% reptiles, 0,9% mammals and 0,9% categorized as others. There was a wide variety of species (374), most of them birds (79,1%). The most received species were Sicalis flaveola e Saltator similis, 17,1% e 17% respectively. From all of the received species, 17,6% were endangered. Concerning the origin of the received animals, seizure was the most representative of the studied period (89,5%). The voluntary surrender corresponded to 10,5% of the received animals. The received animals were registered in 13.074 records, but only 9.766 (74,7%) had the correct local identification, therefore 54.575/74.008 (73,8%) were georreferenced. The spatial analysis identified the receipt of animals from 199 cities of Minas Gerais. Belo Horizonte and its Metropolitan Region were the locals with the highest concentration of occurrences, 81,7%.
Conclusions:
In this context, this study suggests the improvement and intensification of environmental education and supervision in those specific areas.

007

Frequency of Leptospira spp.-infected synanthropic and wild rodents captured in dairy farms from Southern Chile

Gustavo Monti[1], Miguel Salgado[2], **Jhuliana Luna**[1], Barbara Otto[3], [1]Universidad Austral de Chile, Valdivia, Chile; [2]Universidad Austral de Chile, Valdivia, Chile; [3]Universidad Austral de Chile, Valdivia, Chile.
Contact: jhuly_kath@hotmail.com

Purpose
To describe frequency of rodents infected and exposed to Leptospira spp. and their characteristics, that were captured in selected dairy farms from southern Chile
Methods
A longitudinal study design was used. The target species were, Mus musculus (MM), Rattus rattus (RR) and Rattus norvegicus (RN) as synanthropic species whether Abrothrix olivaceus (AO) and Abrothrix longipilis (AL) as wild species; as being reported as most frequent within dairy premises.
Rodents from 7 farms with known status about the bacteria were captured using conventional techniques and cages were distributed within the premise. Following sedation and prior to humanitarian euthanasia, it was measured body temperature, examined for clinical signs and sex, measured length and weight, age was estimated with this information. Additionally, it was collected kidneys for culture and blood for MAT.
Results
It has been trapped 83 rodents and 58% of them were synanthropic species. There were differences between the diversity of species captured in each farm and also between the seroprevalence within-farms. Overall seroprevalence was 11,1%. The most frequent seropositive species were wild (21%) against synanthropic species (5%). For wild species; AL adults were more prevalent (25 vs 0%), whereas for AO it was the opposite (14 vs 25%). For synanthropic species: RN adults were more prevalent (8 vs 0%), whereas for RR it was the opposite (0 vs 15%). There was one synanthorpic (RR) rodent with isolation.
Wild rodents were trapped mainly in forest, bushes and backyards nearby the buildings of the farm and only in one farm some individuals were trapped nearby human or animal premises. In contrast synanthropic species were trapped within most buildings (milking parlor, hay storage and houses) and few of them were trapped in the forest or outside places.
Conclusions
Results suggest that Leptospira spp. is circulating within rodent population, but lower than expected and groups of rodents have different transmission patterns.
Relevance
Given the zoonotic character of the bacteria and the closeness with human and cattle, Leptospira still is an important pathogen to be considered.
Study was funded by FONDECYT # 1141070 grant.

008

The relative importance of different wildlife species in the reservoir community for human African trypanosomiasis

Harriet Auty[1], Robert Fyumagwa[2], Richard Hoare[3], Kim Picozzi[4], Susan Welburn[4], Sarah Cleaveland[5], [1]SRUC, Inverness, United Kingdom; [2]Tanzania Wildlife Research Institute, Arusha, Tanzania, United Republic of; [3]P O Box CH 77 Chisipite, Harare, Zimbabwe; [4]University of Edinburgh, Edinburgh, United Kingdom; [5]University of Glasgow, Glasgow, United Kingdom. Contact: harriet.auty@sruc.ac.uk

Rhodesian Human African trypanosomiasis (HAT) is an important zoonosis caused by sub-species of Trypanosoma brucei and transmitted by tsetse flies. A range of species form a host community that maintains HAT transmission. Wilderness areas, where tsetse feed on a range of wildlife hosts, have been identified as a priority for understanding HAT transmission. The relative importance of different wildlife species within the HAT reservoir community is not well understood, and depends on both the ability of the species to maintain and transmit infection and the rate of tsetse feeding.

This objective of this study was to assess the relative contribution of different wildlife to the HAT reservoir community in Serengeti National Park, Tanzania. Prevalence in wildlife was assessed through PCR of opportunistically collected blood samples from a range of species. Tsetse feeding patterns were determined by cytochrome B sequencing of tsetse blood meal samples. These field-collected data, along with published data, were used to assess the relative contribution of each species by calculating the change in the community reservoir potential when each species was removed, and the proportion of infected vectors that become infected from each species.

Species with the highest prevalence of T. brucei s.l. included bushbuck (50%), reedbuck (33%), impala (18%), hartebeest (18%) and eland (17%). Despite these species being rarely fed on, removing them from the model reduced the community reservoir potential. Removing elephant or giraffe, frequently fed on but rarely infected, increased it, indicating a role in dampening transmission. Despite infecting >20% of infected vectors, warthog still play a dilution role, because they are fed on so frequently but have low prevalence.

Heterogeneity in host vector contact rates and infectiousness drive the epidemiology of HAT in wilderness areas. This study represents a significant step in understanding HAT ecology, and contributes to our knowledge of how human disease risk might change, spatially or temporally, with different wildlife compositions or different host dynamics, which could offer opportunities to reduce risk.

009

Factors influencing the success of an aerial vaccination program of foxes against rabies in Montenegro

Joerg Henning[1], Paolo Tizzani[2], Carsten Potzsch[3], Srdjan Šašić[4], Paolo Viviani[5], Nikolai Pejovic[6], Ricardo J. Soares Magalhaes[1], Mevlida Hrapović[6], [1]University of Queensland, Gatton, Qld, Australia; [2]Office International des Epizooties, Paris, France; [3]EpiVetGermany, Berlin, Germany; [4]Wildlife consultant, Podgorica, Montenegro; [5]Veterinary consultant, Rome, Italy; [6]Veterinary Administration, Podgorica, Montenegro. Contact: j.henning@uq.edu.au

Sylvatic rabies has been eradicated from most of Central Europe, but cases still occur in the Balkan. Oral rabies vaccination of foxes is an effective method for controlling the disease, but clusters of rabies cases might still remain. The aim of this study was to evaluate the success of aerial vaccination campaigns conducted in autumn 2011 and in spring 2012 in Montenegro. Planes used for bait delivery were equipped with GPS to georeference the location of the bait release. Rabies vaccine was embedded in a feed mixture attractive for foxes, which also contained tetracycline as an indicator for bait ingestion. To monitor the bait uptake and the serological responses, foxes were shot by hunters. From each fox a blood sample was collected for detecting rabies vaccine antibodies. In addition canine teeth were removed to detect presence of tetracycline and to determine the age of the foxes. A one square kilometre vector grid was overlaid over Montenegro and values of vaccination coverage, population density and environmental risk factors were extracted for each grid cell. Logistic regression was used to identify if the serological status of a fox (positive/negative) was influenced by the proposed risk factor (i.e. the individual fox risk factor or the risk factor associated with the corresponding grid cell). Of 175 shot foxes 142 foxes (81.1%) had consumed baits. Of these a total of 79 (55.6 %) tested positive for rabies vaccine antibodies. In the univariate analysis the variables associated with the seropositivity of foxes ($p<0.2$) were bait density, mean NDVI, mean fox density, mean total carnivore density, mean distance from water areas, mean distance from pastures, killing location of foxes and intactness of the carcass. In the final multivariable model only fox density was associated with seropositivity of foxes (OR=1.40, 95% CI 1.07, 1.83). The results indicate that locations of higher fox density might require more intense monitoring and specific actions. Factors that could have influenced the probability of foxes not developing rabies vaccine antibodies might have been conditions influencing vaccine viability after bait delivery, such as the ground temperature during the vaccination campaigns.

010

Epidemiology of canine distemper and canine parvovirus in domestic dogs and wild canids in urban and rural areas of the Araucanía region in Chile.

Gerardo Acosta-Jamett[1], Dominique Surot[2], Manuel Cortés[1], Víctor Marambio[1], Cristóbal Valenzuela[1], Antulemu Vallverdú[1], Michael P. Ward[3], [1]Universidad Austral de Chile, Valdivia, Chile; [2]Universidad de Chile, Santiago, Chile; [3]The University of Sydney, Sydney, Australia. Contact: gerardo.acosta@uach.cl

Purpose: Our goal was to assess whether the seroprevalence of canine distemper virus (CDV) and canine parvovirus (CPV) in domestic dogs is higher in urban versus rural areas of the Araucanía region in Chile; to assess risk factors for exposure; and to determine whether wild canids in this region have been exposed to these pathogens. *Methods:* The study was conducted at three sites consisting of a pair of urban and rural areas where a household cross-sectional questionnaire survey was conducted from 2009 to 2012. Blood samples were obtained from domestic dogs and wild canids. Multivariate logistic regression and spatial analysis were carried out. *Results:* Overall, 1,161 households were interviewed of which 71% were located in urban areas. A total of 501 blood samples from domestic dogs and 40 from wild canids were analysed. The overall CDV and CPV seroprevalences in domestic dogs were 61% (CI90%: 58%-70%) and 47% (CI90%: 40%-49%), and 89% (CI90%: 85%-92%) and 72% (CI90%: 68%-76%), in urban and rural areas, respectively. Three species of wild canids were sampled: the culpeo (*Lycal*opex *culpaeus*), the chilla (*Lycalopex griseus*) and one of the most endangered canid species in the world, Darwin's fox (*Pseudalopex fulvipes*). Overall CDV and CPV seroprevalences in wild canids were 10% and 8%, respectively. All four *P. fulvipes* sampled were seronegative to both pathogens. *Conclusions:* Higher seroprevalence found in domestic dogs in urban areas compared to either rural domestic dogs or wild canids suggests that urban domestic dogs might be a maintenance host for CDV and CPV in this region. *Relevance:* Surveillance and control of these pathogens in urban dog populations is needed to protect wild canids, including endangered species.

011

The effect of surgical and chemical sterilization of male free-roaming dogs in southern Chile on behaviour and serum testosterone levels.

Elena Garde[1], **Raphael Vanderstichel**[2], Guillermo Pérez[1], María J. Forzán[2], James Serpell[3], [1]The Global Alliance for Animals and People, Valdivia, Chile; [2]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada; [3]School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA, Contact: rvanderstich@upei.ca

Background. Population control and management of free-roaming domestic dogs is of interest due to the threat these animals pose to people, other animals and the environment. Current sterilization procedures for male dogs include surgical and chemical methods, however, little is known about the effect of either method on serum testosterone (T) levels and behaviour.
Objective. Investigate changes in T and behaviour following chemical and surgical sterilization male free-roaming dogs (FRDs) in southern Chile.
Methods. A total of 174 dogs were enrolled in a field trial and assigned to one of three groups: surgical sterilization, chemical sterilization or control. Each dog was monitored pre- and post-intervention using video recordings and GPS collars. Blood T levels were determined at four time periods (six months prior to treatment, at the time of treatment, four, and six months post-treatment). Videos were transcribed using a one-zero sampling method.
Results and Conclusions. After treatment, all of the surgically castrated dogs had T concentrations below 1.0 ng/ml. Chemical sterilization had a variable effect on T, but in most dogs there was no long-term effect (only approximately 1/3 of dogs showed a reduction resembling that of surgical castration). Surgically castrated dogs had no reduction of sexual activity or aggression when compared to their pre-sterilization behaviour. Chemically sterilized dogs showed a statistically significant increase in dog-directed aggression, but no change in sexual activity. We found no change in home range size in any group between the pre- and post-intervention measurements, and there was no consistent association between T and behavioural changes in any of the study groups.
Relevance. This study, relevant to communities struggling with the control of FRDs, presents the first detailed behavioural observations following surgical and chemical sterilization in male FRDs.

012

Organochlorines in California sea lions - temporal trends and associations with cancer and infectious disease

Nistara Randhawa[1], Frances Gulland[2], Gina Ylitalo[3], Robert deLong[3], Jonna Mazet[1], [1]University of California, Davis, CA, [2]The Marine Mammal Center, Sausalito, CA, [3]National Oceanic and Atmospheric Administration, Seattle, WA, Contact: nrandhawa@ucdavis.edu

Organochlorine contaminants (OCs) are widespread in the marine environment and adversely impact human and animal health. California sea lions, being long-lived apex predators, which accumulate OCs in their lipid-rich blubber layers, are useful sentinels for exposure to and effects of marine sourced OCs. We sought to evaluate blubber OC levels, specifically polychlorinated biphenyls (PCBs) and dichlorodiphenyltrichloroethane (DDTs), in 310 sea lions sampled between 1992 and 2007: 204 stranded sea lions along the coast of central California; 60 healthy males from Puget Sound, Washington State; and 46 females from San Miguel Island, southern California. Lipid-normalized contaminant concentrations were analyzed using general linear models and logistic regression to ascertain temporal trends; comparison between stranded and healthy sea lions; and association of OC concentrations with sex, age, and presence of cancer or fatal infectious disease.
Adult males had the highest mean lipid-corrected blubber OC concentrations. Contaminant levels in stranded adults decreased across the study period. Cancer was almost eight and six times more likely in animals with higher summed PCBs and DDTs, compared to those with lower levels. Infectious diseases were around seven and five times more likely in animals with higher OCs. Mean OC loads were significantly higher in stranded sea lions than in healthy live captured animals ($P<0.05$).
Environmental OC contamination has important health implications for California sea lions, increasing risk of cancer and infectious disease. While levels of OCs appear to be decreasing in sea lion tissues in recent years, their presence in the environment warrants concern for animal health, as well as humans eating contaminated seafood from the same system.

013

Incidence and risk factors for clinical feline herpesvirus (FHV) infection within a large cohort of cheetahs (*Acinonyx jubatus*) housed in zoos

Carmel Witte[1], Nadine Lamberski[2], Florin Vaida[3], Bruce A. Rideout[1], Laura L. Hungerford[4], [1]San Diego Zoo Institute for Conservation Research, Escondido, CA, [2]San Diego Zoo Safari Park, Escondido, CA, [3]University of California, San Diego, School of Medicine, San Diego, CA, [4]University of Maryland School of Medicine, Baltimore, MD, Contact: cwitte@sandiegozoo.org

Purpose: Feline herpesvirus (FHV) infection is endemic among zoo-housed cheetahs (*Acinonyx jubatus*). While some cheetahs experience a self-limiting, mild rhinotracheitis, others acquire a chronic, severe upper-respiratory disease and debilitating cutaneous and ocular ulcers. The purpose of this study was to evaluate the association between dam and offspring clinical FHV and to identify risk factors for clinical disease in cheetahs. Methods: Medical records from cheetahs born in 6 zoos over a time period spanning up to 20 years (1988-2007) were abstracted to identify cases of FHV and estimate disease incidence through 18 months of age. Cox proportional hazards models, with robust sandwich variance estimators to account for correlation among cheetahs with the same dam, were used to estimate hazards ratios and 95% confidence intervals for the association of dam clinical disease with development of FHV and identify other risk factors. Results: Cumulative incidence was 35% (50/144). No association between dam and offspring clinical FHV was identified (HR:1.2, 95%CI:0.5-2.9, p=0.79). Significant, adjusted predictors of disease included having a primiparous dam (HR:3.0, 95%CI:1.3-7.0, p=0.01), and pre-parturition vaccination of the dam with an attenuated vaccine regime (HR:37.1, 95%CI:8.6-159.5, p<0.001). A killed-virus vaccine was not significantly different from no vaccine (HR:1.7, 95%CI:0.4-6.7, p=0.48). Conclusion: Recognition that clinical FHV in the dam was not a robust predictor of disease development in cubs and identification of other predictive factors have implications for cheetah management. Relevance: This study is the first population-level evaluation of risk factors for FHV in cheetahs and confirms the importance of this disease.

014

Enterobacteriaceae producing extended spectrum β-lactamases recovered from wild birds in Ohio

Dimitria A. Mathys[1], Blake A. Mathys[2], Dixie F. Mollenkopf[1], Avery E. Strait[1], Joshua B. Daniels[3], Thomas E. Wittum[1], [1]The Ohio State Unversity, College of Veterinary Medicine, Columbus, OH, [2]Ohio Dominican University, Columbus, OH, [3]The Ohio State Unversity, College of Veterinary Medicine, Columbus, OH, Contact: mathys.18@osu.edu

Purpose: Extended-spectrum β-lactamases confer bacterial resistance to critically important antimicrobials. Livestock, including dairy cattle are an important reservoir for zoonotic food-borne transmission of extended-spectrum cephalosporin (ESC) resistant bacteria. Our aim is to describe the role of wild birds closely associated with dairy facilities and water systems in the epidemiology of ESC resistance on dairy farms**Methods**: We sampled wild migratory and resident songbirds either immediately outside of or 600 feet away from free stall barns on dairy farms. A cloacal/fecal and external surface swab from each songbird was obtained. Cloacal swabs from wild ducks, either live-caught or hunter-harvested along the central flyway were obtained. All samples were inoculated into BPW, then into MacConkey broth containing cefotaxime, and onto MacConkey agar with cefoxitin, cefepime, or meropenem to identify the bla_{CMY}, $bla_{\text{CTX-M}}$, and carbapenemase phenotypes. Genotypes were confirmed using standard PCR. **Results**: Three hundred and forty-six songbirds were sampled on three Ohio dairies. Eleven (3.2%) and ten (2.9%) songbirds were carrying bla_{CMY} and $bla_{\text{CTX-M}}$, respectively. There was no difference in the prevalence of either gene between migratory and resident birds. However, prevalence of both genotypes was higher among birds sampled immediately outside the dairy barns compared to those sampled 600 feet away. Six hundred and eighty-two wild ducks were sampled. Two hundred and thirty (33.7%) and two (0.29%) produced cefoxitin-resistant and cefepime-resistant isolates, respectively. **Conclusion:** Our results suggest that wild songbirds and ducks can serve as mechanical and/or biological vectors for Enterobacteriaceae with resistance to ESCs. However, the low rates we observed suggest that it is unlikely that wild birds play an important role in the dissemination of bacterial resistance genes. **Relevance:** Wild songbirds and waterfowl may have direct or indirect contact with livestock feces. As a result, these birds may play a limited role in the ecology of ESC bacterial resistance genes, including their transmission between farms.

015

Assessment of wild boar/domestic pig interactions through the use of questionnaires in Corsica.

Ferran Jori[1,2], Anne Relun[1], Bastien Trabucco[1,3], François Charrier[4], Oscar Maestrini[4], Daniel Cornelis[1], Sophie Molia[1], David Chavernac[5], François Casabianca[4], **Eric M. C. ETTER**[1,6], [1]CIRAD, Montpellier, France; [2]Botswana College of Agriculture, Gaborone, Botswana; [3]INRA, Corte, France; [4]INRA, Corte, France; [5]CIRAD, Montpellier, France; [6]University of Pretoria, Onderstepoort, South Africa. Contact: eric.etter@cirad.fr

Purpose: Corsica is a French Mediterranean Island with traditional extensive pig farming where free ranging pigs often interact with an abundant and widespread population of wild boars and feral pigs. Hunters and small-scale farmers in rural areas are often privileged observers of interactions between wild and domestic pigs (IWDP) and open questionnaires are a valid and easy way to obtain qualitative and quantitative information on the nature, duration and seasonality of those interactions.
Methods: A total of 86 persons (25 strict farmers, 20 strict hunters and 41 hunters and farmers) were interviewed in this manner in the 6 main production areas of Corsica to obtain qualitative and quantitative information on IWDP, which are suspected to be very common. A principal component analysis allowed to determine the variables linked with the IWDP. According to these first results, correlation matrices allowed to confirm and quantify these relations.
Results
IWDP were highly seasonal and concentrated in the autumn months (mostly November). Most commonly reported direct interactions were mating (60% of farmers), fighting (56% of farmers) and foraging together (36% of farmers). Some farming and hunting practices such as fencing or hunting beat seemed to have a significant negative influence on the occurrence of IWDP. Men driven interactions through the availability of carcass offal from hunted or slaughtered domestic and wild pigs were commonly reported by 68% of farmers and 90% of hunters. High IWDP induced farmers to castrate their females.
Conclusions: The use of semi-structured interviews proved to be a very efficient and cheap method to gather information about the occurrence of natural and men driven interactions between domestic and wild pigs that can be used to design awareness campaigns or to identify hot spot areas for infectious disease transmission between domestic and wild animals.
Relevance: IWDP remain widespread and represent a serious constraint in the control and eradication of swine infectious diseases such as African Swine Fever present in the neighboring Sardinia since 1978, or Aujeszky disease which remains present in Corsica while eradicated from France mainland.

016

Agent-based modeling of respiratory disease transmission in chimpanzees to quantitatively evaluate the performance of syndromic surveillance

Tiffany Wolf[1], Wenchun A. Wang[2], Dominic A. Travis[1], Elizabeth V. Lonsdorf[3], Thomas Gillespie[4], Iddi Lipende[5], Karen Terio[6], Anne Pusey[7], Beatrice Hahn[8], Ian Gilby[9], Carson Murray[10], Randall Singer[11], [1]University of Minnesota, St. Paul, MN, [2]University of Saskatchewan, Saskatoon, SK, Canada; [3]Franklin and Marshall College, Lancaster, PA, [4]Emory University, Atlanta, GA, [5]Gombe Stream Research Center, Kigoma, Tanzania, United Republic of; [6]University of Illinois Zoo Pathology Program, Chicago, IL, [7]Duke University, Durham, NC, [8]University of Pennsylvania, Philadelphia, PA, [9]Arizona State University, Tempe, AZ, [10]George Washington University, Washington, DC, [11]University of Minnesota, St. Paul, MN, Contact: wolfx305@umn.edu

Purpose: Surveillance of syndromic disease in wildlife is novel. Accordingly, associated methodologies for outbreak detection and assessment of surveillance system performance are highly needed. Since 2004, syndromic surveillance has been employed in Gombe National Park, Tanzania, to collect observational data on several major disease syndromes affecting free-living chimpanzees. Our team utilized 9 years of syndromic data for a qualitative assessment of system performance and development of algorithms for respiratory disease outbreak detection. Here we describe the continuation of that effort with a quantitative assessment of surveillance sensitivity, or the probability that a respiratory disease outbreak is detected by the system in place.
Methods: To do this, empirical data on community demographics, social contacts and frequencies of observation by surveillance were integrated with an agent-based, network disease model to simulate disease transmission and surveillance of respiratory outbreaks previously observed. Out of 2000 Monte Carlo simulations of disease introduction, 1064 outbreaks were produced, with mean duration of 5.1 weeks and mean cumulative incidence of 36 cases in a community of 60 individuals. Two algorithms of weekly outbreak detection were examined, one producing an outbreak signal when 2 or more cases were detected, and the other signaling when case prevalence exceeded 15.6% of those observed.
Results: Surveillance sensitivity was estimated as 66% (95% Confidence Interval: 63.1, 68.8%) and 59.5% (95% Confidence Interval: 56.5%, 62.4%) for weekly count and prevalence thresholds, respectively. In addition to differences between detection algorithms, differences were also observed in surveillance sensitivity between quarters of the year.
Conclusions: Overall, disease model simulations revealed important temporal differences in outbreak characteristics, which are likely impacting surveillance system performance.
Relevance: Through this work, we were able to identify the best algorithm for respiratory outbreak detection and key strategies to improve syndromic surveillance performance in a free-living chimpanzee population.

017

Indigenous and scientific knowledge regarding ticks and tick-borne diseases in wildlife-livestock interface areas in Zimbabwe

Michel de Garine-Wichatitsky[1], Lenin Jomane[2], Musa Tivapasi[3], Melody Belgherbi[4], Thokozani Hove[3], Eric Garine-Wichatitsky[5], Jean Wencelius[5], Davies Pfukenyi[3], Billy Mukamuri[6], Alexandre Caron[1], [1]CIRAD/RP-PCP, Harare, Zimbabwe; [2]Government Veterinary Services, Harare, Zimbabwe; [3]University of Zimbabwe, Harare, Zimbabwe; [4]Université Paris Oue, Nanterre, France; [5]Université Paris Ouest, Nanterre, France; [6]University of Zimbabwe, Harare, Zimbabwe. Contact: degarine@cirad.fr

Purpose:
Tick-borne diseases (TBD), including heartwater, anaplasmosis, babesiosis and theileriosis impact severely on livestock productions in sub-Saharan Africa. The causative pathogens have been isolated from wild ruminants but their roles in the transmission to cattle remain unclear. We report on the perceptions by local farmers and serological evidence of TBD transmission in the Great Limpopo Transfrontier Conservation area in Zimbabwe.
Methods:
The comparative study design included three villages: 1) porous interface (direct livestock/wildlife contacts); 2) fenced interface (only indirect contacts); 3) non-interface negative control (no wildlife). Blood samples were taken from cattle at dip-tanks in 2007-2009 and analysed using I-ELISA for Anaplasma marginale, and IFAT for Babesia bovis, B. bigemina, Ehrlichia ruminantium and Theileria parva. Interviews of individual farmers including “free listing” of livestock disease names were performed at dip-tanks in 2008-2009. A questionnaire survey on TBD awareness and impacts was also performed in the three villages in 2014.
Results:
At all sites, we found very high herd prevalence (>80%) of A. marginale and E. ruminantium, and relatively low levels for the two babesiosis (1-20%). Evidence of T.parva was only found at the porous interface. Except for T. parva, comparisons of TBD prevalence among sites were not significantly different ($\chi 2$, $P>0.05$). TBD ranked high in the lists of livestock diseases established by local farmers (heartwater, babesiosis and anaplasmosis among the 10 most frequently cited). Although most farmers respondents (n = 379; 49.1%) believed that ticks were shared between livestock and wildlife, most of them did not know or doubted that TDB are shared (63.0%).
Conclusions:
The serological study did not allow clear conclusions regarding transmission of TBD between livestock and wildlife, which was also reflected by farmers’ perceptions. Additional studies using molecular techniques and/or longitudinal surveys are needed.
Relevance:
This study illustrates the opportunity for the involvement of indigenous knowledge and perception in co-constructed studies of complex epidemiological studies

018

An alternative approach for managing non-legislated swine diseases in Canada

John Berezowski[1], Chris Byra[2], Egan Brockhoff[3], Dan Hurnik[4], Christian Klopfenstein[5], Harold Kloeze[6], Luc Bergeron[7], George Charbonneau[8], Francois Cardinal[9], Travis Herntier[10], Iqbal Jamal[11], [1]Veterinary Public Health Institution, Vetsuisse Fakultät, University of Bern, Liebefeld, Switzerland; [2]Greenbelt Swine Veterinary Services, Chilliwack, BC, Canada; [3]Prairie Swine Health Services, Red Deer, AB, Canada; [4]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada; [5]Le Centre de développement du porc du Québec, Québec, QC, Canada; [6]Canadian Food Inspection Agency, Owen Sound, ON, Canada; [7]Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec, Québec, QC, Canada; [8]South Western Ontario Veterinary Services, Stratford, ON, Canada; [9]Consultants Avi-Porc, Drummondville, QC, Canada; [10]FD Solutions, Winnipeg, MB, Canada; [11]AQL Management Consulting, Edmonton, AB, Canada. Contact: john.berezowski@gmail.com

Background

Current, accurate information is required by all decision makers, including farmers, veterinarians and disease control agencies, to respond to epidemics and to reduce the impact of endemic diseases. Canada has excellent surveillance infrastructure for creating information to deal with diseases covered by legislation, but there is a gap for non-legislated swine diseases

Objective

To design and pilot an alternative approach for reducing the impact of non-legislated swine diseases in Canada

Innovation

The Canadian Swine Health Intelligence Network (CSHIN) has two parts: 1) a network of veterinarians, disease specialists and producers, who monitor changing swine health issues, discuss and prioritize health issues, develop and communicate strategies for dealing with health issues and coordinate regional responses; and 2) a web-based veterinary practice surveillance network. The CSHIN focused on providing value to veterinarians and farmers. It was governed by the swine industry with input from governments, veterinarians and swine specialists

Summary results

The CSHIN collected and analyzed animal health data, coordinated and communicated disease control efforts during the term of the project and afterwards. The model developed for the CSHIN has been adopted and funded by industry and government in western Canada and is being considered for other regions in the country and for other livestock

Conclusions

The CSHIN produced useful information, assisted veterinarians to respond to national disease risks and was valued by industry, veterinarians, researchers and government agencies

Relevance

Alternative surveillance models that focus on delivering information and disease management coordination to veterinarians and farmers have potential to form the foundation for sustainable non-legislated disease surveillance and control infrastructure

019

Measuring progress on the control of porcine reproductive and respiratory syndrome (PRRS) at a regional level: the N212 area regional control (ARC) program as a working example

Pablo Valdes-Donoso[1,2], Lovell S. Jarvis[2], Dave Wright[1], Andres Perez[1], [1]University of Minnesota, Minneapolis, MN, [2]University of California Davis, Davis, CA, Contact: pvaldesdonoso@ucdavis.edu

Purpose: Due to the highly transmissible nature of porcine reproductive and respiratory syndrome (PRRS), a disease heavily impacting swine production, implementation of regional programs to control the disease is critical. Because PRRS is not reported in the US, numerous voluntary area regional control (ARC) programs have been established. Yet, there is no formal framework to measure ARC progress on disease control.
Methods: Using information from the ARC N212 program collected from June 2012 to July 2014, an outline to assess the evolution of an ARC program is suggested. The composition of site types (sow site=1, nurseries/finishers=2) enrolled was evaluated by a repeated measures analysis of variance test (ANOVARM). Trends of active participation, noted as the decision to either share or not share swine PRRS status in the program, were evaluated using a general linear mixed-effects model (GLMEM). An ANOVARM was used to compare cumulative incidence between sites and years of the study, and a spatio-temporal point process was used to assess distribution of incident cases. A GLMEM was fitted to evaluate factors related to temporal trends of PRRS load.
Results: Farm enrollment increased, but the proportion of site types did not vary over time. A significant ($p<0.001$) rise of shared swine PRRS status was found to vary among counties and sites, with type 2-sites less prone to report. PRRS incidence was significantly ($p<0.001$) lower in type 1-sites and during the second year of the study. Space-time aggregations were identified at spatial windows of <3km and temporal windows of <5wks throughout the study period. PRRS load also significantly ($p<0.001$) decreased, with a negative correlation between proportion of stable sites and degree of shared PRRS status.
Conclusions: An outline to measure ARC progress on PRRS control was established. While the disease has decreased over time, spatio-temporal aggregations remained in the area. However, the increase in tendency to share PRRS status may help in disease control.
Relevance: These results may be incorporated into parameterized models to better understand PRRS dynamics, and in turn establish efficient ways to control disease at a regional level.

020

Modeling effects of waning maternal immunity on influenza A transmission in wean-to-finish pigs

Nitipong Homwong, John Deen, University of Minnesota, Saint Paul, MN, Contact: homwo001@umn.edu

Influenza A virus (IAV) is considered one of the top three respiratory diseases in terms of frequency of appearance in North American swine herd. Waning immunity is the probability of an individual pig *i* not protected by immunity at age *t*. It has been reported that 80% of growing pigs do not have maternal immunity against IAV at an entry of finishing facilities. Therefore, the objectives of this study were to 1) estimate the rate of waning maternal immunity of IAV-H1N1 and 2) perform a simulation of epidemic curves of different proportions of maternal immunity.

15 weaned pigs from 15 immune sows were bled every week in total 14 weeks. Sera were tested for IAV-H1N1 using IDEXX ELISA. The SP ratio data were modeled using binomial regression with clog-log link to estimate the rate of waning maternal immunity. A stochastic-MSIR model using Gillespie's direct method was constructed simulating 500 weaned pigs. Parameters in the stochastic models were and transmission rate (β) and recovery rate (γ), 0.646 and 0.23 day^{1}. Scenarios were combinations of initially-infected pigs (I=1, 5, and 10) and proportions of pigs having maternal immunity at weaning (pM=0.5, 0.7 and 0.9) (9 scenarios). Statistical modelling and simulations were performed in R. Estimated waning maternal immunity rate for IAV H1N1 was 0.013 day^{-1} (95%CI: 0.010, 0.016). The average time to lack of maternal immunity was 77.06 days (95%CI 60.28-93.85). Based on our stochastic-MSIR epidemic simulation, a scenario of initially infected pigs (I=1) and proportion of pigs having maternal immunity (pM=0.9) was found to not occurring an epidemic. In pM=0.5 with I=5 or 10 scenarios, epidemics may be occur. Similarly for a pM=0.7 and I=10 scenario, an epidemic may or may not occur. For any of a pM=0.5 scenario, an epidemic can occur at any point in time during a wean-to-finish period with more than 1 epidemic curve.

In a health management perspective, uniformity of maternal immunity of weaned pigs plays a crucial role in enhancing IAV transmission. Waning maternal immunity has interfered with vaccination to create more subclinical infections. Veterinarians should focus on the herd immunity management to control the transmission of IAV in wean-to-finish pigs.

021

Emergence of influenza A viruses in swine on a small scale, and factors important for influenza infection control

Zvonimir Poljak, Juliana B. Ferreira, Helena Grgic, Robert Friendship, University of Guelph, Guelph, ON, Canada. Contact: zpoljak@uoguelph.ca

Purpose:
Infection control of influenza A viruses in swine (IAV-S) relies on immunization and on reducing contact among pigs. Infection control can be challenging because of existing variability among strains. Emergence of IAV on a small scale is also poorly documented in most species. Thus, the objective of this project was to evaluate dynamics of IAV-S in a production system with multiple sources of animals, and to evaluate effectiveness of control measures. This objective was achieved by a combination of observational study design, virological and serological testing, full genome sequencing of IAV-S, and simulation studies using an in silico model of the nursery herd.

Methods:
The production system selected for this study had a history of outbreaks of a flu-like disease. A 2000-head nursery barn from this system was included; ~80 pigs were included in 2 longitudinal studies at entry to nursery and were sampled weekly. Nasal swabs were tested for IAV presence by isolation in MDCK cells, serological testing was conducted using HI assays, and full genome sequencing was conducted using Illumina MiSeq. The simulation model was a stochastic difference equation SIR model, which also incorporated compartment of maternally immune animals (homologous and heterologous). Population was further stratified into four strata to reflect the outline of the barn. Four infection control strategies were evaluated using 1,000 iterations: 25% or 95% of pigs with homologous immunity, each with 1 or 30 infectious animals at the start of the cohort.

Results:
The results of the baseline strategy consistently reproduced the pattern observed in study 1. Disease control under this scenario was not achievable. Disease control under alternative strategies was achieved with different success.

Conclusions:
Relying on immunization alone was not sufficient to consistently control circulation of IAV-S in a simulation model, unless additional control measures are taken. Validity of recommendations was evaluated against the results obtained in observational study 2.

Relevance:
The results of this study contributes to understanding of the emergence of IAV and to design of control measures for IAV in swine populations.

022

Time series analysis of seasonality of influenza A infection in United States swine herds

Nitipong Homwong[1], Cesar Corzo[2], John Deen[1], [1]University of Minnesota, Saint Paul, MN, [2]PIC, Hendersonville, TN, Contact: homwo001@umn.edu

Influenza A virus (IAV) is considered to be one of the top three respiratory diseases affecting North American swine. The estimated cost of IAV in market pigs ranges between $3.23 and $10.41/head depending on the association with other respiratory pathogens. There are different serologic studies demonstrating the presence of IAV antibodies in North American swine. Presently there is no data on seasonal patterns for IAV in swine; therefore the objective of this study was to re-attempt to evaluate seasonality of IAV in United States swine herd using an active surveillance database.

The database contained the IAV-PCR results of 16,170 nasal swabs that were collected on a monthly basis from 32 farms between 2009 and 2011 as part of an active surveillance program for IAV was conducted in the Midwestern United States. With 7 farms withdrawing from the program, 26 pig farms were analyzed by stationary time series using Fourier spectra and modeled with log-binomial regression. Numbers of periodic signals in Fourier spectra were decomposed as a sum of sinusoids and tested by likelihood ratio test. A final model was selected by AIC. Based on the final model, the effective reproductive number (R_E) was estimated from the force of infection (ψ) and expected pig ages. The ψ was estimated by an exponentiation of the periodic signal means. The confidence intervals for seasonality were estimated by delta method. Statistical modeling was performed in R.

The based-line prevalence of IAV was 20%. The periodic amplitude was 10% of the prevalence. The IAV prevalence was reached to a trough in December and to a pinnacle in June. Seasonal IAV in growing pigs was strong and it was periodic with low amplitude composed of one periodic signal. In the US, the ψ for seasonal IAV was 0.20 (95%CI 0.16, 0.23) $month^{-1}$. The R_E for seasonal IAV in pigs was 1.4 (95%CI: 1.2-1.6), which was rather similar to that in humans of 1.3 (95% CI 1.2-1.4).

The seasonality of influenza A virus in US swine herd was elucidated with strong-periodic, low amplitude and low seasonal transmission rate. The times series analysis with Fourier spectra is helpful to identify seasonality of influenza A virus transmissions in US pig population with an active surveillance data.

023

Impact of husbandry practices on Swine Influenza A Virus dynamics within a farrow-to-finish pig farm: a stochastic metapopulation modeling approach

Charlie Cador[1], Nicolas Rose[1], Fabrice Mahé[2], Mathieu Andraud[1], [1]Anses, Ploufragan, France; [2]Mathematics Research Institute, Rennes, France. Contact: charlie.cador@anses.fr

Purpose:
Swine Influenza has been shown to persist in an enzootic form in farrow-to-finish farms. Field studies showed that Swine Influenza A Virus (SIV) can infect weaned piglets at a fixed-age with recurrent occurrence in successive batches. However, the transmission process between batches is still not well understood. The aim of this study was to analyze the conditions for persistence and recurrence of SIV in farrow-to-finish pig herds reared with different batch-rearing systems.

Methods:
A stochastic metapopulation model has been developed to represent the within-herd dynamics of SIV. To analyze the role of the herd structure on SIV spread and persistence, two subpopulations were considered, corresponding to breeding sows and growing pigs, and interacting during lactating stage. This population dynamics was coupled with a SIV epidemiological model based on an extended SIRS model, accounting for the partial passive immunity protection in neonatal piglets. Airborne transmission was featured by a between-batch transmission rate related to the current prevalence of shedding pigs. Initiated by the introduction of one infected gilt in the service room, the minimal conditions for virus spread and persistence between batches were evaluated.

Results:
Between-batch transmission was found necessary to reproduce recurrent infections at fixed age in growing pigs' population as observed in field conditions. The herd structure, driven by the batch-rearing system, was shown as a pivotal factor favoring SIV spread. Short-time intervals between successive batches were found more at risk for SIV persistence at the herd-level.

Conclusions:
The model showed that a lack of internal biosecurity between batches in the nursery sector could partially explain the spread and maintenance of the virus from batch to batch. Limiting air-flows between the different herd-premises could prevent from recurrent infections at fixed-age.

Relevance:
Our model allowed analyzing the impact of batch-rearing systems on within-herd SIV persistence in the context of single strain circulation. This model should be extended to consider multiple strains as observed in field conditions.

024

Simulation of outbreak mechanisms of respiratory disease in finishing pigs caused by Actinobacillus pleuropneumoniae

Arjan Stegeman, Don Klinkenberg, Tijs Tobias, Annemarie Bouma, Leo van Leengoed, Utrecht University, Utrecht, Netherlands. Contact: j.a.stegeman@uu.nl

Purpose
Infection with A. pleuropneumoniae may result in pigs with respiratory disease as well as in non-diseased carrier pigs. However, what actually happens during an acute outbreak episode of pleuropneumonia is unclear. The aim of this study is to test two potential underlying mechanisms for such outbreaks, by identifying conditions for occurrence of such outbreaks under these mechanisms, using mathematical modelling. The first mechanism assumes that a common risk factor causes all cases directly by changing the host pathogen interaction in already colonised pigs (trigger mechanism). The second mechanism assumes that a transmission chain is started by the first case, inducing disease in the infected contact pigs (transmission mechanism).
Method
First, a characteristic outbreak of pleuropneumonia was defined by conducting a review of the literature; defining an outbreak at 12 weeks of age and affecting 50% of animals and lasting 4 days. Next, two mathematical models were developed to simulate outbreaks of A. pleuropneumoniae, one for the trigger mechanism and one for the transmission mechanism.
Results
Mathematical models showed that a characteristic outbreak could be caused under both mechanisms. However, the transmission mechanism needed a 50 times higher transmission rate for diseased pigs than described in literature for colonised pigs. Furthermore, the trigger mechanism showed that outbreaks in young pigs must be rare, as these are not yet colonised, which is supported by literature.
Conclusion
We conclude that outbreaks of A. pleuropneumoniae on endemic farms are most likely explained by exposure of already infected pigs to a trigger.
Relevance
This implies that control of disease caused by A. pleuropneumoniae has to focus on reducing transmission by colonised pigs and by preventing the occurrence of a trigger.

025

Modelling Hepatitis E virus transmission in pigs: when an animal pathogen increases the risk of human exposure to a zoonotic agent

Nicolas Rose[1], Mathieu Andraud[1], Morgane Salines[1], Elodie Barnaud[2], Florent Eono[1], Patricia Renson[3], Olivier Bourry[3], Nicole Pavio[2], [1]Anses, PLOUFRAGAN, France; [2]UMR 1161 Virology ANSES/INRA/ENVA, Maisons-Alfort, France; [3]Anses, PLOUFRAGAN, France. Contact: nicolas.rose@anses.fr

Purpose:
Hepatitis E virus (HEV) can cause enterically-transmitted hepatitis in humans. The zoonotic nature of Hepatitis E infections has been established in industrialized areas and domestic pigs are considered as the main reservoir. The dynamics of transmission in pig herds needs therefore to be understood to reduce the prevalence of shedding pigs at slaughter and prevent contaminated pig products from entering the food chain.

Methods:
Transmission experiments are powerful tools to address quantification of pathogen transmission and identify factors related to transmission characteristics. In this study, the features of HEV transmission were analyzed through replicates of transmission trials involving HEV-inoculated and contact SPF pigs (3I x 3C). The impact of Porcine Reproductive and Respiratory Syndrome virus (PRRSv), a highly prevalent immunosuppressive pathogen in swine populations, was addressed by comparing transmission parameter estimates in PRRSv / HEV co-infected pigs (3 replicates, 18 pigs) with HEV-only inoculated pigs (6 replicates, 36 pigs).

Results:
In HEV-only inoculated pigs, a large inter-individual variability was observed in response to infection with an average latent period lasting 6.9 days [5.8; 7.9] and an average infectious period of 9.7 days [8.2; 11.2]. In PRRSV co-infected pigs, HEV shedding was delayed by a factor of 1.9 and dramatically extended (48.6 days [27.9; 84.6]). Direct transmission rate was estimated 4.7 times higher in case of co-infection than in HEV-only infected pigs (0.70 and 0.15 per day respectively) and susceptibility to environmental contamination was also enhanced. The majority of co-infected animals (14/18) had HEV in the liver at the autopsy stage (49-52 DPI) (none during single HEV infection).

Conclusions:
During single HEV infection, the virus was eliminated rapidly, in contrast to the co-infection with a swine immunosuppressive pathogen such as PRRSV that leads to chronic HEV infection and may dramatically increase the risk of human exposure to HEV.

Relevance:
A global approach, including control of animal-health related pathogens, is needed for public health prevention strategies.

026

Online monitoring of pig motion for a cost-reduced early detection of infection

Marta Martínez Avilés, Eduardo Fernández-Carrión, Guillermo Angulo Aragón, José Mª López García-Baones, **José Manuel Sánchez-Vizcaíno**, Universidad Complutense de Madrid, Madrid, Spain. Contact: jmvizcaino@ucm.es

Purpose: The cost implied in the regular testing of herds located in areas at high risk of exposure, i.e., sentinel sampling, with the regular obtention of negative results have discouraged active surveillance efforts in Europe. There is a need to develop new methods for surveillance that will help maintain a high sensitivity of the system at a reduced cost.
Methods: Individual changes in motion of attenuated African swine fever virus-experimentally-infected pigs were measured through an eartag-embedded accelerometer. A specific software to process Internet Protocol video camera images measured the number of herd movements per hotspot during an established time period. Motion measurements were compared with the detection of infection measured by the observation of fever, clinical signs and PCR blood-test results. We assessed the economic performance of the online system with a traditional sentinel testing scheme.
Results: The results of a first experiment showed that when the animal is infected, the motion frequency changes significantly. The herd movement changes were detected before infection was confirmed by PCR or the observation of clinical signs, but at the same time as fever. Additional results will be presented that verify and validate these first results with the use of improved accelerometers that sample at higher frequency. The initial investment would be recovered from the second year onwards.
Conclusions: We present alternative ways of detecting infection in pigs early with the use of biosensors that can reduce the current cost of sentinel sampling for early detection of infection.
Relevance: This is the first time that sensors are used in pigs and the first time that sensors are used for the purpose of surveillance. In addition, costs of sentinel sampling could be reduced with the use of technology to obtain data from animals remotely.

027

Implications of subclinical infection with PED virus for preventive measures

Satoshi Sekiguchi[1], Naoki Koike[1], Kazuhiro Hata[2], Nobuyuki Marumoto[2], Shinji Watanabe[3], Yosuke Sasaki[1], Junzo Norimine[1], Masuo Sueyoshi[1], [1]University of Miyazaki, Miyazaki, Japan; [2]Miyakonojo Livestock Hygiene Service Center, Miyazaki, Japan; [3]National Institute of Infectious Diseases, Tokyo, Japan. Contact: sekiguchi@cc.miyazaki-u.ac.jp

Purpose: PED (Porcine Epidemic Diarrhea) has become widely spread in many Asian countries from 2012 and caused economic loss due to high morbidity and mortality in neonatal piglets. In Japan, PED cases were usually detected with syndromic surveillance using clinical signs and symptoms. In contrast, active serosurvey enables to detect both infected animals showing clinical signs and subclinically infected animals from infected farms. Additionally, systematic survey at a slaughterhouse is very useful in terms of collecting samples, biosecurity and animal welfare. Thus, the aim of this study was to perform active serosurvey to detect infected animals and analyze the implications of subclinical infection of PED virus.
Methods: Blood samples of growing-finishing pig were collected at the slaughterhouse in the Kyushu area from March 2014 to July 2014. 43 samples were collected from 9 case farms and 184 samples were from 34 other farms. The neutralization test (NT) was used to detect PED infection using Vero cells (KY-5) and PED virus strain (NK94). The relationship between risk factors and infected farms were analyzed using Spearman's rank correlation coefficient and Pearson’s chi-squared test. All the statistics in the present study were performed using statistic software R (version 3.0.1).
Results: Seropositive animals were detected in all case farms (100%), and in 5 out of 34 non-case farms (14.7%). The results indicated that an active serosurvey system was more sensitive, and more useful to detect infected farms, than a syndromic surveillance system in a slaughterhouse. A significant positive correlation was observed between slaughterhouse trucks and infected farms. This study also provided evidence for the relationship between slaughterhouse trucks and infected farms.
Conclusions: These data supported the possibility that the spread of PED virus from an infected farm to another uninfected farm could be caused by slaughterhouse trucks shipping infected animals.
Relevance: The data obtained from this study was fed back to livestock hygiene service centers and meat inspection centers to utilize for effective preventive measures against PED outbreak.

028

Farmers' knowledge and sensitive behavior towards African swine fever in Madagascar

Tiana N. Randrianantoandro, Hiroichi Kono, Satoko Kubota, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan. Contact: omjao@hotmail.fr

African swine fever (ASF) was first detected in 1998 in Madagascar. Currently, there is no fully effective treatment or vaccine available for it. To control the spread of ASF, Malagasy Government prohibits selling of ASF-infected pigs. Unfortunately, ASF remains an endemic disease and there is a need for its eradication in order to ensure smallholder farmers' income. In the present study, we examined whether Malagasy pig farmers sell ASF-infected pigs instead of reporting suspected cases of ASF to the veterinary office or local authority. The objective was to estimate the proportion of pig farmers who sell infected pigs without reporting the infection, according to their knowledge level about ASF. Farmers' knowledge about ASF was assessed by using five questions and each correct answer is equivalent to one point. Then, the indirect questioning technique, called Item count technique (ICT), usually used to estimate the proportion of people engaged in sensitive behavior such as drug use or risky sexual behavior, was used. Besides, some respondents were asked directly whether they sell ASF-infected pigs. A total of 201 farmers in Antananarivo Avaradrano District were interviewed face to face. As results, 59% of pig farmers have low level of knowledge about ASF. The proportion of farmers who sell ASF-infected pigs ranges from 75 to 86%. For high knowledge and low knowledge group, the estimate from ICT was higher, but not statistically significant than that from direct questioning (DQ). The insignificant difference between the estimates from ICT and that from DQ indicates that farmers do not consider selling ASF- infected pigs as sensitive behavior, in other words, farmers admit without hesitation that they sell ASF-infected pigs; despite the law that prohibits it. However, the proportion of farmers selling ASF-infected pigs from ICT method is lower ($p=0.094$) from farmers with high level of knowledge than that from farmers with low level of knowledge. This result indicates that knowledge about ASF has positive impact on farmers' behavior. Therefore, there is a need of improving farmers' knowledge for successful control of ASF. Yet, knowledge improvement should be complemented with law enforcement.

029

Within herd transmission and reproductive number of African swine fever in pig herds in southwestern Nigeria

Emmanuel J. Awosanya[1], Zhao Lu[2], Babasola Olugasa[1], Yrjo Grohn[2], [1]University of Ibadan, Ibadan, Nigeria; [2]Cornell University, Ithaca, NY, Contact: emmafisayo@yahoo.com

Purpose: African swine fever (ASF) is a trans-boundary fatal viral disease of both domestic and wild pigs. The disease has become enzootic in southwestern Nigeria and poses threat to farmers' livelihood. The aim of this study was to investigate within herd transmission of ASF and estimate its basic reproductive number in pig herds within southwestern Nigeria.
Methods: We constructed a modified deterministic Susceptible-Exposed-Infectious-and-Recovered pig (SEIR) model, using parameters derived from a cross sectional survey and the literature. Basic (R0) and effective (Re) reproductive numbers were computed using next generation matrix approach. We performed global uncertainty analysis (UA) and sensitivity analysis (SA) using Simlab(R) version 2.2 Software. The ordinary differential equations of the SEIR model were solved using Runge-Katta (rk4) algorithm.
Results: The within herd ASF transmission model gave a predicted prevalence of 7%, which was close to the survey data prevalence of 11% (95% CI 9 - 14). R0 and Re values were estimated as 6 and 1 respectively. There was a seasonal effect on ASF prevalence; however, there was no significant difference in the average value of R0 between the dry (7) and wet (6) seasons. Model parameters such as rate of infectiousness before onset of clinical signs (σ), transmission rate (β) and rate of infectiousness with clinical signs (δ) were positively correlated with ASF prevalence, while culling rate (μ) and recovery rate (r) were negatively correlated with ASF prevalence.
Conclusions: ASF transmission in southwestern Nigeria appears to mimic more of a subacute than chronic course and that clinically healthy recovered pigs contribute little to the prevalence of ASF. Aside from transmission rate, rate of infectiousness before onset of clinical signs is critical to ASF prevalence.
Relevance: Culling of infected pigs and elimination of chronic carriers should reduce ASF prevalence in southwestern Nigeria

030

Quantification of transmission of African swine fever virus by chronically infected animals and through indirect environmental contact

Phaedra Eblé[1], Eefke Weesendorp[2], Bernie Moonen[1], Sjaak Quak[1], Thomas Hagenaars[2], Willie Loeffen[1], [1]Central Veterinary Institute of Wageningen UR (CVI), Lelystad, Netherlands; [2]Central Veterinary Institute of Wageningen UR (CVI), Lelystad, Netherlands. Contact: phaedra.eble@wur.nl

The introductions in Poland and the Baltic states in 2014 resulted in new interest for ASF in Europe. In Europe, transmission of ASFV will mainly be caused by direct contact between infected and non-infected pigs or through indirect contact with contaminated materials. Animals that survive an ASF infection and become carriers can shed virus for a long period of time and might play an important role in the epidemiology of ASF. For the implementation of efficient control measures, knowledge about transmission of ASFV is needed. The objective of the current study was to quantify ASFV transmission by carriers and indirect virus transmission.

Four groups of five pigs were inoculated with ASFV strain Netherlands ’86. Six pigs survived the acute phase of the infection and became carriers. Four weeks after inoculation, the carriers were moved to six new pens. In each pen, one contact animal (C1) was added for 13 days. Then the contact pigs were removed and 6 new contact pigs (C2) were added for 13 days. Blood and OPF samples were regularly taken and tested for the presence of virus by qPCR. Transmission rate parameters were estimated for each contact period and for the overall period. The four pens in which the inoculated pigs had originally been housed, were repopulated with two sentinel piglets each, for a period of 14 days. Blood, OPF and environmental samples were regularly taken and tested for the presence of virus by qPCR.

None of the C1 contacts and two of the C2 contacts became infected with ASFV. Transmission rates were estimated as 0 (0-0.038, 95% CI) and 0.036 (0.012-0.099) day-1 for each of the 13 day periods, or 0.015 (0.002-0.038) day-1 overall, which is much lower than in the acute phase of infection. With an estimated infectious period of approximately 40 days, the partial reproduction ratio R for the carrier phase would be 0.6 (if a carrier has contact with one naïve pig on average at any time). None of the sentinel pigs became infected.

For ASF infections in wild boar, transmission by carriers and environmental contamination, although limited, may still be a crucial factor for transmission of ASFV because apparently healthy carriers can transmit virus over long distances and cause new spatial foci of infections.

031

Case-control study to detect protective factors on pig farms with low *Salmonella* prevalence

Richard P. Smith[1], Victor Andres[2], Tanya Cheney[1], Rob Davies[2], [1]APHA - Weybridge, Addlestone, United Kingdom; [2]APHA - Weybridge, Addlestone, United Kingdom. Contact: richard.p.smith@apha.gsi.gov.uk

The prevalence of *Salmonella* and *Salmonella* Typhimurium (ST) in UK pigs is among the highest in Europe, highlighting the risk to public health and the need to investigate on-farm controls. However, identification of such controls has been difficult with the wide range of risk factors detected previously indicating potentially complex interactions.

A detailed investigation was conducted to detect the protective factors associated with pig farms maintaining a low (<10%) *Salmonella* prevalence. Routine surveillance of slaughtered pigs identified farms that

maintained a low seroprevalence over 4 separate years. Each farm was enrolled as a case to compare against 2 matched controls from the same geographical region and production type, selected randomly from the pig industry.

Each of the 57 participating farms was visited once to collect farm and animal group data. Pooled and individual floor faeces samples were collected from a representative selection of pens and buildings, with ~200 collected on average. Two risk factor analyses were completed: a farm-level logistic regression comparing case against control farms; and a sample-level mixed-effects model examining risk factors for *Salmonella*

presence, with sample type/ age group included as an *a priori*. The case farms had a significantly lower *Salmonella* prevalence (pooled 4.3%;

individual 0.1%) than the controls (19.4%; 6.7%). The serovars detected also differed, with those of public health importance (ST, monophasic ST) detected from two case farms (*S*. 4,12:i:-) and 23 control farms. ST was the most prevalent serovar on control farms.

The two models identified significant associations, including variables related to feed (type, addition of acid products/ antibiotics), factors related to effectiveness of cleaning and disinfection (feeder/drinker types, flooring and ventilation, frequency of scraping), biosecurity (use of bootdips, feed lorries entering farm), batch production and scouring problems. The results are discussed in relation to similar international studies and to

providing the case farms as exemplars, to improve farmer education, and to help guide future cost-benefit studies.

032

A cohort study investigating the factors that led to emergence of porcine epidemic diarrhea virus through feed during early phase of 2014 Canadian outbreak

Terri OSullivan, **Zvonimir Poljak**, Robert Friendship, Cate Dewey, University of Guelph, Guelph, ON, Canada. Contact: zpoljak@uoguelph.ca

Purpose: Porcine epidemic diarrhea virus (PEDV) emerged in Canada in Jan 2014. Potentially contaminated feed (PCF) was implicated as the source of the virus resulting in a voluntary feed recall by the involved feed company. Challenge studies demonstrated that porcine epidemic diarrhea (PED) could be reproduced in pigs inoculated with the PEDV-positive ingredient spray dried porcine plasma (SDPP). However, inoculation of pigs with the complete feed did not reproduce PED. This created skepticism about the role of the PCF in the introduction of PEDV into Canada. The objectives of this study were to determine the probability of a PED outbreak for producers that received the PCF and to evaluate if there was a difference in the likelihood of a PED outbreak between producers that received PCF (exposed) and producers that did not receive PCF (non-exposed).
Methods: Data used were the feed company's (FC's) database containing all sales of feed to customers containing SDPP as an ingredient and sales of feed that contained a SDPP alternative of non-animal origin; the FC's database containing data obtained as a result of recall; and diagnostic data confirming cases of PEDV from the population. Data were analyzed using Kaplan-Meier (KM) survival curves, log-rank test, and Cox's proportional hazard model.
Results: KM estimates of survival curves indicated that exposed customers had a higher likelihood of experiencing PED (Log Rank P=0.012). The number of feed deliveries did not affect the probability of a PED outbreak (P=0.11). When considering all factors in the Cox's proportional hazard model the hazard of experiencing PED in the exposed customers was 36.6 times higher than in the non-exposed (P=0.02). A dose-response was clearly demonstrated meaning that as more contaminated SDPP in a complete feed was utilized by a customer the hazard of a PED outbreak increased (P<0.001). A time–varying covariate approach was also applied to the data and yielded comparable results.
Conclusions: Exposure to PEDV contaminated SDPP increased the hazard of a customer PED outbreak during the incursion of PEDV into Canada.
Relevance: This study supports that contaminated feed was involved in the incursion of PEDV into Canada.

033

Evaluation of porcine reproductive and respiratory syndrome control methods using agent-based modelling

Andreia G. Arruda[1], Zvonimir Poljak[1], Amy Greer[1], Robert Friendship[1], Jane Carpenter[2], [1]University of Guelph, Guelph, ON, Canada; [2]Ontario Swine Health Advisory Board, Stratford, ON, Canada. Contact: arrudaa@uoguelph.ca

Purpose:
Porcine reproductive and respiratory syndrome (PRRS) is an endemic swine disease in North America, and even though elimination is possible, virus re-introduction and recurrent outbreaks are common. Gilt acclimation is a procedure commonly used and can be achieved using vaccination (modified live vaccine), or immunization based on exposure to the PRRS virus resident to the herd.
The objective of this project was to investigate which of the control measures mentioned above would best minimize the likelihood of an outbreak in a typical Ontario farrow-to-wean swine site compared to a baseline of no control measures implemented. Secondary objectives were to investigate how the duration of infection and number of infectious animals introduced would affect the overall size of such an outbreak.
Methods:
A stochastic, agent-based model was developed in order to capture different animal characteristics such as disease state and location in the farm for female pigs and produced offspring, as well as heterogeneity of contacts. The model was created using Anylogic®7.1.2, and the outcome of interest was the maximum number of infected animals resulting from re-introduction of the virus into herds of different compositions. One hundred model iterations were generated for each scenario and sensitivity analysis was conducted for the parameters mentioned in the secondary objectives.
Results:
Model results demonstrate that both PRRS control strategies produced a higher frequency of simulations resulting in no outbreak after the introduction of the virus, compared to the baseline scenario. A decrease in the duration of infectiousness resulted in an overall reduction in the maximum number of pigs infected. Finally, the frequency of no outbreaks occurring decreased as the number of infected animals introduced in the herd increased.
Conclusions:
In conclusion, our findings suggest that homologous virus exposure would decrease the likelihood of occurrence of large PRRS outbreaks the most; and attempts to reduce the introduction of infected animals are valuable in decreasing the likelihood of major outbreaks.
Relevance:
Modelling can be a useful approach to investigate disease control methods.

034

How would classical swine fever spread in Great Britain? Data fit and predictions

Thibaud Porphyre[1], Kokouvi Gamado[2], Carla Correa-Gomes[3], Aaron Reeves[3], Harriet K. Auty[3], George J. Gunn[3], Glenn Marion[2], Mark E. J. Woolhouse[1], [1]University of Edinburgh, Edinburgh, United Kingdom; [2]Biomathematics & Statistics Scotland, Edinburgh, United Kingdom; [3]Scotland's Rural College, Inverness, United Kingdom. Contact: t.porphyre@ed.ac.uk

Purpose: Classical swine fever (CSF) is a notifiable, highly contagious viral disease of swine which results in severe sanitary and economic consequences in affected countries. In order to improve preparedness for disease incursion, it is critical to have some understanding of how disease would spread should it be introduced into a CSF-free country.
Methods: In Great Britain (GB), the last epidemic of CSF occurred in 2000 and involved 16 farms located in East Anglia, a major pig-rearing area in GB. Based on these data, we used a Bayesian framework to infer both the extent of the local disease spread and the rate at which infected farms are detected during active surveillance. These inferences informed a spatially explicit, premises-based model used to explore the risk of widespread dissemination of CSF, through both local spread and animal movements, in the British pig industry.
Results: We found that CSF infection would locally spread from primary sites but the probability of spread beyond 5 kilometers was limited. The performance of active surveillance in GB in 2000 was found to be similar to that reported in other member states, with an average of 31.7 days required to detect an infected premises (95% Cr.I. 11.2 - 72.7). When projecting inference over GB, the overall probability of epidemic take-off remained consistently low throughout the year despite increasing the duration of the silent period, varying from 0.028 to 0.078. When 8 weeks of silent spread was considered, the probability of epidemic take-off was strongly spatially dependent, with few geographic areas showing a take-off probability greater than 0.15. Widespread outbreaks (>50 farms) were nevertheless possible, regardless incursions occurring in low or high risk areas.
Conclusions: These results suggest that, although rare, widespread epidemics of CSF would be possible in GB at any time of the year and regardless of the duration of the silent period.
Relevance: Knowledge of spatial and temporal variation in the probability of epidemic take-off are key components for surveillance planning and resources allocation, and this work provides a valuable stepping stone in guiding policy on CSF surveillance and control in GB.

035

Estimating transmission of cattle brucellosis in West Africa

Anna Dean[1], Esther Schelling[2], Bassirou Bonfoh[3], Abalo Kulo[4], Gad Boukaya[5], Guillaume Fournié[6], [1]World Health Organization, Geneva, Switzerland; [2]Swiss Tropical and Public Health Institute, Basel, Switzerland; [3]Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Abidjan, Côte D'Ivoire; [4]Ecole Supérieure d'Agronomie, Université de Lomé, Togo; [5]Ministère de l'Agriculture, de l'Elevage et de la Pêche, Lomé, Togo; [6]Royal Veterinary College, London, United Kingdom. Contact: deanan@who.int

Purpose:
Brucellosis is a neglected zoonosis with a major impact globally on livestock production, livelihoods, food security and human health. The transmissibility of brucellosis has never been estimated in livestock in sub-Saharan Africa. A serological survey conducted in 25 villages in northern Togo in 2011 provided the first population-representative seroprevalence data for livestock in West Africa (cattle: 9.2%, 95%CI:4.3-18.6% ; small ruminants: 0%). The purpose of this study is to estimate the transmissibility of cattle brucellosis in northern Togo in order to inform the design of appropriate disease control strategies.

Methods:
A deterministic age-structured mathematical model was developed to simulate the spread of brucellosis between cattle. Cattle were considered to move from the susceptible to infected state. Females were considered infectious after their first parturition and remained infectious until death. Transmission was estimated by fitting the model to the results of the serological survey in Togo. Given the level of uncertainty surrounding characteristics of the cattle population dynamics, the model was fitted for different scenarios.

Results:
For all scenarios, the basic reproductive number (R0) was below 1.3. This low value suggests that a moderate level of implementation of control interventions, such as vaccination, would be sufficient to eliminate brucellosis within cattle.

Conclusions:
In an agropastoral setting in West Africa, cattle brucellosis is endemic. The model will now be expanded to a metapopulation structure to account for clustering within villages. This will allow the modelling of transmission within and between villages, which will better inform the design of strategies for brucellosis control in cattle. Detailed results will be presented at the ISVEE conference.

Relevance:
In addition to the direct relevance of these results to livestock health in sub-Saharan Africa, there are important public health and economic implications. Reducing the burden of neglected zoonoses such as brucellosis can improve the health of communities and provide a route out of poverty.

036

Using Bayesian ensemble methods for epidemiological projections: a case study of a Foot and Mouth Disease outbreak

Lindsay M. Beck-Johnson[1], Tom Lindström[2], Michael J. Tildesley[3], Colleen T. Webb[1], [1]Colorado State University, Fort Collins, CO, [2]Linköping University, Linköping, Sweden; [3]University of Nottingham, Sutton Bonington, United Kingdom. Contact: L.Beck-Johnson@colostate.edu

Purpose

Epidemiological modeling is a rapidly developing field that has produced extremely useful models for understanding disease spread. As a result, many countries utilize information from models to inform preparedness and response plans for the event of a disease outbreak. However, since there are multiple models for any given disease, it can be difficult to select a single model on which to base a preparedness plan. Ensemble modeling is a technique in which the predictions or outputs of multiple models can be combined into a single, interpretable prediction. This method is used frequently in weather forecasting and climate change predictions but has seldom been used in epidemiology. A recently developed Bayesian ensemble modeling method for epidemiological situations has shown this technique could be used for outbreak preparedness and/or response. Foot and Mouth Disease (FMD) outbreaks carry significant economic consequences for the infected country so preparedness and response planning for FMD outbreaks is a high priority for FMD-free countries. Consequently, policymakers often use FMD models as a key part of making these plans.

Methods

Working with six FMD simulation models, using data from the 2001 UK FMD outbreak, we explored whether ensemble methods could improve model predictions early in an outbreak situation. The models were parameterized using data two weeks after the beginning of the control program and simulated forward in time.

Results

We found that the ensemble analysis performed well and, importantly, the ensemble distribution did better at capturing the observed data than the individual models alone.

Conclusions

These preliminary results suggest that the ensemble method could be a powerful tool for epidemiological applications. Ensemble models have the potential to reduce the confusion caused by multiple individual models that predict different things about the same outbreak, and that have the potential to present a single, interpretable, prediction based on the varying predictions.

Relevance

Ensemble analysis has the potential to improve our ability to make epidemiological predictions, which would be an enormous benefit for animal and public health globally.

037

Preserving privacy and maintaining meaningful epidemiological predictions

Marleen Werkman[1], Michael J. Tildesley[2], Ellen Brooks-Pollock[3], Matt J. Keeling[4], [1]Central Veterinary Institute, Lelystad, Netherlands; [2]University of Nottingham, Sutton Bonington, United Kingdom; [3]University of Bristol, Bristol, United Kingdom; [4]University of Warwick, Coventry, United Kingdom.
Contact: marleen.werkman@wur.nl

Purpose
Mathematical models form an integral part of epidemic preparedness planning and real-time forecasting. State-of-the-art models involve detailed data, these data are often not available or, if available, these are often not published in the public domain due to privacy concerns. However, sharing data will hugely benefit developing, optimising and training disease simulation models. To avoid privacy problems, policy makers may consider sharing aggregated data which could feed into a metapopulation model. However heterogeneity of farms may not be captured with these data. Therefore, we investigate the feasibility of using a metapopulation model to predict epidemic dynamics and identify the most optimal control strategy in a highly heterogeneous landscape.
Methods
In this study we use the individual farm-based model developed and utilised during the UK 2001 FMD outbreak (Keeling et al., 2001) and have developed an analogous metapopulation model. The 2010 UK agricultural census was provided by the DEFRA and contained farm location, size and species composition. As farm composition and size have been shown to play a major role, we adapt our standard metapopulation model to incorporate heterogeneity of farm size. For both metapopulation models, farms are divided into grids based on their Easting and Northing coordinates of the farmhouse. To investigate the effects of the resolution of the grids on model outcomes, we vary the grid resolution from 200 metres to 10 km.
Results
The adapted approach performed substantially better than the standard metapopulation model in predicting the final epidemic size, identifying risk areas, determining the likelihood of epidemic take-off and identifying the most optimal control strategy; however, in terms of spatial spread the standard and adapted metapopulation model gave comparable results.
Conclusions & relevance
In cases where a metapopulation model is preferred over an individual farm-based model, using the adapted metapopulation model with grids of 4 km provide the most optimal balance between privacy and detailed model outputs.

038

Estimating genetic differences in hosts' susceptibility and infectivity for infectious diseases.

Floor Biemans, Piter Bijma, Mart de Jong, Wageningen UR, Wageningen, Netherlands. Contact: floor.biemans@wur.nl

Transmission of an infectious disease is affected by susceptibility and infectivity of the host individuals involved. Susceptibility, the relative probability that an individual gets infected when subjected to infectious individuals, is a trait affecting the disease status of the individual itself; it is measured as a direct genetic effect. Infectivity, the ability to infect other individuals, affects the diseases status of others; it is therefore measured as an indirect genetic effect (IGE). An IGE is a heritable effect of an individual affecting the phenotype of another individual. Current genetic studies on infectious diseases focus is on susceptibility only. Differences in infectivity, however, can have major effects on disease transmission. Identifying highly infective individuals can contribute to preventing disease outbreaks. Here we investigate methods to estimate host genetic effects on susceptibility and infectivity based on binary data on the disease status of individuals.

A simulation study of disease transmission over time was performed. Genetic heterogeneity was modeled in a diploid host population with two unlinked loci, one for susceptibility and one for infectivity. Endemic disease transmission was simulated with a SIS-model. At several points in time the population state was determined by counting the number of susceptible and infectious individuals of each genotype. These data were analyzed using a generalized linear model with a complementary log-log link function and relative gene effects for susceptibility and infectivity were estimated back. Genetic differences were estimated correctly for susceptibility and for infectivity when observation intervals were short and/or genetic differences were large. This model can be used in livestock genetic improvement by selecting animals with favorable genetic effects for susceptibility and infectivity.

The model has been applied to field data on Digital Dermatitis (DD), an infectious claw disease in dairy cattle. By combining transmission data on DD with high density single-nucleotide polymorphism data of the individual cows, genomic regions affecting susceptibility and infectivity can be identified.

039

Modelling the transmission of Peste des Petits Ruminants in Ethiopia and optimal vaccination coverage

Guillaume Fournié[1], Agnès Waret-Szkuta[2], Laike M. Yigezu[3], Dirk U. Pfeiffer[1], François Roger[4], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]National Veterinary School of Toulouse, Toulouse, France; [3]National Veterinary Institute, Debre-Zeit, Ethiopia; [4]CIRAD-EMVT, Montpellier, France. Contact: gfournie@rvc.ac.uk

Purpose:
Peste des petits ruminants (PPR) is a highly contagious viral disease of small ruminants with a substantial economic impact on production systems. Eradicating PPR within the next 15 years is a joint objective of the FAO and the OIE. Although a vaccine is available, the transmission of the virus (PPRV) has never been quantified in any setting. This knowledge is essential in order to design and implement effective vaccination campaigns. Our aim was to estimate the level of PPRV transmission using data from a national serological survey conducted in Ethiopia (1999-2000) prior to the first vaccination campaign, including over 10,000 sheep and goats.

Methods:
We developed a stochastic spatially-explicit metapopulation model. The total Ethiopian small ruminant population was divided into 5100 populations, each defined by an area of 15km by 15km. PPRV spread was simulated within and between these populations. Sedentary and pastoralist populations, which prevailed in the highlands and lowlands, respectively, were further differentiated. Age and species (sheep or goats) were accounted for. The model was fitted to the serological survey results using Approximate Bayesian Computation.

Results:
Results showed that PPRV transmission was higher within pastoralist than sedentary populations. Moreover, transmission was high between pastoralist populations, suggesting a high level of mixing. While PPRV could not become endemic within a single pastoralist population, it could remain endemic within the pastoralist system as a whole. Although viral spill-over from pastoralist to sedentary populations was frequent, the level of PPRV transmission among sedentary herds was low and unlikely to allow endemicity. The high turn-over in small ruminant populations meant that vaccinated animals are rapidly replaced by susceptible animals. Therefore, vaccination campaigns should be conducted annually in order to maintain the vaccination coverage above the herd immunity threshold.

Conclusions:
Vaccination campaigns should be conducted annually and target pastoralist populations.

Relevance:
This study provides the first ever estimation of PPRV transmission to guide vaccination policy.

040

Modelling CCHF (Crimean Congo Haemorrhagic Fever) spread to identify major factors and test control strategies

Thierry Hoch[1], Eric Breton[1], Mathilde Josse[1], Ahmet Deniz[2], Esin Guven[3], Zati Vatansever[4], [1]INRA, Nantes, France; [2]Etlik Central Veterinary Control & Research Institute, Ankara, Turkey; [3]Ataturk University, Erzurum, Turkey; [4]Kafkas University, Kars, Turkey. Contact: thierry.hoch@oniris-nantes.fr

Purpose:
Crimean Congo Haemorrhagic Fever (CCHF) is an emerging zoonotic disease. The causative agent is a virus (CCHFV), mainly transmitted by ticks of the species *Hyalomma marginatum* in Eastern Europe and Turkey. The Turkish outbreak in 2002 is associated with a previous decline in agricultural activities that led to an increase in suitable habitats for ticks, which resulted in great exposure of humans and domestic animals to ticks. In order to test scenarios for the control of pathogen spread, we have developed a mechanistic dynamic model.
Methods:
Design of a model to apply to a vector-borne disease is based on coupling a population dynamics model, here applied to the tick *H. marginatum,* with a model of CCHFV transmission. Our model takes into account the major processes involved in tick population and pathogen dynamics. It also considers the influence of abiotic (temperature and vapour saturation deficit) and biotic factors (host, *i.e.* hare and cattle, densities) on disease spread. The basic reproduction number (R_0) for CCHFV infection was calculated thanks to the estimation of the next-generation matrix. Using R_0 as output variable, the model was thereafter used to test control strategies and especially the effect of various acaricide treatments, differing by their starting date, their duration and the number of applications.
Results:
Comparison with data showed that the model is able to reproduce realistically the observed dynamics for tick population and pathogen spread. Simulation results indicate that acaricide treatments could have valuable effects provided that the acaricide is applied early (day 100 in the year), regularly (at least 3 times a year) and over several years. A global sensitivity analysis for abiotic and biotic factors showed that, even though temperature has a strong impact on model outputs, host densities also play a role.
Conclusions:
In addition to acaricide treatment, one way to decrease pathogen spread could be to act on wildlife hosts, especially hares, for instance by isolating wildlife populations from domestic animals.
Relevance:
The kind of model we have developed provides insight into the ability of different strategies to control pathogen spread.

041

Quantifying the impact and transmission of zoonotic pathogens. Development of novel methods using Lassa fever data

Giovanni Lo Iacono[1], Andrew Cunningham[2], James L. N. Wood[1], [1]University of Cambridge, Cambridge, United Kingdom; [2]Institute of Zoology, Zoological Society of London., London, United Kingdom. Contact: gianni.loiacono@phe.gov.uk

Purpose:
Zoonotic diseases are serious threats to humans. An important example is Lassa fever (LF), a rodent-borne, viral haemorrhagic disease common in West Africa; a significant proportion of the disease is due to human-to-human transmission. There are two fundamental, but under-studied, stages in zoonotic transmission: `spillover', i.e. transmission of pathogens from animals to humans, and `stuttering transmission', when limited human-to-human transmission occurs. We focused on questions such as:
i)If we have quantified pathogen dynamics in the reservoir, with some knowledge of the mechanism of contact, can we estimate the likelihood of spillover events?
ii)Can we tease apart how much the disease is transmitted by animals and how much by humans?
Methods:
We developed a unified theoretical framework for spillover and stuttering transmission based on a generalization of Poisson processes which include memory of past human infections (for stuttering chain) and depletion of susceptibles.
Results:
The methodology was validated with an agent based model and applied to LF, for which we have data of hospitalized patients at Kenema Hospital in Sierra Leone. The approach provides a recipe to calculate:
i)The distribution of spillover events, from knowledge of the mean and variance in key factors (e.g. the human population size, pathogen prevalence in, and human exposure to, the reservoir).
ii)The relative contributions of human-to-human vs animal transmission
For the case of LF, the approach indicates what missing information is required to allow full reproducibility of the empirical data (seasonality in the rodent abundance and infection prevalence, reporting bias)
Conclusions:
We formulated, tested and applied a methodology for spillover and stuttering chain, providing a practical tool to estimate the risk of spillover and to disentangle the contribution of animal-to-human from human-to-human transmission. Current knowledge gaps in the dynamics of LF were identified.
Relevance:
Methodologies like this are of crucial importance for the scientific and public health communities to assess risks associated with spillover and to plan preventive interventions and responses.

042

How critical is vaccination of cattle for control of Brucella melitensis on endemic mixed-ruminant farms? - a dynamic transmission model parameterized with field data

Wendy Beauvais, Imadidden Musallam, Javier Guitian, Royal Veterinary College, Hatfield, United Kingdom. Contact: wbeauvais@rvc.ac.uk

Purpose

Brucella melitensis is one of the causative agents of brucellosis, a neglected zoonosis, and is traditionally understood to infect mainly small ruminants. However, seroprevalences of up to 20% have been found in cattle in mixed-ruminant settings where *B. melitensis* is the predominant agent. The inter-species transmissibility of *B. melitensis* has not been extensively studied. Although licensed vaccines are available to protect against *B. melitensis* in small ruminants and *Brucella abortus* in cattle, none have been licensed for use against *B. melitensis* in cattle.

The objective of this study was to investigate how critical vaccination of cattle is, for the control of *B. melitensis* in mixed-species settings.

Methods

A dynamic transmission compartmental model was built in R (R Core Team, 2014) to represent a herd, and transmission parameters (cow to cow, sheep to sheep, cow to sheep and sheep to cow) were estimated based on data from 187 closed sheep and /or cattle herds, a subset of 504 randomly-selected farms in Jordan where *Brucella melitensis* predominates (Musallam et al, 2015). It was assumed that endemic stability had been reached in these herds and that *Brucella melitensis* was the predominant species present.

Results

According to the model, assuming a vaccine efficacy of 80% and homogenous mixing of cattle and sheep, a mass vaccination program of sheep and cattle followed by annual vaccination of replacements on a typical Jordanian farm would reduce the % of infected animals to less than 0.5% in 5-7 years. With vaccination of sheep only, the time taken increased by up to 18 months for farms with less than 20% cattle, and to over 20 years for farms with more than 80% cattle. Sensitivity analysis suggested the conclusions were robust.

Conclusion

Given the model assumptions, vaccination of cattle may be critical for the control of *B. melitensis* in settings with mixed-species farms if: 1) >20% of animals on the farm are cattle and 2) sheep and cattle mix freely.

Relevance

Although modeling studies have important limitations, the results underline the need for efficacy data for cattle vaccines against *B. melitensis* and for thorough, sustained vaccination policies, in order to control *B. melitensis.*

043

Mathematical Modeling of Influenza A Virus Dynamics within Swine Farms and the Effects of Vaccination

Meggan E. Craft, Jennifer Reynolds, Lauren White, Montserrat Torremorell, University of Minnesota, St Paul, MN, Contact: craft@umn.edu

Purpose:
Influenza A virus infections are widespread in swine herds across the world. Influenza negatively affects swine health and production, and represents a significant threat to public health due to the risk of zoonotic infections. Swine herds can act as reservoirs for potentially pandemic influenza strains.
Methods:
In this study, we develop mathematical models based on experimental data, representing typical breeding and wean-to-finish swine farms. These models are used to explore and describe the dynamics of influenza infection at the farm level, which are at present not well understood. In addition, we use the models to assess the effectiveness of vaccination strategies currently employed by swine producers, testing both homologous and heterologous vaccines.
Results:
An important finding is that following an influenza outbreak in a breeding herd, our model predicts a persistently high level of infectious piglets. Sensitivity analysis indicates that this finding is robust to changes in both transmission rates and farm size. Vaccination does not eliminate influenza throughout the breeding farm population. In the wean-to-finish herd, influenza infection may persist in the population only if recovered individuals become susceptible to infection again. A homologous vaccine administered to the entire wean-to-finish population after the loss of maternal antibodies eliminates influenza, but a vaccine that only induces partial protection (heterologous vaccine) has little effect on influenza infection levels.
Conclusions:
Therefore, influenza is challenging to eliminate on swine farms with current management practices.
Relevance:
Our results have important implications for the control of influenza in swine herds, which is crucial in order to reduce both losses for swine producers and the risk to public health.

044

Estimation of H1N1 swine influenza A virus transmission parameters in pigs with different initial immune statuses

Charlie Cador[1], Séverine Hervé[2], Mathieu Andraud[1], Stéphane Gorin[2], Frédéric Paboeuf[3], Nicolas Barbier[2], Stéphane Quéguiner[2], Céline Deblanc[2], Gaëlle Simon[2], Nicolas Rose[1], [1]Anses, Ploufragan, France; [2]Anses, Ploufragan, France; [3]Anses, Ploufragan, France. Contact: charlie.cador@anses.fr

Purpose:
Recurrent influenza infections in swine operations are characterized by swine influenza A virus (SIV) infections occurring at a fixed age, when a significant part of the piglets still have SIV maternally derived antibodies (MDA). Those passive antibodies are known to provide partial protection towards infection but their impact on transmission characteristics is not well known.

Methods:
A transmission experiment involving 72 specific pathogen free (SPF) piglets with or without MDA was carried out to evaluate the impact of MDA on SIV transmission. In each group (MDA+/MDA-), the transmission trial included 2 seeder-pigs with 4 direct- and 5 indirect-contact piglets (3 replicates per group). Individual viral shedding was monitored using RT-PCR carried out on nasal swabs taken on a daily basis. Blood samples were taken to monitor MDA waning (ELISA test). A non-linear mixed effect model was used to estimate the parameters governing antibody kinetics in MDA+ piglet. Long term projections of individual profiles were derived to estimate the duration of passive immunity. The impact of contact structure and initial serological statuses of the piglets on shedding duration was investigated using survival analysis. The assessment of protection conferred by MDA with regard to SIV transmission was based on a SIR framework accounting for differential transmission rates depending on piglets' initial serological statuses and contact structure. Transmission rates were estimated using maximum likelihood method.

Results:
The model of antibody kinetics in MDA+ piglets showed a persistence of passive immunity higher than 7 weeks. Contact structure and MDA status did not significantly influence the duration of shedding. Based on estimates of the transmission rate in MDA+ piglets and shedding duration a reproduction number significantly higher than 1 was obtained.

Conclusions:
MDA protection does not prevent early-life SIV transmission which may participate to SIV persistence in swine herds.

Relevance:
Understanding SIV transmission according to the immune status and the contact structure between weaned piglets is pivotal to identify control points for recurrent SIV infection prevention.

045

The modelled spread of severe footrot in Norway if no elimination program had been implemented

Gry M. Grøneng[1], Synnøve Vatn[2], Anja Bråthen Kristoffersen[1], Ola Nafstad[2], **Petter Hopp**[1], [1]Norwegian Veterinary Institute, Oslo, Norway; [2]Animalia - Norwegian Meat and Poultry Research Centre, Oslo, Norway. Contact: petter.hopp@vetinst.no

Severe footrot was detected in Norway in 2008, and in 2009, an elimination program was initiated by the sheep industry in collaboration with the Government.
Footrot is a contagious disease where the main infective agent is *Dichelobacter nodosus* (*D. nodosus*). *D. nodosus* can be divided into a virulent and benign type by laboratory methods. These methods were firstly implemented in Norway in 2009. The term severe footrot have therefore been used in Norway to include both flocks diagnosed with virulent *D. nodosus* and flocks where the two types have not been distinguished, but the flock is expected to be infected with virulent footrot because of severe clinical signs. The development and spread of *D. nodosus* is dependent on climatic factors and density of sheep. Footrot have spread to two counties and a total of 121 flocks have been diagnosed with severe footrot in Norway since 2008. During 2014, only two flocks were diagnosed with severe footrot, and both are under sanitation to eliminate the disease from the flock.
The aim of this study was to estimate the spread of severe footrot in the Norwegian sheep population, if no elimination program was implemented.
A stochastic compartment model was developed where the spread of footrot within each of the 19 counties in Norway were modeled separately. The within county spread was based on the observed spread of footrot in Norway, and the climate and density of sheep flocks within each of the counties. In addition, a between county spread was included in the model by three possible routes; movement of sheep and cattle between counties and use of shared mountain pastures, where sheep from several counties could mix.
By 2013, the disease was estimated to have spread to six counties and 16% of the sheep flocks would have been infected in Norway. By 2035, 16 counties were estimated to have the disease and 64% of the sheep flocks were infected with severe footrot. Such an extensive spread of footrot would result in welfare problems and large economic losses for the sheep industry in Norway. This shows the importance of the early implementation of an elimination program for footrot in Norway.
The model can be used for other diseases and in other areas when the relevant input factors are used.

046

Towards understanding the interactions between farm management, antimicrobial usage, pig health and MRSA contaminations using an agent-based model

Egil A. J. Fischer[1], Thomas J. Hagenaars[2], Natasha I. Valeeva[3], Tim Verwaart[4], [1]Universiteit Utrecht, Utrecht, Netherlands; [2]Wageningen UR, Lelystad, Netherlands; [3]Wageningen UR, Wageningen, Netherlands; [4]Wageningen UR, Den Haag, Netherlands. Contact: e.a.j.fischer@uu.nl

Purpose:
The prevalence of antimicrobial resistance (AMR) in livestock has increased in the last decades threatening human and animal health. Reduced antimicrobial use is needed to decrease the prevalence of AMR. Antimicrobial (AM) usage is complex due to interaction of biological processes and farmers' decisions. These decisions are driven by economic considerations, but also by motivations, cognitions and social networks. Little is known about integrated influence of such aspects on adaptation of the farmer's management behavior of AM usage, affecting AMR.
Here, this complex adaptive system (CAS) of MRSA and antimicrobial usage in fattening pig farming was investigated for a better insight. Additionally we evaluated:
•The effect of policy interventions to reduce AM usage levels
•The resilience of reduced AM usage levels against the outbreaks of livestock diseases
Methods:
An agent-based model was developed in which farmers take decisions based on their observations of health problems on the farm and their beliefs and motivations. The motivations are influenced by information on public health effects of AM usage, pressure from peers and incentives arising from policies. Each farm consisted of a number of pens with pigs, which were healthy, diseased by an endemic or emerging disease, and are either contaminated with MRSA or not. Pigs were treated with AMs based on their health status and the decision of the farmer.
Results:
The agent-based model was calibrated to data on MRSA prevalence, AM usage and endemic disease prevalence.
Different hypotheses are investigated with this tool. The importance of the effects of outbreaks of infectious diseases and pressure from peers and policy are shown.
Conclusions:
We constructed an agent-based model capturing the essentials of MRSA epidemiology and the use of AMs in the Netherlands. We can show how policy interventions can potentially change the usage of AMs and its robustness of reduced AM usage levels against outbreaks of infectious diseases. We have created a useful tool for advising policy.
Relevance:
AMR is an increasing problem in veterinary public health, but the effect of policies to reduce AM usage are not always evident.

047

Genetic-epidemiological modelling of gastrointestinal parasitism in sheep.

Mathilde Saccareau[1], Carole R. Moreno[1], Gabriel Ciappesoni[2], Bruno Goffinet[1], Robert Faivre[3], François Brun[4], Stephen Bishop[5], [1]French National Institute for Agricultural Research (INRA), Castanet-Tolosan Cedex, France; [2]Instituto National de Investigacion Agropecuaria (INIA), Canelones, Uruguay; [3]French National Institute for Agricultural Research (INRA), Castanet-Tolosan Cedex, France; [4]Association de coordination technique agricole (ACTA), Castanet-Tolosan Cedex, France; [5]The Roslin Institute and Royal (Dick) School of Veterinary Studies, Edinburgh, United Kingdom. Contact: mathilde.saccareau@toulouse.inra.fr

Purpose:
The gastrointestinal parasite is the most pervasive challenge in grazing small ruminants, leading to considerable production loss. Its control with the use of anthelmintic treatments is no longer sustainable due to the development of parasitic resistance to these anthelmintic. So we need to find complementary strategies: host nutrition, grazing management, targeted selective treatments, breeding for resistance to parasitism.

Methods:
A previous deterministic, dynamic model (Laurenson et al. 2011) was developed for *T. Circumcincta* in growing lambs (from weaning, during less than four months). From this model, we developed a model to account for these different strategies, and predict their consequences on productivity and level of parasitism in lambs and ewes. We added the possibility of housing the reproducing ewes and a supplementary module offered the opportunity of managing the different age classes of the flock, mating the females with selected sires and having new females entering the flock each year: therefore, we have a sustainable flock simulated over several years which allows the investigation of alternatives to the use of anthelmintic as a long-term option (several years). Further to this, we proposed a set of parameters for modeling infection by one of the most frequent parasite *H. Contortus* (instead of *T. Circumcincta* previously modeled).

Results/Conclusions:
To validate our new model, we used a unique Uruguayan data set in which the flock was naturally infected by *H. Contortus* (several years of parasitism infection measures are available during growing and parturition periods of female sheep). In parallel, we had conducted a sensitivity analysis in order to identify the parameters resulting in the bigger output traits variations, therefore we are estimating them.

Relevance:
This improved model is helpful to investigate many situations without having to resort to many experiments which require infestations costly in terms of animals, and could be adapted to other species (like goats). An important issue of our model is to advise farmers on the optimal proportion of genetically resistant animals to introduce in the flock in order to control parasitism infection.

048

Bio-economic simulation modeling: How to control Paratuberculosis on dairy farms?

Carsten Kirkeby[1], Kaare Græsbøll[1], Søren S. Nielsen[2], Lasse E. Christiansen[3], Nils Toft[1], Erik Rattenborg[4], Tariq Halasa[1], [1]National Veterinary Institute, Frederiksberg C, Denmark; [2]Department of Large Animal Sciences, University of Copenhagen, Frederiksberg C, Denmark; [3]DTU Compute, Kgs. Lyngby, Denmark; [4]SEGES, Aarhus, Denmark. Contact: ckirkeby@gmail.com

Purpose:
Paratuberculosis is a widespread chronic infection causing decreased milk production, decreased farming profitability and reduced animal welfare in cattle. Infection is caused by Mycobacterium avium ssp. paratuberculosis (MAP). Current data suggest that the prevalence in dairy herds without control is much lower than suggested by previous models. Furthermore, data from Danish dairy herds suggest that test-and-culling may be an efficient strategy. Therefore the aim of this study was to build a simulation model that was calibrated to the current situation in order to evaluate strategies for disease control. Such a framework should also include important mechanisms such as an age-dependent sensitivity of ELISA tests and mechanistic modelling of MAP shed in manure on the farm.
Methods:
We developed a new bio-economic simulation model including these mechanisms and calibrated the model to a dataset of herds without any control actions against spread of MAP. Likewise, we modelled control actions mechanistically, adjusted to the effects estimated from real data. We also allowed build-up of MAP shed in manure in five farm compartments to mechanistically simulate disease transmission.
Results:
We found that the three most commonly implemented controls actions only had a weak impact on the prevalence on their own, although they were actually able to reduce the prevalence. The most efficient control action for reducing the prevalence was a test-and-cull strategy, which was able to eradicate MAP from the herd based on simulations in a herd with an average initial prevalence.
Conclusions:
This control action was also found as the most profitable strategy, because it did not cause extra expenses and resulted in high marginal revenue.
Relevance:
The results are valuable for farmers who want to optimize their control strategy for MAP and maximize profit.

049

Meta-analysis of the transmission of Mycobacterium avium subsp. paratuberculosis in experimentally infected sheep to inform mathematical modelling

Nelly Marquetoux[1], Rebecca Mitchell[2], Peter Wilson[1], Mark Stevenson[3], Anne Ridler[1], Cord Heuer[1], [1]Massey University, Palmerston North, New Zealand; [2]Cornell University, Ithaca, NY, [3]The University of Melbourne, Melbourne, Australia. Contact: nelly.marquetoux@gmail.com

Purpose:
A state-transition model was developed to evaluate the economic effects of interventions for on-farm control of paratuberculosis in sheep. The model required pathways and parameters describing within-host progression of Mycobacterium avium subsp. paratuberculosis (MAP). Because the pathophysiology of the progression of ovine paratuberculosis is complex and still poorly understood the objective of this work was to systematically evaluate findings from published infection experiments to identify suitable model parameter estimates for our model

Methods:
Twenty experimental and natural infection studies with MAP were subjected to systematic review and meta-analysis. The state-transition model was parameterized by the results of the meta-analysis.

Results:
We identified two possible pathways following infection with MAP in sheep and the rates at which sheep entered and stayed in latent and shedding states. Age at infection and MAP inoculum doses had significant effects on the fate of infected sheep ($p<0.05$) with higher MAP doses decreasing the time to onset of fecal shedding while higher age at infection decreased the odds of progressing to clinical paratuberculosis.

Conclusions:
Meta-analysis of natural or experimental infection studies of sheep with paratuberculosis can improve the current understanding of the pathophysiology of MAP infection and contribute towards building biologically relevant mathematical models for this disease.

Relevance:
This study provided a robust framework for mathematical modeling of ovine paratuberculosis.

050

Spread and control of Johne's disease in an enzootic cattle region: a multi-scale model to evaluate complex strategies combining biosecurity and trade regulations

Pauline Ezanno[1], Gaël Beaunée[1], Elisabeta Vergu[2], [1]INRA, Oniris, Nantes, France; [2]INRA, Jouy-en-Josas, France. Contact: pauline.ezanno@oniris-nantes.fr

Purpose
Johne's disease is a worldwide enzootic disease of cattle inducing a large economic impact for dairy producers due to production losses and early culling of cows. This chronic disease is characterized by a long incubation period, and diagnostic tests used in routine are poorly sensitive. Hence, observing the disease spread in the field is hardly possible, whereas there is a need for evaluating control strategies. Our objective is to better understand the spread of Mycobacterium avium subsp. paratuberculosis (Map) at a regional scale using a modelling approach, and to compare through simulations control strategies combining biosecurity measures (early culling, hygiene improvement, calf management) and tests at purchase.
Methods
We developed the first multi-scale mechanistic model of Map spread between dairy cattle herds, accounting for stochastic within-herd dynamics (demography and infection), indirect local transmission, and incorporating data on animal trade and on herd-specific size and management. We modeled all of the 12,857 dairy herds located in Brittany (France) having more than 15 dairy females. Data from 2005 to 2013 was used to calibrate each herd size and demographic rates, and to define trade events. We assumed initially 30% of the herds to be infected.
Results
Each measure tested alone or in combination with tests at purchase succeeded in slowing down the regional Map spread, but not in decreasing the proportion of infected herds. More than two measures had to be combined to effectively reduce the herd-level prevalence. However, in that latter case, only a moderate level of implementation of each measure was required, indicating the operational potential of such combined strategies.
Conclusions
Our study highlights the challenge of controlling Map spread in an endemically infected region because of poor test characteristics and frequent trade movements.
Relevance
Our model is a flexible and efficient tool to help collective animal health managers in defining relevant control strategies at a regional scale, accounting for regional specificities in terms of contact network and farms' characteristics.

051

A coupled epidemiological-economic model for measuring the burden of poultry disease on the rural poor in Madagascar

Cassidy Rist[1], Calistus N. Ngonghala[2], Andres Garchitorena[2], Thomas R. Gillespie[1], Matthew H. Bonds[2], [1]Emory University and Rollins School of Public Health, Atlanta, GA, [2]Harvard Medical School, Boston, MA, Contact: rist.dvm@gmail.com

Background: Over 70% of the rural poor rely on livestock as a fundamental economic and nutritional resource; however, a high burden of infectious disease limits their productivity. Economic models used to measure the burden of livestock diseases traditionally account for income lost, but do not reflect long-term interactions between poverty and disease or incorporate the impact of these interactions on important components of human capital, i.e. human health and nutrition.
Objective: We estimate the economic burden of poultry disease on rural households in Madagascar based on the premise that human capital and poultry productivity are complementary inputs for generating household income, and that human capital is also supported by poultry production.
Methods: The dynamic relationship between poultry disease and economic outcomes is modeled by coupling well-established susceptible-infectious-susceptible (SIS) disease-type models with a simple economic growth model. We parameterize this coupled model with household-level survey data collected from the Ifanadiana District in Madagascar, where over 72% of households own poultry.
Results: Our model captures income lost from decreased poultry production, and incorporates feedbacks between poultry productivity and human capital in disease burden estimates. The majority of model simulations predicted a 10-25% loss of monthly income for poultry-owning households under current disease conditions.
Conclusion: Diseases that limit poultry productivity threaten the subsistence of poor households in ways that are directly comparable to the effects of human disease; not only through direct loss of income, but also by undermining immediate and long term human capital accumulation.
Relevance: Results provide new insight on how feedbacks between human and livestock productivity exacerbate the economic impact of livestock disease on the rural poor. Elucidating these feedback mechanisms is particularly important for the global health and development communities who seek to include livestock disease prevention strategies as components of broader human health and development initiatives.

052

Success Factors for Strengthening a One Health Strategy in Nine Asian Countries

Roger Morris, Peter Jolly, Joanna McKenzie, Massey University, Palmerston North, New Zealand.
Contact: roger.morris@morvet.co.nz

An integrated approach has been developed to deal with emerging diseases in nine Asian countries - Afghanistan, Bangladesh, Bhutan, China, India, Mongolia, Nepal, Pakistan, Sri Lanka.
Joint Masters training has been provided for over 100 medical doctors, veterinarians and wildlife specialists in epidemiological investigation and delivery of disease control and health risk management, through a blended program of distance and in person teaching. Graduates also undertake a Fellowship jointly managed by national epidemiology centres and Massey University, in which Fellows work with a wider group of participants to investigate and evaluate control policies for zoonotic diseases of importance in their country..
This process is facilitated by a suite of software tools called HandiPlan (Human and Animal Disease Investigation Planning Toolbox). HandiPlan is built inside IRIS (Incident Response Information System), a database system capable of dealing with different types of disease risks and events. The five HandiPlan components can be applied to any country in the world. HandiMap builds a national risk landscape from satellite-derived environmental indicators and national data based on epidemiological evidence and national knowledge of a particular disease. HandiSpread, a spatial simulation model, evaluates alternative surveillance and/or control strategies. If the disease is considered a threat, HandiResponse determines an optimum surveillance portfolio. If the disease is currently occurring in the country, HandiManager evaluates alternative control policies. Both tools use HandiSpread to model the effects of different strategies. HandiEcon carries out economic analysis to select optimum strategies for the disease. Example analyses have been developed for brucellosis and avian influenza, which will be used to illustrate applications of the toolbox.
One Health Hubs have been developed in each country, supported by a software system, Hubnet, which facilitates collaboration and information sharing amongst these One Health networks, within and between countries.

053

The quantitative benefit of a “One Health” approach to study complex health issues: a systematic review

Laura C. Falzon[1], Isabel Lechner[1], Ilias Chantziaras[2], Lucie Collineau[3], Aurelie Courcoul[4], Maria-Eleni Filippitzi[2], Riikka Laukkanen-Ninios[5], Carole Peroz[6], Jorge P. Ferreira[3], Merel Postma[2], Pia G. Prestmo[7], Clare J. Phythian[8], Eleonora Sarno[9], Gerty Vanantwerpen[10], Timothee Vergne[11], Douglas Grindlay[12], Marnie L. Brennan[12], [1]Veterinary Public Health Institute, Liebefeld, Switzerland; [2]Veterinary Epidemiology Unit, Ghent University, Belgium; [3]SAFOSO AG, Liebefeld, Switzerland; [4]University Paris Est, Maisons-Alfort Cedex, France; [5]Department of Food Hygiene and Environmental Health, Helsinki, Finland; [6]LUNAM Universit, ONIRIS, Nantes, France; [7]School of Veterinary Sciences, Bristol, United Kingdom; [8]NMBU, Sandnes, Norway; [9]Institute for Food Safety and Hygiene, Zurich, Switzerland; [10]Department of Veterinary Public Health and Food Safety, Ghent University, Belgium; [11]Veterinary Epidemiology, Economics and Public Health group, London, United Kingdom; [12]Centre for Evidence-Based Veterinary Medicine, University of Nottingham, United Kingdom. Contact: laura.falzon@vetsuisse.unibe.ch

Purpose: One Health (OH) promotes a holistic approach to address complex issues. As the OH movement has been gaining momentum, it is important to quantify the added benefit of this approach to enable its adoption by multiple stakeholders. The aim of this study, a joint project between residentsof the European College of Veterinary Public Health, was to systematically identify and summarize primary research describing a quantitative benefit of an OH approach.Methods: Peer-review publications and grey literature reporting original research on the quantitative benefit of an OH approach, and published after 1910, were considered. The American Veterinary MedicalAssociation (2008) definition of OH was used, while “quantitative benefit” specified both monetary and non-monetary benefits. An electronic search using a comprehensive set of search terms was performed in 4 electronic databases. Additional publications were identified via expert consultation, information solicited from an eco-health list-serve, and manual searches of references. Independent reviewers screened abstracts for relevance followed by full-publication review. Relevant data will be extracted from included publications.Results: A total of 49937 publications were identified (49885 and 52 publications through electronic and additional search, respectively). After removing duplicates, 42094 abstracts were screened for eligibility; of these, 553 were deemed relevant for full-publication review. So far, 195 publications have been screened, of which 82 were included. These studies describe a collaboration between animal and human (n=47), human and environment (n=28), animal and environment (n=3), or all three sectors (n=3). Both monetary (e.g. reduced costs) and non-monetary benefits (e.g. reduced number of cases) are described.Conclusions: Further analysis will provide us with information on the health issues addressed, and how many studies focused on monetary vs. non-monetary benefits. Relevance: Results obtained so far illustrate that a number of studies were able to quantify the added value of this approach, providing a tangible measure by which to promote the OH approach among decision-makers.

054

Is there are need for One Health Surveillance?

John Berezowski[1], Judy Akkina[2], Victor Del Rio[3], Katrina DeVore[4], Fernanda Dorea[5], Celine Dupuy[6], Melody Maxwell[3], Vivek Singh[7], Flavie Vial[1], Laura Streichert[4], [1]Veterinary Public Health Institution, Vetsuisse Fakultät, University of Bern, Liebefeld, Switzerland; [2]United States Department of Agriculture, Animal and Plant Health Inspection Service, Veterinary Services,, Fort Collins, CO, [3]Pan American Center for Foot-and-Mouth Disease, Pan American Health Organization, Rio de Janeiro, Brazil; [4]International Society for Disease Surveillance, Boston, MA, [5]Swedish Zoonosis Centre, Department of Disease Control and Epidemiology, National Veterinary Institute (SVA), Uppsala, Sweden; [6]French Ministry of Agriculture, Lyon, France; [7]Public Health Foundation of India (PHFI), Indian Institute of Public Health (IIPH),, Hyderabad, Telangana, India. Contact: john.berezowski@gmail.com

As One Health (OH) continues to grow, alternative health infrastructure may be needed to support it. Since most population health surveillance is domain specific; as opposed to OH which crosses multiple domains, changes to surveillance may be required to optimize OH practice. The surveillance needs for OH practice have yet to be defined. A project was initiated to: 1) determine if there is a perceived need for a new type of surveillance (One Health Surveillance or OHS); 2) identify some of the challenges to the implementation of OHS; and 3) propose some solutions

The project had two parts: 1) an email survey of surveillance stakeholders working in different health domains, and 2) a workshop held at the Annual Conference of the International Society for Diseases Surveillance (ISDS) held in Philadelphia, PA, on Dec 10-11, 2014

A total of 185 questionnaires were returned from 44 countries. 85% of respondents reported that OHS would benefit them in their work. However, there were differences between people working in different domains; between respondents from developed or developing countries and between surveillance practitioners and decision makers. Three main challenges to OHS were identified: 1) training and resources, 2) tools and methodologies and 3) cross-agency communication and collaboration

There were 61 workshop participants from 6 countries, who identified solutions, including: cross domain staff exchanges, tools for data integration, and adapting reportable diseases to multiple domains

This study captured some of the attitudes of a group of surveillance stakeholders towards OHS, provides support for the value of OHS and presents some strategic approaches to moving OHS forward.

This work was supported by the ISDS: http://www.syndromic.org/ and the Skoll Global Threats Fund: http://www.skollglobalthreats.org/

055

A concrete regional “One health” surveillance system and management of epidemics: a success story in the South West Indian Ocean

Eric CARDINALE[1], **Harena Rasamoelina-Andriamanivo**[2], harimahefa razafimandimby[2], Richard Lepec[2], Loïc Flachet[2], [1]CIRAD, Sainte Marie, Réunion; [2]Indian Ocean Commission, Ebène, Mauritius. Contact: harena.rasamoelina@coi-ioc.org

Purpose
In 2005, a Chikungunya epidemic hit tens of thousands of people in the Indian Ocean region. This event revealed that health information sharing within the Indian Ocean Commission (IOC) countries (Comoros, Madagascar, Mauritius, France/Reunion and Seychelles) was critical. At the same time, zoonoses like Rift Valley fever and other animal diseases with high economic impact like Peste des petits ruminants burst out endangering food security in the region.
Methods
To support the control of these emerging infectious diseases, two regional surveillance networks (human and animal), operational since 2009, were merged in 2013 into a unique “SEGA One health” network. It aims at strengthening surveillance systems at national and regional level, improving response to health risks and building capacity. This network is coordinated by a unit based at the IOC and involves focal points from human and animal health ministries, laboratories and research institutions. The network activities include health events monitoring through regular conference calls and meetings, web-surveillance, support for national surveillance systems and outbreak investigations, arboviruses quality control program for laboratories, training program and “one health” surveillance programs at national and regional level.
Results
A weekly epidemiological bulletin is widely distributed (240 issues since 2009), twenty outbreaks have been investigated since 2013 (plague, dengue, Rift valley fever⋯). Eight national surveillance systems have been strengthened with an emphasis on information and communication technologies and specific “One health” programs have been initiated such as cysticercosis in Madagascar, leptospirosis in Seychelles, antibiotic-resistance and insecticide-resistance monitoring programmes at regional level. Another originality of this network is its close interactions with researchers through regular workshops and research studies. Priorities are defined by health managers and research results are considered in State control strategy.
Conclusion: One health is no more a concept but a reality
Relevance: The only way to better understand and tackle diseases

056

Economic assessment of zoonoses surveillance in a "One Health" context: A conceptual framework

Sara Babo Martins[1], Jonathan Rushton[2], Katharina DC Stärk[1], [1]Royal Veterinary College/SAFOSO, Liebefeld, Switzerland; [2]Royal Veterinary College, Hatfield, United Kingdom. Contact: sara.martins@safoso.ch

Cross-sectoral collaboration between animal and public health has been highlighted as a means to improve the management of zoonotic threats. This includes surveillance systems for zoonoses, where enhanced integration and sharing of information are seen as key to improved public health outcomes. Yet, there is a lack of evidence on the economic returns of such collaboration, particularly in the development and implementation of surveillance programmes.

The economic assessment of surveillance in this context needs to be underpinned by the understanding of the links between zoonotic disease surveillance in animal populations and the wider public health disease mitigation process, and how these relations impact on the costs and benefits of the surveillance activities. We examine these concepts and present a conceptual framework of these links as a basis for the economic assessment of zoonoses surveillance. The overall aim of this work is to support the prioritization of resource allocation to surveillance of zoonoses by exploring if a uniform approach to document the association between surveillance of zoonotic diseases in the animal population and the economic benefits for the public health sector can be developed.

Monetary, non-monetary and intermediate or intangible cost components and benefit streams of three conceptually distinct stages of zoonotic disease mitigation were identified. In each stage, as the wider disease mitigation objective varies so does the use of information generated in the animal populations in public health decision making and consequently the associated cost components and benefit streams. Steps and tools for an economic assessment are presented taking into account these links.

Results of the application of this framework to selected case studies are presented. First applications showed that the framework is practical and complete. It is suggested that the framework would add value in the regular evaluation of One Health surveillance.

The presented framework can be directly applicable in ongoing surveillance programmes targeting zoonotic diseases, and inform planning of effective and efficient future surveillance programmes for zoonoses.

057

West Nile virus integrated surveillance in Emilia-Romagna: an example of One Health approach in Italy

Marco Tamba[1], **Giulia Paternoster**[1], Antonino Caminiti[1], Annalisa Santi[1], Giorgio Galletti[1], Romeo Bellini[2], Paolo Bonilauri[1], Alba Carola Finarelli[3], Roberto Cagarelli[3], Andrea Mattivi[3], Paola Angelini[3], Claudio Gualanduzzi[3], Silvano Natalini[3], Claudio Velati[4], Mattia Calzolari[1], Michele Dottori[1], [1]Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia-Romagna, Brescia, Italy; [2]Centro Agricoltura ambiente 'Giorgio Nicoli', Crevalcore, Italy; [3]Regione Emilia-Romagna, Bologna, Italy; [4]Regional Blood Centre, Regione Emilia-Romagna, Bologna, Italy. Contact: giulia.paternoster@izsler.it

Purpose:
West Nile virus (WNV) circulates in nature between mosquitoes and birds, and can cause neuroinvasive disease in humans. As iatrogenic transmission via blood transfusion is possible, the National Blood Centre has established that WNV Nucleic Acid Test (NAT-PCR) on blood donations shall be timely introduced in a province after the notification of West Nile neuroinvasive disease in humans (WNND). Testing shall be then continued until 30 November and repeated from 1 July to 30 November in the following year. In 2014, NAT-PCR testing started after the notification of WNV circulation detected by the integrated surveillance system for WNV in place in the Emilia Romagna region (ER), Italy.
This work describes how the results of the integrated surveillance could be used to establish also the end of the testing period for blood donations.
Methods:
The ER integrated surveillance system includes: entomological monitoring; active and syndromic surveillance of wild birds; syndromic surveillance of horses; active surveillance on patients with neuroinvasive disease. Mosquitoes, birds and humans are tested by Real Time RT-PCR, while horses are tested by a commercial IgM ELISA. Positive samples are sent to the National Reference Centres for confirmation, sequencing and lineage determination.
Results:
In 2009 and 2010, the surveillance system detected the circulation of a lineage 1 WNV strain. In 2009, nine WNND human cases occurred in three out of the nine ER provinces, while none was notified in 2010. In 2011 and 2012, neither virus circulation nor WNND cases were detected. In 2013, WNV lineage 2 circulation was detected and 20 WNND cases occurred in five provinces. In 2014, lineage 2 WNV was again detected and seven WNND cases occurred in five provinces. The entomological and veterinary surveillance have always detected virus circulation before the occurrence of WNND cases (average: 34.3 days; median: 30; range 20-54) and no WNND cases occurred more than 30 days after the last WNV detection in mosquitoes, horses or birds.
Conclusions:
Therefore also the end of testing could be adapted to the results of the integrated surveillance.
Relevance:
This approach could be cost saving in terms of avoided NAT-PCR.

058

Operationalizing One Health using the One Health Systems Mapping and Analysis Resource Toolkit

Katey Pelican[1], **Tracey Lynn**[2], Kaylee Myhre[1], Heidi Kassenbourg[1], [1]College of Veterinary Medicine, University of Minnesota, St. Paul, MN, [2]Veterinary Services, USDA-APHIS, St. Paul, MN, Contact: tracey.v.lynn@aphis.usda.gov

Coordination and collaboration across human, animal, and environmental health sectors are essential to meet the Global Health Security Agenda (GHSA) targets for "a world safe and secure from global health threats posed by infectious diseases." While progress is being made, many evaluation and assessment efforts focus on individual sector infrastructure and capacity. Additional tools are needed that bring the sectors together in positive, interactive dialogue to further operationalize "One Health" within their jurisdiction.

The One Health Systems Mapping and Analysis Resource Toolkit (OH-SMART), jointly developed by the University of Minnesota (UMN) and the U.S. Department of Agriculture (USDA), is a step-wise, structured approach by which a network of agencies review and visualize their procedures and processes for interdisciplinary coordination of complex issues at the human-animal-environmental interface. During the experiential workshops, participants create systems-based maps of cross-sectoral interactions, analyze them to identify current and desired operational best practices, and develop mutually prioritized actions needed to strengthen the system of prevention, early detection, and rapid, effective cross-sectoral response.

UMN and USDA piloted OH-SMART in the United States in Minnesota and at a USDA-led conference with over 30 U.S. states participating. Several of these states have since applied OH-SMART to strengthen their One Health system; examples include multi-sector response to a zoonotic disease outbreak associated with a petting zoo and tornado response with companion animal sheltering. The successful university-government partnership that created OH-SMART could be replicated in other countries to support further application of OH-SMART, including as a useful means to synergize between tools used for assessment of national capacities, e.g., the WHO-OIE Operational Framework for Good governance at the human-animal interface. At the end of the workshop, participants will have an understanding of how to use OH-SMART to improve collaborations with other sectors to address issues at the human-animal-environmental interface.

059

One Health graduate program as opportunity to bridge the gaps between animal health, public health and food safety sectors in developing Western Balkan countries

Nihad Fejzic[1], Sabina Seric-Haracic[1], Aida Hodzic[2], Semra Cavaljuga[3], Valeria Grieco[4], [1]University of Sarajevo Veterinary faculty, Sarajevo, Bosnia and Herzegovina; [2]University of Sarajevo Veterinary faculty, Sarajevo, Bosnia and Herzegovina; [3]University of Sarajevo Faculty of medicine, Sarajevo, Bosnia and Herzegovina; [4]University of Milano Faculty of veterinary medicine, Milano, Italy. Contact: nihad.fejzic@vfs.unsa.ba

Purpose:One Health (OH) is advocated as sound solution for current increasing interdependencies between environment, human and animal health. In line with many OH initiatives worldwide is effort to create OH master program that will run simultaneously on several Universities in Western Balkan (WB) countries. As a part of this effort, questionnaire survey of stakeholders in public health sectors in selected WB countries (Bosnia and Herzegovina, Kosovo) was done. Methods:This paper reports result of the survey, particularly regarding self-assessed proficiency of health workers (animal and human) and most priority training needs within the OH framework. Targeted respondents were veterinary and medicine professionals working in faculties, government bodies, institutes, primary health care as well as senior year veterinary and medicine students. Results:Survey responses were appropriately balanced between countries, veterinary and medical professions, gender and predefined age categories. Average respondent dealing with animal or human public health most commonly deals with variety of tasks, most frequently with food safety and epidemiological surveillance. Respondents working predominantly on these tasks view their relevant skills as adequate. However, concern rises for self-evaluated competency in respondents occasionally involved (in case of an incident). Only 15,7% of respondents were familiar with OH concept. We investigated intensity of previous formal and informal education in contrast to current needs for training for following groups of public health disciplines:
-epidemiology, prevention and control of zoonoses,
-occupational health,
-hygiene and quality of food,
-health economics and
-public health management.
Conclusions:Our results show that less extensive training in public health disciplines during previous education does not automatically translates to most currently required training needs in the region. Relevance: Even though most of respondents were interested in one year OH master program in domicile/neighboring country, only 14,3% (20) scaled perceived individual benefits to be sufficient for them to finance entire costs.

060

One Health in practice - challenges and drivers for collaborative development of zoonotic disease management in Sweden

Ann Lindberg[1], Anna Brådenmark[2], Holly Cedervind[3], Lena Hult[4], Cecilia Jernberg[5], Mats Lindblad[6], Roland Lindqvist[6], Jenny Persson-Blom[7], Håkan Ringberg[8], Ulf Törnebladh[9], Anders Wallensten[5], Marianne Elvander[10], [1]Swedish National Veterinary Institute, Uppsala, Sweden; [2]Swedish Association of Local Authorities and Regions, Stockholm, Sweden; [3]County Administrative Board of Värmland, Karlstad, Sweden; [4]Board of Agriculture, Jönköping, Sweden; [5]Public Health Agency of Sweden, Stockholm, Sweden; [6]National Food Agency, Uppsala, Sweden; [7]Swedish Work Environment Authority, Stockholm, Sweden; [8]Swedish Society for Communicable Disease Prevention and Control, Malmö, Sweden; [9]National Board of Health and Welfare, Stockholm, Sweden; [10]Swedish National Veterinary Institute, Uppsala, Sweden. Contact: ann.lindberg@sva.se

Purpose: Integrated surveillance and control of zoonotic infections across the animal health-public health (AH-PH) interface is a cornerstone in European food safety legislation. Still, financial, legal and organisational factors can act as constraints to efficient cross-sectoral collaboration. The aim of this paper is to give an example of successful development of AH-PH collaboration, transforming One Health (OH) from a vision into practice.
Methods: Over 18 years, Swedish authorities have consciously improved their co-operation from passive-consultative, via reactive-operative, towards proactive coordination of strategies for the control of zoonoses. Several collaborative processes have been subject to joint development; data sharing, outbreak management, communication, risk assessments and definition of long-term strategies and priorities. At current, using program theory, an analysis is being conducted with the aim of identifying bottlenecks in the effective governance of the 'zoonoses system', to create a basis for continuous improvement of system processes with the objective to make best use of available resources and, ultimately, to protect public health.
Results: In addition to collaborations becoming more efficient and satisfying, an important strategic output has been the high-level endorsement of "green papers" for six zoonoses of high public health impact, followed by joint prioritisation of actions identified as critical to improve their management. These documents have subsequently been used to guide operations planning within the AH-PH administrations. A recent initiative, emerging out of these green papers, is a trans-sectoral evaluation of the surveillance system for the zoonoses in question.
Conclusions: Traditionally, policies and control chains follow sectors, and to make transversal collaborations sustainable alternative incentives have to be developed. This paper identifies key success factors as well as challenges experienced when turning OH into practice.
Relevance: An example of how inter-agency policies supporting a OH approach can become institutionalized without enforcement of new legislation or organizational changes.

061

One health economics must be different

Simon R. Ruegg, University of Zürich, Zürich, Switzerland. Contact: srueegg@vetclinics.uzh.ch

Purpose:
In One Health, the joint consideration of human, animal and environmental health, we suggest to regard living systems as complex non-linear dynamical systems (CNLDS). This approach has not only methodological implications, but also reveals some blind spots in conventional approaches. Here we explore the consequences of the thermodynamic properties of CNLDS on economic evaluation.
Methods:
All living beings are open CNLDS nested within larger systems, where the global ecosystem represents the largest scale. It is characterised by a stable attractive state, namely a steady state of material, energy and information flow, with minimal entropy. Any zoological taxon participating in this system has evolved in a niche to which it is optimally adapted, contributing to the minimal global entropy. Domestication of animals represents a dissipative state of that system, which requires entropy for its maintenance.
Results:
This entropy can be drawn from three sources: (1) man in form of labour and vigilance, (2) the environment in form of natural resources to support biodiversity and ecosystem resilience, and (3) the domesticated animal in form of compromised welfare and health.
The concept of economic optimisation focuses on human benefit by reducing (1), thereby inevitably increasing the strain on (2) and (3) to maintain the thermodynamic state of the system. Furthermore, economic valuation by definition disregards ecosystems-services or transfers that are not reflected in human consciousness and/or trade. Thus, it will inevitably fail to consider unknown contributions to the global system from the environment and animals. These will only reveal to human consciousness once their contribution is critically compromised. Consequently, economic evaluation is inevitably retrospective and cannot account for future positive or negative aspects.
Conclusions:
Animal husbandry produces benefits from a human perspective, but requires contributions from animals and the environment. One health economics thus must assess which thermodynamic costs are environmentally tolerable and define the husbandry practices that respect this limit, instead of optimising systems at low scale.

062

Roaming behaviour of domestic dogs in Aboriginal and Torres Strait Islander communities in northern Australia

Salome Dürr[1], **Michael P. Ward**[2], [1]Veterinary Public Health Institute, Liebefeld, Switzerland; [2]The University of Sydney, Camden, Australia. Contact: Michael.ward@sydney.edu.au

Background:
Rabies is probably the most severe zoonosis transmitted by dogs, which serve as the main reservoir population of this disease. Rabies is absent from Australia but the risk of incursion from neighbouring, rabies endemic Indonesia is possible. Large populations of free-roaming domestic dogs in Aboriginal communities in remote Northern Australia would enable establishment of rabies after incursion. Knowledge on roaming behaviour of these dogs would inform preparedness plans, but such information was lacking.
Objectives:
The objectives of this study were to estimate home range (HR) and utilization distribution (UD) of 69 domestic dogs in six indigenous communities in northern Australia applying four different methods: the minimum convex polygon, the location-based kernel density estimation, the biased random bridge (BRB), and Time Local Convex Hull (T-LoCoH).
Methods:
GPS collars were attached to dogs for a period of 1-3 days and positions were recorded every minute. Data were cleaned and HR and UD calculated using the four indicated methods using R software.
Results:
Median core HRs (50% isopleth) were estimated to range from 0.2 to 0.4 ha and the more extended HR (95% isopleth) from 2.5 to 5.3 ha, depending on the method used. The HR and UD shapes were found to be generally circular around the dog owner's house. Some individuals roamed much more with a HR size of 40-104 ha and covered large areas of their community or occasionally beyond.
Conclusions:
Only BRB and T-LoCoH methods integrate the consecutiveness of GPS locations into the analysis, a substantial advantage. Advantages of the BRB method include a more realistic analytical approach (kernel density estimation based on movements rather than on locations), the ability to deal with irregular time periods between consecutive GPS fixes and parameter specification which respects the characteristics of the GPS unit used. The BRB method was therefore the most suitable method for UD estimation in this dataset.
Relevance:
These results can further be used to inform transmission parameters for canine infectious disease models, such as a rabies spread model in Australia.

063

Estimating the population of free-roaming and owned dogs and gastro-intestinal parasite burden in owned dogs in the city of Quito, Ecuador.

Colon J. Grijalva[1], Heather S. Walden[1], Patti C. Crawford[1], Julie K. Levy[1], Rommel L. Vinueza[2], Jorge A. Hernandez[1], [1]University of Florida, Gainesville, FL, [2]Universidad San Francisco de Quito, Quito, Ecuador. Contact: jgrijalvar@ufl.edu

Background: In 2011, authorities of Quito, Ecuador, approved an Ordinance to promote public health and animal welfare. Two limitations are that current population of dogs is not known, and the relationships between dog abundance, socio-economic factors, prevalence of dog with gastro-intestinal (GI) parasites and pet ownership responsibility has not been investigated in Quito.
Objectives: (i) To estimate the population of stray and owned dogs in Quito (ii) To examine relationships between studied household factors and pet ownership responsibility and (iii) To estimate the prevalence of and household factors associated with a positive diagnosis of GI parasites in owned dogs.
Methods: Stray and owned dogs from 65 parishes in Quito were considered for inclusion in this study. To accomplish the first objective, space-based, random sampling procedures recommended by the World Society for the Protection of Animals were used. A survey with instruments (indexes) to investigate Living Conditions (LCI) and Pet Ownership Responsibility (PORI) was prepared. Canine fecal samples were collected for diagnosis of GI parasites. Linear regression models were used to calculate dog abundance parameters (e.g., human-to-dog ratios). Logistic regression was used for identification of investigated factors associated with PORI and a positive diagnosis of GI parasites.
Results: Data from 16 investigated parishes revealed an estimated human:free-roaming dog ratio=49:1; a human:owned dog ratio=3.5:1. A low human:free-roaming dog ratio was associated with high poverty rates (β=-0.77; r=0.77; R2=0.59; $p<0.01$), households with low PORI were associated with low LCI and ≥2 dogs in the households ($p<0.01$). The overall prevalence of households with dogs with GI parasites was 28% (95%CI =21, 37%). *Ancylostoma spp* was the most frequent parasite. We failed to identify risk factors associated with a positive diagnosis of GI parasites in dogs.
Conclusions: The problems of stray dogs and lack of pet ownership responsibility are associated with poverty.
Relevance: We have generated baseline data for Quito that is composed by demographic, health and pet ownership responsibility indicators.

064

Dog overpopulation and disease burden on Santa Cruz Island Galapagos

Nicole M. Diaz[1], Gabriella S. Mendez[1], C. Jaime Grijalva[1], Heather S. Walden[1], Marilyn Cruz[2], Eduardo Aragon[3], **Jorge A. Hernandez**[1], [1]University of Florida, Gainesville, FL, [2]Agencia de Regulación y Control de la Bioseguridad y Cuarentena para Galapagos, Santa Cruz, Galapagos, Ecuador; [3]Universidad Central del Ecuador, Quito, Ecuador. Contact: hernandezja@ufl.edu

Purpose: To estimate the dog population and disease burden on Santa Cruz Island, Galapagos.
Methods: We used a probabilistic spatial sampling approach for selection of neighborhoods, blocks, and households with or without dogs. In addition, we used a cross sectional study approach for estimation of disease prevalence and identification of exposure factors associated with previous exposure to canine distemper virus (CDV) and other pathogens. The study sample included 101 dogs.
Results: The human:dog ratio = 6:1 which extrapolates to 2500 dogs. More female dogs (50%) were spayed, compared to male dogs (30%) (P = 0.04). Prevalence of dogs with positive antibody titers to CDV = 36% (95% CI = 26, 47%). We observed an interaction effect between rural residence and spay/neuter status on seropositivity to CDV.
Conclusions: Because vaccination is prohibited, the dog population on Santa Cruz is susceptible to an outbreak of CDV with potential spill over to marine mammals. Burden of other pathogens will be presented at the symposium.
Relevance: Dog overpopulation and diseases are threats to endemic island species on the Galapagos. Although sterilization campaigns to control dog population growth have been successfully implemented, published data on sterilization and resulting population trends are lacking. We provide evidence the current dog population in Santa Cruz Island is two times more than a recent dog count in March 2014, and local culture against sterilization of male dogs remains a limiting factor for reducing reproduction. Prevalence of previous exposure to CDV was higher in spayed/neutered rural dogs; perhaps, we hypothesize, due to illegal vaccination or direct and indirect transmission between infected and susceptible dogs during mass gatherings. Study results provide the most comprehensive assessment of dog overpopulation and disease burden on the Galapagos to date.

065

Antimicrobial resistant *Escherichia coli* in hospitalised companion animals and their hospital environment

Gina Pinchbeck[1], Ian Tuerena[1], Tim Nuttall[2], Nicola Williams[1], [1]University of Liverpool, Neston, United Kingdom; [2]University of Liverpool, Neston, United Kingdom. Contact: ginap@liv.ac.uk

Background: Antimicrobial resistance (AMR) among *E. coli* has previously been shown to be higher in hospitalised animals compared to animals in the community; hence pets may be at risk of nosocomial colonisation and infection with these organisms.
Objective: The aim of this study was to determine the prevalence of AMR *E. coli*, including important AMR phenotypes (e.g. extended spectrum beta-lactamase (ESBL) and AmpC producers), from both the faecal microflora of animals hospitalised in referral practices and their practice environment.
Methods: Dogs and cats hospitalised overnight at five referral hospitals in the northwest UK were sampled. Environmental samples were collected once per week from each practice. Full susceptibility testing was performed on all isolates according to BSAC guidelines. The presence of bla_{ESBL} and bla_{AmpC} genes were established using PCR and sequencing techniques.
Results: 333 faecal samples were collected from 214 animals. The adjusted prevalence of resistance types among faecal samples were: clavulanic acid potentiated amoxicillin (CAPA) 14%; ciprofloxacin 9.2%; multidrug resistance (MDR) 13.1%); ESBL-producer 14.0% and AmpC-producer 7.7% . Of 257 environmental samples 47 (18.3%) contained AMR *E. coli* with resistant isolates more likely to be found in outside walking areas and ward floors than tables and keyboards.
Multilevel, multivariable regression models showed there was significant variation by practice. Neurosurgery and soft tissue surgery cases were at increased risk of several resistance outcomes compared to medical and orthopaedic cases. Use of fluoroquinolones and CAPA were associated with increased risk of ESBL. Isolation of environmental AMR isolates and increased hospitalisation time were also associated with increased isolation of AMR.
Conclusions and relevance: AMR was present in hospitalised animals and the practice environment. Antimicrobial use, hospitalisation, case type and practice were associated with acquisition of AMR isolates. Further studies are needed to determine the impact of antimicrobial stewardship and infection control measures on colonisation with AMR bacteria in veterinary healthcare.

066

Epidemiological modelization of canine leishmaniasis: proposal of a didactical tool to understand vectorial diseases

Ana Muniesa, Ana Peris, Ignacio de Blas, Universidad de Zaragoza, Zaragoza, Spain. Contact: animuni@unizar.es

Purpose: Canine leishmaniasis (CL) is a parasitic disease caused by *Leishmania infantum* and transmitted by sandflies that mainly affects dogs. There are a number of publications about this topic, but some essential aspects of the epidemiology of the transmission dynamics are not sufficiently clear yet. The aim of this work was to develop a software that simulates the dynamics of *L. infantum* infection in dog populations to study temporal evolution of infection taking into account possible risk factors related to the transmission and maintenance of the disease in endemic populations: the habitat (urban vs rural), the abundance of Phlebotomus and its activity level related with temperature, and the dog density and their intrinsic variables (sex, age and aptitude).
Methods: A simulation tool was developed using a model that combines stochastic methods based on random generation, simple and conditional probabilities, linear and logistic regressions and iterative procedures. Data for validation and calculation of the model coefficients correspond to a cohort study carried out in Zaragoza (Spain) during two years (2006-2008). The implementation was performed on a web server with PHP and MySQL.
Results: An interactive model was available to improve understanding the role of different factors about the dynamics of CL, such as temperature, dog density, population structure (age-sex stratification), dog aptitude, health status, treatment application… Relationship between sex and dog aptitude has been revealed as an interesting confounding factor.
Conclusions: The development of this model will allow us to predict the impact of climate change in CL and other vector borne diseases, or evaluate the effectiveness of certain measures of disease control (compulsory slaughter, early diagnosis and treatment).
Relevance: During construction of the model have been identified some important gaps in knowledge of the dynamic transmission, such as frequency of vector infection or life expectancy of dogs depending on their aptitude and health status.

067

Mass vaccination of 70% of dogs can control rabies, even in rapidly-growing populations of free-roaming dogs with high rates of turnover due to births and deaths

Darryn Knobel, Anne Conan, Ross University School of Veterinary Medicine, Basseterre, Saint Kitts and Nevis. Contact: dknobel@rossvet.edu.kn

Rabies is a serious yet neglected public health threat in underserved communities in Africa, where the virus is maintained in populations of owned, free-roaming domestic dogs. Rabies can be controlled through the mass vaccination of dogs against the virus, if at least 40% of the population is immune at any time. The World Health Organization (WHO) recommends that, to achieve control and eventual elimination of dog rabies, programs must ensure that mass dog vaccination campaigns achieve a coverage of at least 70%, and that such campaigns recur, usually annually. It is assumed that this coverage is sufficient to maintain the population immunity above the critical threshold of 40% for at least 12 months, despite dog population turnover due to births, deaths and migrations during this period. The figure of 70% is an empirically-derived consensus, and little work has been done to test this assumption using real data on demographic rates from free-roaming dog populations. We report data from a demographic surveillance system covering all owned dogs in a rabies-affected, underserved community in South Africa. Data span a 24-month period, from 1st January 2012 through 1st January 2014, covering 1,800 dog-years of observation. The objective of the study was to quantify demographic parameters in this population of dogs, and to assess the implications for rabies control through mass vaccination. Annual population growth rate was +18.6% in 2012 and -24.5% in 2013. Crude annual birth rates were 451 puppies born per 1,000 dog-years in 2012 and 313 per 1,000 dog-years in 2013. Crude annual death rates were 406 per 1,000 dog-years in 2012 and 568 per 1,000 dog-years in 2013. This is a highly dynamic population, with rapid turnover and significant heterogeneity in demographic rates over time and across segments of the population. Despite this, we show that routinely achieving 70% vaccination coverage during mass dog vaccination campaigns conducted every 12 months will be sufficient to maintain coverage above the critical threshold, even during periods of rapid growth and high turnover. Our findings are consistent with WHO recommendations to achieve control and eventual elimination of dog rabies in Africa.

068

Estimation of population size and rabies vaccination coverage of free-roaming dogs using mark-resight methods, Bhutan

Tenzin Tenzin[1], Joanna S. McKenzie[2], **Raphael Vanderstichel**[3], Bir Doj Rai[4], Karma Rinzin[1], Yeshey Tshering[1], Rinzin Pem[4], Chenga Tshering[5], Chenga Tshering[5], Narapati Dahal[1], Kinzang Dukpa[1], Sithar Dorjee[6], Sonam Wangchuk[7], Peter Jolly[2], Roger Morris[8], Michael P. Ward[9], [1]National Centre for Animal Health, Thimphu, Bhutan; [2]Institute of Veterinary, Animal and Biomedical Sciences, Massey University, New Zealand, New Zealand; [3]Department of Health Management, Atlantic Veterinary College, UPEI, Charlottetown,, Prince Edward Island, PE, Canada; [4]Regional Livestock Development Centre,, Wangdi, Bhutan; [5]Livestock Sector,, Paro, Bhutan; [6]BAFRA, Thimphu, Bhutan; [7]Public Health, Thimphu, Bhutan; [8]MorVet Limited, Masterton, New Zealand; [9]Faculty of Veterinary Science, University of Sydney, Sydney, Australia. Contact: rvanderstich@upei.ca

Purpose: Capture-Neuter-Vaccinate-Release (CNVR) programs have been implemented in Bhutan to manage the dog population and control rabies, but no detailed evaluation has been done to assess their coverage and impact.
Methods: We compared estimates of the dog population using three analytical methods: Lincoln-Petersen index, the Chapman estimate, and the logit-normal mixed effects model, and a varying number of count periods at different times of the day to recommend a protocol for applying the mark-resight framework to estimate free-roaming dog population abundance. We assessed the coverage of the CNVR program by estimating the proportion of dogs that were ear-notched and visually scored the health and skin condition of free-roaming dogs in Gelephu and Phuentsholing towns in south Bhutan, bordering India, in September-October 2012.
Results: The estimated free-roaming dog population in Gelephu using the Lincoln-Petersen index and Chapman estimates ranged from 612 to 672 and 614 to 671, respectively, while the logit-normal mixed effects model estimate based on the combined two count events was641 (95% CI: 603-682). In Phuentsholing the Lincoln-Petersen index and Chapman estimates ranged from 525 to 583 and 524 to 582, respectively, while the logit-normal mixed effects model estimate based on the combined four count events was 555 (95% CI: 526-587).The total number of dogs counted was significantly associated with the time of day (AM versus PM; P = 0.007), with a 17% improvement in dog sightings during the morning counting events.
Conclusions: We recommend to conduct a morning marking followed by one count event the next morning and estimate population size by applying the Lincoln-Peterson corrected Chapman method or conduct two morning count events and apply the logit-normal mixed model to estimate population size.
Relevance: The mark-resight method is practical in developing countries to estimate the free-roaming dog population and also to assess the vaccination coverage.The findings from this study are expected to guide dog population management and the rabies control program in Bhutan, and elsewhere in the world.

069

Dog and cat population dynamics: modelling different sterilization scenarios to support veterinary public policies management

Aline G. A. Guilloux[1], Ricardo A. Dias[1], Oswaldo S. Baquero[1], Caio F. Moretti[1], Tosca De Lucca[2], Ricardo C. A. Rodrigues[3], Cláudio Castagna[3], Douglas Presotto[3], Yury C. Kronitzky[2], José H. H. Grisi[1], Fernando Ferreira[1], Marcos Amaku[1], [1]University of Sao Paulo, São Paulo, Brazil; [2]Prefecture of Campinas, Campinas, Brazil; [3]Prefecture of Campinas, Campinas, Brazil. Contact: aline_gil@hotmail.com

Dogs and cats have a close relation with humans and many times are treated as family, but are still being relinquished or abandoned. This animals occupy public spaces, some times deprived of basic needs, originating ambiental problems and transmiting zoonotic disease.
The stray populations was controlled trough euthanasia until 2008, in São Paulo state. When it was abolished, shelters have rapidly reached their maximum capacity. Adoption takes time, reducing the capture rate and possibly increasing the stray population. Establish cost-effective policies to control dog and cat population is essential to public authorities and sterilising owned population is a part of it.
This study aimed to compare owned population sterilisation scenarios, modelling population dynamics and cost-effectiveness to support decision making in Campinas municipality. The population control strategy in place is doing isolated mass sterilisation efforts.
Two personal interview census were performed in Jardim Vila Olimpia neighbourhood to mesure population vital parameters (Feb/12 and Jun/13), with a mass sterilisation campaign in between. Hypothetical sterilisation scenarios were compared to this campaign and population dynamics was simulated with mathematical modelling.
When compared to keeping previous sterilisation rates, a single mass sterilisation effort doesn't change population's evolution in 20 years. Analysing local and global sensitivity, the vital parameters with more relative influence in animal population evolution were carrying capacity of the environment, immigration rate and abandonment rate, for both species. An anual mass sterilisation effort would have the best cost-effectiveness ratio after 20 years.
Targeting specific gender or age in sterilisation campaigns could be a helpful to overcome the high reproductive rate. Lengthening the permanence of sterilised animals in the population and improving movement restriction could be achieved trough responsible ownership. These results allow the veterinary public policies stakeholders to make decisions based in scientific evidence and reinforces the need to a continuos effort to control dogs and cats populations.

070

Prevalence of infection by Leishmania infantum in asymptomatic dogs using qPCR and IFAT

Patricia Sebastian, Hector Fuertes, Ana Muniesa, Nabil Halaihel, **Ignacio de Blas**, Universidad de Zaragoza, Zaragoza, Spain. Contact: deblas@unizar.es

Purpose: Canine leishmaniasis (CL) is a relevant parasitic disease that affects dogs in the Mediterranean region. An early diagnosis of infected dogs is a key element in order to control the disease. Our objective was to establish the prevalence of CL in asymptomatic dogs from a defined area comparing two different diagnostic techniques: a real time PCR (qPCR) and a Direct immunofluorescent technique (IFAT).
Methods: An observational cross-sectional study was performed over 98 healthy dogs with similar level of exposition to the vector, living in a periurban area of Zaragoza, an endemic region of CL located in the north-east of Spain. The area was selected in order to avoid bias due to different environmental conditions. The period of the study was in February-March before vectors began their activity.
Results: Agreement between techniques was very poor and it was established by Cohen's kappa coefficient (k=0.048; p=0.314). *Leishmania infantum* specific antibodies were identified in serum using IFAT with an apparent prevalence of 8.16% (95% CI: 4.19-15.29%). A seven times higher apparent prevalence: 58.16% (95% CI: 48.27, 67.44%) was detected by qPCR. The mean value of Ct for qPCR positive dogs was 35.73 ± 1.48.
Conclusions: These values are higher than expected taking into account that only asymptomatic animals were sampled.
Relevance: Serological technique are significantly underestimating the prevalence of the infection in endemic areas, probably due to non-seroconverted animals, which can seriously influence the results of studies trying to clarify the epidemiological studies of this parasite. On the other hand, qPCR is a good technique to detect *Leishmania* protozoa from infected dogs in a more accurate way, being a potential tool to prevent the antibodies development and consequently the clinical disease.

071

Is the tail wagging the dog? Time-to-event analysis of data mined from a veterinary practice management system to investigate the frequency of tail injuries in New Zealand.

Daan Vink[1], Kate Hill[2], [1]Ministry for Primary Industries, Upper Hutt, New Zealand; [2]Massey University, Palmerston North, New Zealand. Contact: Daan.Vink@mpi.govt.nz

Background: Tail docking is discouraged in New Zealand, but not legally prohibited. Pro-choice kennel clubs argue that banning docking would result in a much higher incidence of tail injuries, but the effect of a ban is unclear.
Objectives: To use data mining techniques to investigate tail injuries in dogs in New Zealand, and estimate the impact of a ban on docking.
Methods: Electronic records of dogs were extracted from 16 veterinary clinics using the same practice management system (PMS), covering an 8 year retrospective period. Tail injury cases were identified, and time-to-event analysis was performed to investigate breed and clinic location effects. Non-cases were right-censored by last clinic visit date; a Cox proportional hazards model was subsequently fitted. The excess number of cases that would have occurred if a ban on tail docking had been in place over the study duration was estimated.
Results: Records from 601 dogs which had experienced tail injuries and 44,755 dogs which had not were represented in the data. The overall clinic-level incidence risk was 11.01 cases per 10,000 dogs seen per year. The most common causes were accidents and injury due to a vehicle. The odds of injury were significantly higher on the South Island than on the North Island, and significantly higher in rural clinics than in urban clinics. The hazard ratios were highest for farm and hunting working dogs, and lowest for toy and terrier breeds. If a ban on docking had been in place for the duration of this study, approximately 61 additional cases of tail injury (10%) would have occurred.
Conclusions: Tail injuries were rare. A ban on docking is not likely to result in a substantially elevated rate of injury. Farm dogs and hunting dogs are at highest risk; furthermore, injuries are likely to be underreported in these categories. The higher incidence in South Island rural clinics is likely to be due to confounding.
f) Relevance: Mining of PMS data is shown to be highly effective for the investigation of rare conditions. As the observation period for each dog was determined by the date of injury or the censoring date, time-to-event analysis represented the most appropriate analytic technique to investigate the data.

072

Epidemiology of canine hyperadrenocorticism in primary-care veterinary practices in England

Dan G. O'Neill[1], Jonathan M. Faire[1], David B. Church[2], Paul D. McGreevy[3], Peter C. Thomson[3], Dave C. Brodbelt[1], [1]Royal Veterinary College, London, United Kingdom; [2]Royal Veterinary College, London, United Kingdom; [3]University of Sydney, Sydney, Australia. Contact: doneill@rvc.ac.uk

Purpose

Hyperadrenocorticism (HAC) can severely compromise welfare but limited epidemiological data exist on the general canine population. This study aimed to estimate prevalence and identify risk factors for HAC in a large population of dogs attending primary-care practice in England.

Methods

The VetCompass programme shares de-identified veterinary data for research; 470 clinics have shared 11 million clinical records on 4 million animals. The free-text clinical notes and standard diagnoses (VeNom Codes) of 210,824 dogs attending 119 clinics were searched to identify potential HAC cases and a random subset was verified by manual review. Analyses used Stata Version 13. Prevalence was reported over a one-year period; probability weighting accounted for the sampling protocol. Risk factor analysis used multivariable logistic regression. After backwards stepwise elimination, the area under the ROC curve was evaluated model performance.

Results

Review of 52% of potential cases identified 304 cases. The estimated prevalence was 0.28% (95% confidence interval (CI) 0.25-0.31). There were 127 (41.8%) deaths at a median age of 12.7 years (interquartile range 10.9-14.2, range 5.8-17.6).

Four risk factors were identified: breed, relative bodyweight, age and insurance. Bichons (OR: 6.5, 95% CI 3.5-12.2, P < 0.001) and Yorkshire Terriers (OR: 1.9, 95% CI 1.0-3.5, P = 0.042) had increased odds compared with crossbred dogs. Dogs at or above mean bodyweight for breed had 1.7 (95% CI 1.3-2.3, P < 0.001) times odds compared with dogs below the mean. Increasing age was associated with increasing HAC diagnosis Insured dogs had 3.8 (95% CI 2.7-5.4, P < 0.001) times the odds compared with uninsured dogs. The final model showed good discrimination (area under the ROC curve: 0.951).

Conclusions

About 1-in-400 dogs has a HAC diagnosis. Bichons and Yorkshire Terriers are over-represented.

Relevance

This study highlights the innovative usefulness of large aggregates of veterinary clinical data to explore complex questions on companion animal health. These findings can improve HAC detection using breed, relative bodyweight and age indicators. Insurance may play a role in facilitating diagnosis.

073

Scrotal castration as a safe and effective means of male canine sterilization

Kimberly A. Woodruff[1], Karla Rigdon-Brestle[2], Phil Bushby[1], Carla Huston[3], Robert Wills[3], [1]Mississippi State University College of Veterinary Medicine, Starkville, MS, [2]Humane Alliance, Asheville, NC, [3]Mississippi State University College of Veterinary Medicine, Starkville, MS, Contact: kwoodruff@cvm.msstate.edu

Purpose: For years, a prescrotal surgical approach has been the only accepted method of male dog sterilization. The prevailing thought has been that a scrotal incision will cause more complications including swelling and induction of self-trauma. The focus of this study is to evaluate the hypothesis that there are no differences between the prescrotal and scrotal technique.
Methods: In a collaborative effort between Mississippi State University College of Veterinary Medicine (MSU-CVM) and Humane Alliance, 437 apparently healthy male dogs over the age of 6 months were randomly allocated by coin toss into 2 treatment groups and castrated by either a prescrotal (n=206) or scrotal incision (N=231). Complications were recorded up to 72 hours following the procedure by individual owners and humane organization employees. At MSU-CVM the length of the procedure was recorded to track the difference in efficiency. Data were analyzed for surgical efficiency and the presence or absence of complications. Multivariable logistic regression was used to measure the strength of association between the occurrence of each of the complications and the explanatory variables of method, institution and weight of dog. Differences in duration of surgery by method were assessed by analysis of variance. A p value < 0.05 was considered statistically significant for analysis. Complications were categorized by the presence or absence of hemorrhage, self-trauma, pain and swelling.
Results: Method of castration was not found to be significantly associated with hemorrhage, pain or swelling. Fifty-four animals (prescrotal = 34, scrotal = 20) were recorded as inflicting self-trauma through biting, licking or chewing their incision. The odds of self-trauma were 1.96 times greater ($p=0.04$) in animals undergoing the prescrotal method than in those castrated by the scrotal method. The average time for scrotal castration was 30% faster than prescrotal castration.
Conclusion: Scrotal castration was comparable to traditional prescrotal castration in terms of incidence of most post-operative complications.
Relevance: This study supports scrotal castration as a safe and efficient method of male canine sterilization.

074

A comprehensive review of dog walking correlates for increasing physical activity of both dogs and people

Carri Westgarth[1], Robert M. Christley[1], Hayley E. Christian[2], [1]University of Liverpool, Liverpool, United Kingdom; [2]The University of Western Australia, Perth, Australia. Contact: carri.westgarth@liverpool.ac.uk

Purpose:
Physical inactivity and sedentary behaviour are major threats to population health, with rising levels of obesity in both people and their pets. A considerable proportion of people own dogs, and there is good evidence that dog ownership is associated with higher levels of physical activity. However not all owners walk their dogs regularly. This paper comprehensively reviews the evidence for correlates of dog walking so that effective interventions may be designed to increase the physical activity of dog owners, and improve dog welfare.

Methods:
Published findings from 1990-2012 in both the human and veterinary literature were collated and reviewed for evidence of factors associated with objective and self-reported measures of dog walking behaviour, or reported perceptions about dog walking. Study designs included cross-sectional observational, trials and qualitative interviews.

Results:
There is good evidence that the strength of the dog-owner relationship, through a sense of obligation to walk the dog, and the perceived support and motivation a dog provides for walking, is strongly associated with increased walking. The perceived exercise requirements of the dog may also be a modifiable point for intervention. In addition, access to suitable walking areas with dog supportive features that fulfill dog needs such as off-leash exercise, and that also encourage human social interaction, may be incentivising.

Conclusions:
Current evidence suggests that dog walking may be most effectively encouraged through targeting the dog-owner relationship and by providing dog-supportive physical environments.

Relevance:
Future studies must be of a higher quality methodological design, including accounting for the effects of confounding, and longitudinal designs and testing of interventions in a controlled design in order to infer causality.

075

Risk factors identified for owner-reported feline obesity at around one year of age

Elizabeth Rowe[1], William Browne[2], Rachel Casey[1], Tim Gruffydd-Jones[1], Jane Murray[1], [1]University of Bristol, Bristol, United Kingdom; [2]University of Bristol, Bristol, United Kingdom. Contact: lizzie.rowe@bristol.ac.uk

Purpose:
This study is the first to use prospective data from a longitudinal study ('Bristol Cats') to identify early-life risk factors for feline overweight/obesity at around one year of age.
Methods:
Data analysed were collected via three owner-completed questionnaires (for cats aged 2 – 4 months, 6.5 – 7 months and 12.5 – 13 months) completed between May 2010 and August 2013. Owner-reported body condition scores (BCS) of cats at age 12.5 – 13 months, using a 5-point system, were categorised into a dichotomous variable: overweight/obese (BCS 4 – 5) and not overweight (BCS 1 – 3) and used as the dependent variable. Cat breed, neuter status, outdoor access, type of diet and frequency of treats fed were analysed as potential risk factors. A total of 836 cats were included in the analysis, 7.0% of which were reported by their owners to be overweight/obese at 12.5 – 13 months of age. Significant potential explanatory variables from univariable logistic regression models were included in multivariable logistic regression models built using stepwise forward-selection. To account for potential hierarchical clustering of data due to multi-cat households these were extended to two-level random intercept models. Models were compared using Wald test p-values.
Results:
Clustering had no impact on the analysis. The best fitting multivariable logistic regression model identified two risk factors that independently doubled the risk of feline obesity developing at 12.5 – 13 months of age: feeding dry food as the only or major (≥50%) type of food in the diet at 6.5 – 7 and 12.5 – 13 months of age and restricted or no outdoor access at 12.5 – 13 months of age.
Conclusions:
Results highlight the importance of a cat's early environment in the risk of obesity developing in early adulthood. The amount of food fed, opportunities for exercise and BCS of cats with no or restricted outdoor access and those fed a dry diet should be monitored to reduce the risk of overweight/obesity developing.
Relevance:
Obesity is considered the second most common health problem in pet cats in developed countries. Identifying these risk factors will enable more effective preventative strategies to be developed.

076

Analytical epidemiology of hematuric struvite crystalluria in cats

Chika C. Okafor[1], David L. Pearl[2], Sandra L. Lefebvre[3], Shauna L. Blois[4], Mingyin Yang[3], Mansen Wang[3], Elizabeth M. Lund[3], Cate E. Dewey[2], [1]The University of Tennessee, Knoxville, TN, [2]University of Guelph, Guelph, ON, Canada; [3]Banfield Pet Hospital, Portland, OR, [4]University of Guelph, Guelph, ON, Canada. Contact: okaforch@utk.edu

Purpose: To identify demographic and clinical factors associated with diagnosis of hematuric struvite crystalluria in cats seen at general care veterinary hospitals in the United States and to compare these factors with those identified previously for struvite urolithiasis.
Methods: Electronic medical records of all cats evaluated at 790 general care veterinary hospitals in the United States between October 2007 and December 2011 were reviewed to identify cats that developed hematuric struvite crystalluria (n = 4,032) and control cats with neither history of hematuria nor crystalluria (n = 8,064). Demographic information extracted included diet, age, sex, neuter status, breed, hospital location, and date of diagnosis. Clinical information extracted included urinalysis results, and history of cystitis and diabetes mellitus. Potential risk factors were assessed with univariable and multivariable logistic regression analyses.
Results: Hematuric struvite crystalluria in cats was significantly (p 30 mg/dL, and ketone concentration ≥ 5 mg/dL.
Conclusions:
Hematuric struvite crystalluria and struvite urolithiasis in cats share similar urinary risk factors. However, males had significantly higher odds of the former condition whereas females were at higher risk of the latter. Hence, the diagnosis of hematuric struvite crystalluria may not necessarily predispose cats to struvite urolithiasis or any such predisposition could be occurring in female cats only.
Relevance: Cystitis screening and treatment in cats may be useful in reducing or preventing hematuric struvite crystalluria.

077

Using quantitative bias analysis to estimate the magnitude and direction of outcome misclassification bias in a cohort study of canine epilepsy

Ane Nodtvedt, Norwegain University of Life Sciences, Oslo, Norway. Contact: ane.nodtvedt@nmbu.no

Purpose: The incidence rate of canine epilepsy was estimated based on a Swedish pet-insurance database (Heske et al. 2014, a). The incidence rate ratio (IRR) for the north versus the rest of the country was 0.49 (95% CI 0.44-0.55). The positive predictive value of the diagnosis in the same database was determined by validation against patient chart records (Heske et al. 2014, b). The sensitivity and specificity of the insurance database versus practice records is unknown but must be assumed to be < 100% and therefore likely to introduce misclassification bias of the outcome. Because the access to veterinary specialists will vary by region, this bias might be differential. The aim of the study was therefore to estimate the magnitude and direction of bias introduced by misclassification of the outcome on the IRR of canine epilepsy by region. Methods: A quantitative bias analysis (QBA) was performed, using a probabilistic approach with trapezoidal distributions for Se and Sp. The specificity was assumed to be high (min: 0.90, mode 1: 0.93, mode 2: 0.96, max: 0.99), while the sensitivity was lower and more uncertain (min: 0.50, mode 1: 0.60, mode 2: 0.70, max: 0.80) Furthermore, the sensitivity was assumed to be lower in the northern part of Sweden because of the lower density of veterinary clinics (min: 0.40, mode 1: 0.50, mode 2: 0.60, max: 0.70). The spreadsheet model described by Lash et al. (2009) was used for the bias analysis, and run with 10.000 simulations in Excel on a sample of 2000 dogs, equally distributed between north/rest of Sweden. Results: The observed, uncorrected RR was 0.50 (95% CI 0.38-0.66). When accounting for the misclassification of disease status, the median RR for north was 0.31 (simulation interval: 2.5th percentile 0.02-97.5th percentile 0.87). Conclusion: The magnitude of the effect of misclassification bias on the association between north and the incidence of canine epilepsy was substantial, but the direction of the effect remained the same. Relevance: The QBA provided a practical method of determining size and direction of misclassification bias.

078

Comparing the prevalence of, and agreement between, veterinary and owner-reported clinical signs associated with active cases of equine laminitis in Great Britain.

Danica Pollard[1], Claire E. Wylie[2], Kristien L. P. Verheyen[3], Jonathan R. Newton[1], [1]Animal Health Trust, Newmarket, United Kingdom; [2]Rossdales Equine Hospital, Newmarket, United Kingdom; [3]Royal Veterinary College, Hatfield, United Kingdom. Contact: danica.pollard@aht.org.uk

Purpose:
Recent epidemiological studies of equine laminitis involving first opinion veterinary practices may underestimate true disease frequency as owner-recognised laminitis cases not attended by a veterinarian would be excluded. This study aimed to evaluate owner recognition of equine laminitis by comparing data from cases including both owner-reported and attending veterinarian information.
Methods:
Twenty six veterinary practices were asked to submit purpose-designed laminitis reporting forms (LRFs) for owner-suspected and/or veterinary-confirmed cases of active laminitis attended. Owners and veterinarians independently reported clinical signs via separate LRFs. Paired owner and veterinary LRFs were submitted when owners suspected the horse had laminitis, even if it was not the final veterinary diagnosis. Veterinary LRFs only were submitted when the owner did not suspect laminitis, but it was the final veterinary diagnosis. McNemar tests and Kappa statistics assessed differences in the prevalence of, and agreement between, owner- and veterinary-reported clinical signs.
Results:
Fourteen (53.8%) practices submitted veterinary LRFs, reporting 69 laminitis cases, of which 36 were owner-suspected (52.2%). Paired owner and veterinary LRFs were returned for 32 cases. No 'false positive' cases of owner-suspected laminitis not confirmed by the veterinarian were reported. The only significant differences identified were that veterinarians more frequently reported lameness at walk and difficulty turning (P=0.03) while owners more frequently reported increased hoof temperature (P=0.02). Significant agreement was found for 52% of owner- and veterinary-reported clinical signs pertaining to lameness, stance and abnormalities in the affected feet. Agreement for the majority of clinical signs (10/14) ranged from moderate (Kappa 0.43, P=0.005) to substantial (Kappa 0.74, P<0.001).
Conclusions:
Considerable agreement existed between owner- and veterinary-reported clinical signs of laminitis.
Relevance:
These preliminary results provide some confidence in use of owner-reported data for epidemiological studies of equine laminitis.

079

World Health Organization estimates of the global and regional disease burden of 11 foodborne parasitic diseases, 2010

Paul R. Torgerson[1], Brecht Devleesschauwer[2,3,4], Niko Speybroeck[5], Nicolas Praet[6], Arve L. Willingham[7], Fumiko Kasuga[8], Mohammad B. Rokni[9], Xiao-Nong Zhou[10], Eric M. Fevre[11], Banchob Sripa[12], Thomas Furst[13], Christine M. Budke[14], Hélène Carabin[15], Martyn D. Kirk[16], Frederick J. Angulo[17], Arie Havelaar[18,19,20], Nilanthi de Silva[21],
[1]University of Zürich, Zurich, Switzerland; [2]University of Ghent, Ghent, Belgium; [3]Université catholique de Louvain, Brussels, Belgium; [4]Institute of Tropical Medicine, Antwerp, Belgium; [5]Université catholique de Louvain, Brussels, Belgium; [6]Institute of Tropical Medicine, Antwerp, Belgium; [7]Ross University, Basseterre, Saint Kitts and Nevis; [8]National Institute of Health Sciences, Tokyo, Japan; [9]University of Tehran, Tehran, Iran, Islamic Republic of; [10]Chinese Center for Disease Control and Prevention, Shanghai, China; [11]University of Liverpool, Liverpool, United Kingdom; [12]Khon Kaen University, Kohn Kaen, Thailand; [13]Imperial College, London, United Kingdom; [14]Texas A&M University, College Station, TX, [15]University of Oklahoma Health Sciences Center, Oklahoma City, OK, [16]The Australian National University, Canberra, Australia; [17]Centers for Disease Control and Prevention, Atlanta, GA, [18]Emerging Pathogens Institute, Gainesville, FL, [19]University of Utrecht, Utrecht, Netherlands; [20]National Institute for Public Health and the Environment, Bilthoven, Netherlands; [21]University of Kelaniya, Ragama, Sri Lanka.
Contact: paul.torgerson@access.uzh.ch

Purpose: Foodborne diseases are globally important. We present the first estimates of the global and regional human disease burden of 10 helminth diseases and toxoplasmosis attributed to contaminated food.
Methods: Data were abstracted from systematic reviews, national surveillance data, journal articles, and national estimates of foodborne diseases, to estimate the number of infections, sequelae, deaths, and Disability Adjusted Life Years (DALYs), by age and World Heath Organization region for 2010.
Results: These parasitic disease, resulted in 48.4 million cases (Uncertainty intervals [UI] of 43.4 million-79.0 million) and 59,724 (UI: 48,017-83,616) deaths annually resulting in 8.78 million (UI: 7.62 million - 12.51 million) million DALYs. We estimated that 48% (UI: 38%-56%) of cases of these parasitic diseases were foodborne, resulting in 76% (UI: 65%-81%) of the DALYs attributable to these diseases. Overall, foodborne parasitic disease, excluding enteric protozoa, caused an estimated 23.2 million(UI: 18.2 million - 38.1 million) cases and 45,927 (UI: 34,763 - 59,933) deaths annually resulting in an estimated 6.64 million (UI 5.61 million - 8.41 million) DALYs. Foodborne ascaris infection (12.3 million cases, UI: 8.29 million - 22.0 million) and foodborne toxoplasmosis (10.3 million cases, UI: 7.40million - 14.9 million) were the commonest foodborne parasitic diseases. Human cysticercosis with 2.78 million DALYs (UI: 2.14 million - 3.61 million), foodborne trematodosis with 2.01 million DALYs (UI: 1.65million - 2.48 million) and foodborne toxoplasmosis with 825,000 DALYs (UI: 561,000 - 1.26 million) resulted in the highest DALYs.
Conclusions: These estimates represent an important step forward in understanding the impact of foodborne diseases globally and regionally. The disease burden due to most foodborne parasites is highly focal and results in significant morbidity and mortality among vulnerable populations.
Relevance: While gaps exist, we believe the estimates presented here are the best current source of guidance to support decision makers when allocating resources for intervention, and for research initiatives for foodborne parasitic diseases.

080

Raw milk consumption in the US: how safe is it?

Solenne Costard, Huybert Groenendaal, Francisco J. Zagmutt, EpiX Analytics, Boulder, CO, Contact: scostard@epixanalytics.com

Purpose:
Raw milk consumption is increasingly popular in the US. Its potential contamination with pathogens poses a risk of foodborne illnesses. The objectives of this study were to 1) estimate the current risk of illness and hospitalization due to the consumption of milk and cheese contaminated with Shiga toxin-producing *Escherichia coli*, *Salmonella spp*., *Listeria monocytogenes* and *Campylobacter spp*., 2) estimate the excess risk associated with unpasteurized products, and 3) assess the public health impact of potential scenarios of consumption changes in the US.
Methods:
A novel stochastic risk attribution model developed for the study relied on historical outbreak reports, national statistics and surveys, and published studies.
Results:
In the US, dairy consumption causes on average more than 6,000 illnesses and 25 hospitalizations yearly, mostly due to *Campylobacter spp*. Eighty-nine percent of these illnesses are due to unpasteurized milk and cheese consumed by just 3% and 1.6% of the population, respectively. The mean annualized risks of illness and hospitalization were 237 (95%CrI: 147 - 371) and 84 (59 - 119) times higher for consumers of raw dairy products, respectively.
Raw milk consumption doubled between the mid-1990s and the mid-2000s. If it was to double again, the average number of yearly illnesses would increase by 89%. Better pathogen control on raw milk farms would reduce the disease burden, but not prevent it altogether.
In conclusion, the consumption of raw milk and cheese in the US is associated with a disease risk over 200-fold higher than for pasteurized products, and causes almost 90% of annual illnesses due to dairy consumption. Milk-borne illnesses (and hospitalizations) will increase steadily as raw milk popularity grows, and is likely to be largely driven by campylobacteriosis.
Relevance:
The present study highlights the US disease risk burden from milk and cheese consumption, and estimate the impact of further raw milk consumption increase. The study results have potential implications for policy management and prevention efforts on this hotly debated issue.

081

Using a value chain framework for food safety assessment of broiler and indigenous chicken meat systems of Nairobi

Maud Carron[1], Pablo Alarcon[1], Barbara Haesler[1], Eric Fevre[2], Maurice Karani[2], Patrick Muinde[2], James Akoko[2], Joshua Onono[3], Jonathan Rushton[1], [1]Royal Veterinary College, Hatfield, Hertfordshire, United Kingdom; [2]International Livestock Research Institute, Nairobi, Kenya; [3]University of Nairobi, Nairobi, Kenya. Contact: mcarron@rvc.ac.uk

Purpose:
Research on livestock food systems in developing countries remains limited, yet this context needs to be understood to investigate the epidemiology of zoonoses. The aim of this study was to use a value chain framework to characterize the broiler and indigenous chicken meat systems of Nairobi and their food safety risks.
Methods:
Using such a framework for food safety characterisation at system level is novel and has significant potential in developing countries. Data collection involved 18 focus group discussions and 236 interviews with various poultry meat value chain stakeholders in Nairobi. Analysis included chain mapping and identification of governance and food safety challenges.
Results:
The study identified 10 chain profiles, characterising the broiler and indigenous chicken systems, and production-retailing continuum.
Food safety risks identified were related to lack of biosecurity, cold chain and access to water, poor cleaning and hygiene practices, consumption of sick animals, significant environmental contamination of by-products, and lack of inspection at farm slaughter.
Large companies dominated the governance of the broiler system through the control of day-old chick production. Overall government control was relatively weak leading to minimal official regulatory enforcement. Large companies and brokers were identified as dominant groups in market information dissemination and price setting. No dominant group was identified for indigenous chicken profiles, farming being at household level for local consumption, with quasi non-existent regulations. Lack of industry association was system-wide, creating a barrier for access to capital. Other system barriers included lack of space and expertise, leading to poor infrastructure and limited ability to implement effective hygienic measures.
Conclusions and relevance:
Optimal food safety and disease control strategies should consider the structure of the poultry meat system and stakeholder interactions to ensure effective programmes. This study provides a new perspective for epidemiologists and public health officers to address food safety risks in full understanding of the food system context.

082

Simulation study evaluating the ability of the USDA-FSIS poultry inspection system to predict the risk of consumer exposure to Salmonella from chicken

Randall Singer[1], Shaun Kennedy[2], [1]University of Minnesota, Saint Paul, MN, [2]The Food Systems Institute, Saint Paul, MN, Contact: singe024@umn.edu

Purpose: *Salmonella* continues to be a significant public health concern in the U.S., and although the prevalence of *Salmonella* has decreased in many meat products, salmonellosis rates in the U.S. have remained steady since 2003. The objective of this study was to evaluate whether current or planned inspection of poultry by USDA-FSIS is likely to be a sufficient public health indicator of consumers' risk of exposure to *Salmonella* on chicken distributed into commerce.
Methods: Models were developed to represent the introduction pathways, persistence and heterogeneity of *Salmonella* in poultry systems and the resulting prevalence and microbial load in chicken flocks entering normally functioning processing plants. *Salmonella* prevalence and load on chicken carcasses and in the further processed products were estimated from data obtained from U.S. broiler companies and from USDA-FSIS baseline testing.
Results: The results of the simulations demonstrated that the new inspection strategy being implemented by USDA-FSIS is appropriate for identifying systemic and consistent problems but is unlikely to recognize temporally specific spikes where substantial amounts of product are entering commerce with levels of *Salmonella* that would be considered higher risk due to microbial loads above a typical infectious dose.
Conclusions: The data show that high *Salmonella* loads, not prevalence, entering the plant are temporally clustered, and consequently, an inspection strategy based on presence/absence with a limited sampling frequency is likely to miss temporal clustering of high *Salmonella* load production birds. Given that poultry production companies' management of *Salmonella* is based on both public health risk and "regulatory risk," a company could pass its regulatory performance standard testing and still be putting a significant amount of contaminated product into commerce.
Relevance: This model was based on *Salmonella* on raw products that are not-ready-to-eat. This recognizes that even though all risk would theoretically be eliminated by proper food handling and cooking, neither poultry companies nor regulatory authorities can assume the efficacy of consumer behavior.

083

Value chain analysis as a tool for assessing food safety risks in the Nairobi pork food system

Patrick Muinde, International Livestock Research Institute, Nairobi, Kenya. Contact: P.Muinde@cgiar.org

Purpose
In Nairobi, with 3.1 million consumers and 30,000 pigs, the pork system may represents a major source of zoonotic pathogens. Yet, this system and its public health risks have not been described. The study used value chain analysis, a well-known method in economics, to investigate zoonosis and food safety risks practices in the Nairobi pork food system.
Methods
A cross-sectional study of the Nairobi pork system collected data through 25 focus group discussions and 436 individual interviews with farmers, traders, abattoir owners, large companies' managers, retailers, government officers and consumers. Data were analysed to identify, describe and quantify the main pork chain profiles, their associated zoonosis and food safety risks practices and their link to governance, the distribution of benefits and barriers to improving the system.
Results
Six pork chain profiles were identified with the 'large integrated company' profile accounting for 62% of pork marketed through abattoirs. Pigs in slums were channelled directly to consumers and butchers or through less integrated markets. Main zoonosis and food safety risk practices for city pig keepers were: handling and consumption of sick pigs; and swill and scavenging feeding. In less integrated abattoirs these risks were: lack of traceability, cold chain systems and adequate cleaning and sterilising practices and equipment. For the retailers, there was a lack of hygiene linked to poor infrastructure, scarcity of water and cleaning practices. Large companies govern the high end market for pork where barriers to improvements were less. In the lower end poor profit margins and unequal benefit distribution led to issues on around investments in infrastructure, cold chains and human capacity building plus difficulties with meeting feeding and animal health costs.
Conclusions
This study identified the main zoonoses and food safety risk practices and the people involved in risk taking activities to help future control programmes in the Nairobi pork system.
Relevance
The integration of value chain and analysis of risks practices proved useful and represent the way forward for epidemiologist working in developing countries.

084

Enhancing antimicrobial stewardship: predictors of selective antimicrobial use practices among dairy calf producers

Greg Habing, Gustavo Schuenemann, Catherine Djordjevic, The Ohio State University, Columbus, OH, Contact: habing.4@osu.edu

Purpose:
Calf-raising operations provide a unique microbial niche, where immature intestinal flora, dense animal populations, and frequent application of antimicrobials may facilitate the emergence of antimicrobial resistant pathogens. In the U.S.A., producers report that 18% of calves receive an antimicrobial for diarrhea prior to weaning, often with antimicrobials designated as “critically important” to human medicine. The overall objective for this research was to understand the decision criteria for antimicrobial use (AMU) for calf diarrhea. We hypothesized that selective AMU is associated with herd-level predictors, including the presence of veterinarian-written treatment protocols and producer attitudes about the impact of AMU in livestock.
Methods:
Surveys were mailed to 1,100 randomly selected Grade A dairy producers in Ohio and Michigan, USA. Producers were asked to indicate current treatment practices for a series of case descriptions with increasing severity. Based on the responses, producers were categorized as applying antimicrobials for all, select, or none of the described cases. The survey included potential predictors, including herd size, age, education, veterinarian-written protocols, and attitudes about the public health impact of AMU in livestock.
Results:
In total, 481 (44%) producers returned the survey, and 10%, 55%, 30% of producers reported applying antimicrobials to all, select, or none of the cases described in the survey, respectively. Based on initial ordinal univariable logistic regression, more selective therapy was significantly ($P < 0.05$) associated with a higher level of concern about the public health impact of AMU. However, selective therapy did not have a univariable association with herd size, age, education level, or the presence of a veterinarian written protocol. Results of a multivariable model will be presented.
Conclusions:
The reported AMU practices of dairy calf producers were significantly associated with producer attitudes about the impact of AMU on public health.
Relevance: These data are useful to design methods to improve antimicrobial stewardship among dairy calf producers.

085

Delivery of farm animal post-mortem examinations for surveillance through an academic-private partnership in England

Alasdair J. C. Cook[1], Ingrid E. M. den Uijl[1], James Wiseman[1], Johanna C. Penell[1], Sara Robertson[2], [1]University of Surrey, GUILDFORD, United Kingdom; [2]Animal & Plant Health Agency (APHA), Addlestone, United Kingdom. Contact: alasdair.j.cook@surrey.ac.uk

Purpose: Defra conducted a review of surveillance of farmed livestock to reduce costs and improve evidence on new or re-emerging threats to animal health for policy-makers. This review led to a procurement exercise for delivery of post-mortem examinations (PMEs) of farmed livestock on behalf of Defra's Animal & Plant Health Agency (APHA). The University of Surrey (UoS) in collaboration with a private veterinary practice was awarded a contract to deliver surveillance PMEs for several areas of England.

Methods: To fulfil this contract, UoS operates a new booking in, data collection and reporting system. PMEs are requested by private veterinary surgeons and subjected to a triage process to ensure the submission is of surveillance value. Relevant data, including farm address, animal identity and clinical signs are captured on a dedicated UoS database Carcases are directed to the most appropriate PME site, which may be at UoS or at one of a number of Fallen Stock sites. The PME is conducted by a trained veterinary surgeon and the results are entered onto PathPal ™ an android app developed by UoS and then transmitted to the UoS database. Reports for the individual case are generated from the database and regular summaries are automatically submitted to APHA for inclusion in the national surveillance database.

Results: The service began in February 2015 and once fully operational , is expected to receive around 100 PME submissions each month. It is intended that the same process will also manage a private PME service for all submission to the UoS own pathology centre.

Conclusions: The PME surveillance service demonstrates the capacity for an academic-private collaboration to contribute to national surveillance of animal health. Engagement with third parties has enabled Government to benefit from an innovative approach to surveillance including the automation of data collection and submission via PathPal™.

Relevance: The UoS approach may serve as a model for delivery of surveillance in other countries. In addition, the PathPal™ app could be used by other vets whether in private practice, research or Government to ensure the systematic capture of gross PME findings.

086

Water public health in Vietnam: small scale livestock and mitigation of emerging infectious diseases.

David Hall, **Quynh Ba Le**, University of Calgary, Calgary, AB, Canada. Contact: qble@ucalgary.ca

Purpose:
Our research examined the relation between water public health, small scale integrated farming, limited biosecurity, and mitigation of emerging infectious diseases (EIDs) in Vietnam.
Methods:
We collected data from 600 farms in North and South Vietnam (Thai Binh and An Giang provinces) using questionnaires, semi-structured interviews, and water quality testing (E. coli, turbidity, and pH). Water samples were collected from participants' wells or rain water cisterns and analyzed in government laboratories using WHO standardized methods. Probit analysis was used to investigate the association of demographic variables with E. coli levels in drinking water and EID mitigation strategies.
Results:
The typical profile of our participants was a 45 year old married individual with two children, six or seven years of formal education, low income (c. $1200 p.a.), and nine years farming experience. Farmers raised fish, poultry, a few pigs or cattle, and some crops (e.g., rice). Most participants had basic awareness of avian influenza prevention, but very limited knowledge of water-borne diseases such as E. coli. Respondents were predominantly male (71%). More than 90% of participants claimed they boiled and/or filtered their water used for drinking (rain or well water). Water test results revealed that more than 80% of samples contained unacceptable levels of E. coli (10 to several thousand cfu's). Probit analysis revealed significant association of demographic variables with E. coli levels in drinking water, including age ($p<0.01$), presence of and number of livestock on farm ($p<0.01$), history of vaccinating poultry against H5N1 ($p<0.05$), and declared interest in public health training ($p<0.01$).
Conclusions:
Levels of E. coli in respondents' drinking water are unacceptably high. They have a basic understanding of public health concepts but are not using preventive practices to mitigate waterborne emerging infectious disease. Increased awareness of water public health and livestock waste management is recommended.
Relevance:
These findings are relevant for public health programs targeting small scale mixed farms in Southeast Asia.

087

Poultry trading networks in Bangladesh: identification of market's trading characteristics and implications for poultry virus spread and targeted control measures.

Natalie R. S. Moyen[1], Garba Ahmed[2], Suman Gupta[2], Rahman Khan[2], Taufiq Imtiaz Khan[2], Nitish Debnath[2], Mat Yamage[2], Dirk Pfeiffer[1], Guillaume Fournie[1], [1]Veterinary Epidemiology, Economics and Public Health group, Royal Veterinary College, London, United Kingdom; [2]Emergency Centre for Transboundary Animal Diseases, Food and Agriculture Organisation of the United Nations, Dhaka, Bangladesh. Contact: nmoyen3@rvc.ac.uk

Purpose: Avian influenza (AI) is endemic in Bangladesh and poultry is mainly sold at live bird markets (LBM), which have an important role in spreading viruses through human and poultry populations. With a growing human population, poultry consumption is expected to continue to increase, and, with it, the quantities of poultry traded at LBM across the country. The network structure connecting the LBMs is likely to be extremely heterogeneous, and being able to identify LBMs which are 'central' to the network will allow design of more effective surveillance and control strategies.
Methods: A cross-sectional survey of 161 LBM across Bangladesh, was carried out to describe the network of contacts between LBMs and poultry farming areas resulting from the trade of poultry. Over 600 poultry traders, from 18 of 64 districts, were interviewed.
Results: Supply was diverse in terms of type of supplier and geographical origin: the LBMs interviewed were supplied by 44 districts. Although 50% of them had a catchment area of 50km or less, 7% sold poultry produced more than 200km away. Almost 50% of the LBMs interviewed had 1 or 2 different suppliers: either 1 or 2 LBMs, or 1 or 2 poultry farming sub-districts, but 3% of the LBMs had at least 10 different suppliers. Sales to poultry traders operating in other LBMs were identified in only 16 of the LBMs in this study. These markets were generally the ones supplied by the greatest number of poultry, and by the greatest number of LBMs and farms. Additionally, these LBMs, also had the largest catchment areas. More than 90% of the LBMs and the poultry farming sub-districts are connected via this trading network, linking distant districts and, impacting the risk of spread of AI throughout the country.
Conclusions: Our study confirms the important role played by LBMs in connecting 2/3 of the districts, in all 7 divisions of Bangladesh. However, heterogeneous supplying characteristics of LBMs suggest that they are at different risks of disseminating virus throughout the poultry trade network.
Relevance: Inclusion of network parameters as risk factors for AI dissemination identified in this study could enhance implementation of targeted surveillance and control measures.

088

Poultry movement in the south of Vietnam, 2009 - 2010

M. A. Stevenson[1], L. V. Nguyen[2], P. V. Dong[3], [1]The University of Melbourne, Parkville Victoria, Australia; [2]Ministry of Agriculture and Rural Development, Hanoi, Viet Nam; [3]Ministry of Agriculture and Rural Development, Hanoi, Viet Nam. Contact: mark.stevenson1@unimelb.edu.au

Purpose:
While complete enumeration of poultry movement networks allows animal health authorities to identify nodes (physical locations) that are major sources and destinations of traded birds and therefore a risk in terms of receiving and distributing infectious diseases such as highly pathogenic avian influenza, these activities are expensive in terms of time and cost, particularly for developing countries. A more practical approach is to conduct a cross-sectional study of poultry movements, allowing node characteristics that render them more likely to receive or distribute poultry to be identified.
Methods:
A cross-sectional study to document commune-to-commune poultry movement events in 19 provinces in the south of Vietnam was carried out between September 2009 and June 2010. The data were analysed as a social network and an exponential-family random graph model developed to quantify the influence of commune-level characteristics on the probability of a movement connection existing between two communes.
Results:
A total of 26,490 commune-to-commune movement events via roads were recorded over the 10 month study period. This involved a total of 3.15 million chickens and 18.14 million ducks. Communes were more likely to be connected if they were urban. As the number of humans per commune increased the odds of a commune-to-commune connection decreased. Increases in the number of poultry-owning households per commune increased the odds of a commune-to-commune connection.
Conclusions:
The number of duck movements and the total number of individual ducks moved were 5 and 6 times greater (respectively) than that recorded for chickens. Poultry were more likely to be moved between communes with relatively large numbers of poultry-owning households. In contrast, communes with large numbers of people were less likely to be connected by poultry movement events.
Relevance:
Assuming a causal relationship exists between a commune's connectivity within a poultry movement network and HPAI H5N1 risk, communes identified as being likely to be connected within a network should be targeted for HPAI H5N1 control and surveillance.

089

Livestock disease spread through animal movements: a temporal network approach

Hartmut H. K. Lentz[1], Thomas Selhorst[2], Franz J. Conraths[1], [1]Friedrich-Loeffler-Institute, Greifswald, Germany; [2]Federal Institute for Risk Assessment, Berlin, Germany. Contact: lentz.h@gmail.com

Livestock trade forms a network of agricultural holdings connected via trade of live animals. These networks are often treated as static objects, although trade is in fact strongly time-dependent. This has a dramatic impact on the possible spreading patterns for infectious diseases.
A static (aggregated) trade network is constructed as follows: if two nodes are connected directly to each other in a time-dependent network, the same connection is present in the static network. A fundamental difference between the static and the time dependent view however, is the consideration of paths, i.e. indirect connections over more than one edge. Concerning paths, the causality of the edges used plays an essential role. In an aggregated network, paths can seem causal, although they do not follow a time-respecting sequence of edges in the real system. This leads to a systematic overestimation of outbreak sizes, if trade networks are treated as static.
We introduce a new method, which allows for the computation of the total causal path structure of a temporal network using the adjacency matrices of its snapshots. In addition, information about the timescales required for path traversal can be derived from the step-by-step derivation of accessibility. This procedure directly yields the distribution of shortest path durations in a temporal network. In addition, we define the new measure causal fidelity that compares the number of paths in a temporal network with its aggregated counterpart. The methods presented here require only basic knowledge linear algebra and can be implemented efficiently. Their capability is demonstrated for livestock trade networks in Germany.
Literature: H Lentz, T Selhorst, and I Sokolov, Phys. Rev. Lett., 2013.

090

Influence of disease control zones on dairy cattle movement patterns

Arata Hidano[1], Carolyn Gates[1], Mark Stevenson[2], Mark Bosson[3], Tim Carpenter[1], [1]EpiCentre, Massey University, Palmerston North, New Zealand; [2]University of Melbourne, Melbourne, Australia; [3]OSPRI, Hamilton, New Zealand. Contact: A.Hidano@massey.ac.nz

Purpose:
Many countries with endemic bovine tuberculosis (bTB) have established control zones around regions where farms with higher infection risk exist. This can significantly influence the structure of cattle movement networks, which has important implications for modelling disease transmission dynamics. Here, movement data from dairy herds in New Zealand were analysed (1) to explore the spatial relationships between network trade communities and the five major disease control areas (DCA) and (2) to identify demographic factors that predict community membership.

Methods:
Dairy cattle movement data from July 2008 and June 2011 were retrieved from the Livestock Improvement Corporation (LIC) database. The movement data were aggregated by year and the Clauset-Newman-Moore algorithm for directed networks was then used to detect communities amongst the LIC dairy farms. The association between community membership and DCA was analysed using Mantel test. A multinomial regression model was constructed to predict the major community membership.

Results:
The geographical distributions of the major network communities were relatively stable over time and we restricted the remaining analyses to data from July 2009 through June 2010. During this period, 747,802 individual animals were moved between the 12,288 LIC farms in 42,149 distinct batch movements. The algorithm detected 408 communities, although only 35 of these communities contained more than 10 farms and the largest five communities included 9,508 farms (77.4%) of the studied population. Farms in the same DCA were more likely to be in the same community ($p<0.001$). In addition to DCA, numbers of culling and new calves born in the previous year were useful predictors for the major community membership.

Conclusions:
The community structure of dairy cattle movements in New Zealand is strongly influenced by DCA. However, there is still significant trade between farms in different DCAs, which may be contributing to the spread of bTB.

Relevance:
It is important to account for network community structure when planning disease control strategies and when developing rules to generate cattle movement patterns in disease simulation models.

091

Network analysis of direct and indirect contacts between dairy farms in the Province of Parma (Emilia-Romagna, IT)

Gianluigi Rossi[1], Stefano Pongolini[1], Giulio A. De Leo[2], Mauro Cavalca[3], Luca Zarenghi[3], Silvano Natalini[4], Luca Bolzoni[1], [1]Istituto Zooprofilattico della Lombardia e dell'Emilia Romagna, Parma, Italy; [2]Stanford University, Monterey, CA, [3]AUSL di Parma, Parma, Italy; [4]Regione Emilia-Romagna, Bologna, Italy.
Contact: gianluigi.rossi@izsler.it

Although live animals exchange is considered the most effective route of disease transmission between farms, the spread through contaminated equipment, vehicles, or personnel proved to be crucial for many epidemics, included the 2001 foot-and-mouth disease in the UK or the worldwide spread of avian flu in 2000s decade. Among farm professional visitors, veterinarians are considered particularly dangerous for disease spread due to their close contact with animals. While between-farm direct contacts (i.e. animals exchange) have been studied in depth over the past 20 years, indirect contacts (e.g. through veterinarians or other operators) have been often overlooked, mainly because of the challenging task represented by data retrieval.
Our work aims to understand the role of indirect contacts due to veterinarians' visits in a potential epidemic spread. Starting from 1349 dairy farms of the Italian Province of Parma, we build two contact networks using data on cattle exchange (direct contacts), and government and private veterinarians (indirect contacts).
We employ network analysis techniques to evaluate network features associated to the two considered routes of transmission. Moreover, we identify farms acting as a super-spreader in the direct contact network and in the indirect one. In particular, we compute for each farm the infectious chain under different assumptions on farm infectious period. Finally, we evaluate the impact of indirect contacts on the overall contact network (which includes both direct and indirect) weighted for the difference in the infective potential with respect to direct contacts.
Direct and indirect networks show non-trivial differences, in particular with respect to the number of connections, the contacts' frequency, and the identity of farms acting as super-spreaders. Furthermore, our results show that, despite their expected low infection probability, the contribution of indirect contacts to a potential epidemic spread can be critical.
Therefore, our work highlights the significant role of indirect contacts, in particular their importance in designing effective surveillance and control strategies.

092

Temporal and spatial characterization of the network of live Atlantic salmon movements in Ireland: implications for disease prevention and control

Tadaishi Y. Rodriguez[1], Simon J. More[2], Fiona Geoghegan[3], Catherine McManus[4], Ashley E. Hill[1], Beatriz Martinez-Lopez[1], [1]University of California Davis, Davis, CA, [2]University College Dublin, Dublin, Ireland; [3]Marine Institute, Rinville, Ireland; [4]Marine Harvest Ireland, Rinmore, Ireland. Contact: tadaishi@gmail.com

Live fish movement has been deemed as having an important role in the transmission of infectious diseases both locally and globally. For that reason, the characterization of the patterns and dynamics of live fish movements in a region or country provides not only a better understanding of how fish diseases can spread but also how to allocate interventions for more cost effective disease prevention and control programs.

Here we analyzed the structure and dynamics of live Atlantic salmon movement network (ASN) in Ireland from 2009 to 2013, using social network analysis and spatial epidemiology methods.

During the study period there were 81 nodes and 494 shipments, corresponding to 71.6 mill fish moved. The number of nodes of the ASN decreased from 59 to 48 while the number of edges and fish moved per year increased from 79 to 104 edges and 11.5 mill to 15.2 mill fish moved. The ASN was disconnected exhibiting a marked seasonality associated to the salmon production cycle.

For every year the ASN exhibited both small-world and scale-free topologies. There was an increase in average path length and clustering coefficient during the study period. Only few sites were highly connected (hubs). Community detection algorithms found a relatively stable community structure over the years, indicating that ASN form a single country-wide compartment. Significant spatial clusters were found for different centrality measures, indicating that hubs tend to aggregate in specific regions of the country. Finally, we have characterized the biosecurity of these hubs in an attempt to further estimate their potential for disease introduction and spread to the rest of the ASN.

The results of these analyses will be used by local stakeholders as an input for risk assessments and for the design and implementation of risk based disease surveillance and control strategies.

093

Bovine tuberculosis in cattle and red deer in Southern Bavaria, Germany - can network analysis explain the routes of transmission?

Julia Boenchendorf[1], **Hartmut H. K. Lentz**[2], Lena Straub[3], Johannes Bracher[4], Sarah Schärrer[5], Mathias Büttner[6], Gabriela Knubben-Schweizer[1], Carola Sauter-Louis[7], [1]Ludwig-Maximilians-University, Oberschleissheim, Germany; [2]Friedrich-Loeffler-Institut, Greifswald – Isle of Riems, Germany; [3]Ludwig-Maximilians-University, Munich, Germany; [4]Ludwig-Maximilians-University, Munich, Germany; [5]Federal Food Safety and Veterinary Office, Bern, Switzerland; [6]Bavarian Health and Food Safety Authority, Oberschleissheim, Germany; [7]Friedrich-Loeffler-Institut, Greifswald, Germany. Contact: Hartmut.Lentz@fli.bund.de

Purpose: Although bovine tuberculosis has been controlled in many European countries, it still plays a role in some European countries, especially due to wildlife reservoirs. Germany has achieved official TB-free status in 1997. Increasing numbers of disease outbreaks were reported in the region of Allgäu, South Germany, from the year 2000 onwards. The disease was observed in cattle and in wild-living red deer and results of DNA fingerprinting indicated a transmission both within species as well as across host species. However, the routes of transmission are not yet sufficiently understood. The purpose of this study was to gain more information about the epidemiology of bovine tuberculosis in that area.
Methods: Movement data of cattle from affected farms and the contacts with cattle from other herds were analysed retrospectively using network analyses. Network analyses are often used to describe trade networks, identifying farms that are potential spreaders of the disease. In our study we used network analysis to describe the spread and transmission of the disease amongst cattle, overlaying the geographical information of cattle grazing areas and locations of hunted deer. Movement data from 2010 to 2014 were obtained from the national cattle movement database (HI-Tier).
Results: Most farms were connected through cattle movements, especially through summer pasture farms grazing cattle from different herds. Such pastures are located in areas, which are also known to be the habitat of red deer. No information is available on direct contact between the two species, but indirect contact is highly likely in these areas.
Conclusions: Network analyses helped to understand the epidemiology of bovine tuberculosis in cattle in Southern Germany. In this context, trade contact with alpine summer pastures seemed to represent a hazard for cattle holdings. However, data on red deer was too sparse to show transmission patterns between red deer and cattle.
Relevance: Network analysis can provide valuable insights into possible connections between farms and transmission pathways.

094

Network analysis of swine value chain: towards efficient zoonotic disease surveillance programs in Vietnam

Eugenie Baudon[1], Tung Duy Dao[2], **Sophie Molia**[3], Leo L. Poon[4], Pham Thi Nga[2], Nguyen Viet Khong[2], Benjamin J. Cowling[4], Malik Peiris[4], Marisa Peyre[5], [1]The University of Hong Kong, CIRAD, Hong Kong, Hong Kong; [2]National Institute of Veterinary Research, Hanoi, Viet Nam; [3]CIRAD, Montpellier cedex 5, France; [4]The University of Hong Kong, Hong Kong, Hong Kong; [5]CIRAD, Montpellier, France. Contact: sophie.molia@cirad.fr

The occurrence of the H1N1 2009 pandemic demonstrated the importance of swine influenza (SI) surveillance, but a systematic surveillance is still lacking especially in less developed countries.
Purpose: The objective was to develop feasible and efficient surveillance protocols suitable to the swine production organization in Vietnam.
Methods: Based on a comprehensive study of the pig value chain in Northern Vietnam using participative methods and network analysis, different surveillance protocols for SI detection were implemented over a one-year period, with serological and virological testing of pigs.
Results: A total of 78 viruses were isolated at a large slaughterhouse where pigs originated mainly from commercial farms. No viruses were isolated from the other protocols focusing on the familial sector. Based on haemagglutinin and neuraminidase sequencing, the subtypes detected included 16 H1N1, 27 H3N2, and 35 H1N2 viruses related to H1N1pdm09, a H3N2 Korean triple reassortant virus, and H3N2 and H1N2 human-like SI viruses isolated in Southern Vietnam in 2010. Further sequencing of internal genes will be performed to identify reassortants. From ELISA results, seroprevalence was high in the slaughterhouses and low in young pigs at the market. Pigs in six out of 17 sentinel familial farms seroconverted during the study but no virus isolation was possible due to the lack of timely reporting of influenza-like illness by farmers. Pending HI test results will show if the viruses isolated in the commercial sector were circulating as well in the familial farms. Based on these observations and on the results of a pilot study carried out concurrently, the potential for the use of syndromic surveillance for virus isolation in the familial sector will be analyzed and discussed.
Conclusions: In Vietnam, no SI virus isolation has ever been successful in the familial sector despite high SI circulation. Surveillance at the large slaughterhouse has been maintained due to successful virus isolation and is a first step toward SI monitoring in Vietnam.
Relevance: The use of innovative methods such as participatory epidemiology and syndromic surveillance may be the key to enhance and sustain surveillance.

095

Evaluation of the trade patterns and social network structure of pig movements in the US and their association with PRRSV transmission.

Kyuyoung Lee[1], Dale Polson[2], Beatriz Martínez-López[1], [1]UC Davis, Davis, CA, [2]Boehringer Ingelheim Vetmedica, Ankeny, IA, Contact: pvmlee@ucdavis.edu

Purpose: The porcine reproductive and respiratory syndrome virus (PRRSV) is responsible of large economic losses in the US swine industry. Ongoing surveillance efforts to control and eradicate PRRSV in the US have provided large number of PRRSV sequences which, coupled with the high PRRSV genetic variability, allows to identify sites related epidemiologically (i.e. PRRSV small genetic distance, same restriction fragment and length polymorphism -RFLP-). However, fundamental questions remains unaddressed: which are the transmission routes that are mostly contributing to PRRSV transmission?, what is the specific role of pig movements in the introduction and spread of specific PRRSV RFLPs? In this study we aim to address the role of pig shipments in the transmission of different PRRSV RFLPs within and between systems using social network analysis (SNA).
Methods: We used more than 200 PRRSV sequences (> 30 RFLP) of open reading frame (ORF) 5 region from PCR-positive field samples and more than 150,000 pig movement records collected over 3 years in different US pig production systems. For each system, yearly directed and weighted networks were built with nodes being pig sites and links being the pig shipments. Each network was assessed for scale-free fitting a power-law distribution and small world properties. Centrality measures were computed for each site and trade communities (i.e. “groups of sites”) were identified using the “Walktrap” algorithm with links weighted on the number of pig moved per shipment.
Results: As a result, we identified groups of sites sharing similar PRRSV RFLPs (where a shared PRRS control program will be highly beneficial) and pig sites where pig movements play a key role for new PRRSV introduction and/or spread.
Conclusions and Relevance: Outcomes of this study will support risk-mitigation strategies to better prevent and control PRRSV transmission through pig shipments in the US.

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Spatio-temporal network analysis of pig movements in Great Britain: implications for disease transmission and control strategies

Claire Guinat[1], Anne Relun[2], Aaron Morris[3], Linda Dixon[4], Dirk Udo Pfeiffer[5], [1]Royal Veterinary College / Pirbright Institute, London, United Kingdom; [2]CIRAD, Montpellier, France; [3]Royal Veterinary College / APHA, London, United Kingdom; [4]Pirbright Institute, Pirbright, United Kingdom; [5]Royal Veterinary College, London, United Kingdom. Contact: cguinat@rvc.ac.uk

Animal movements represent an important means for disease transmission among animal holdings over large geographical distances. Therefore, understanding the dynamic patterns of animal movement networks is needed to inform models of disease spread and target control and risk-based surveillance strategies.

Here, we conduct a spatio-temporal analysis to explore pig movement networks throughout Great Britain (GB) over a 5-year period (2009-2013) with a view to identify spatial and temporal patterns, characterise the monthly network topology and identify trade communities. Descriptive statistics were initially generated including all premise types. A directed and weighted monthly network was then built, considering each premise (only farms, gathering areas and market premises) as a node and each daily pig movement between two premises as an edge.

Over the 5-year study period, the pig movements included 48,976 active premises and 888,613 movements, involving 64,121,604 pigs. Most of the movements originated from farms (96.0%) and gathering areas (3.8%) and were directed to slaughter houses (68.3%), farms (23.7%) and gathering areas (7.8%). The distance covered by 50%, 75% and 95% of the pig movements was 31km, 65km and 175km, respectively. A seasonal pattern was observed, with increased trade movements occurring in autumn and spring. East Anglia, North West, South East and South West England and Yorkshire and Humberside represented the major sources and receivers in term of number of movements and pigs. The monthly network exhibited both scale-free and small-world properties. The 10 largest trade communities including 18% of premises were identified and associated with specific regions, providing a basis for defining zoning areas in the context of control of endemic and epidemic disease spread.

This study demonstrates how the spatio-temporal and functional organisation of pig trade in GB can be investigated to reveal hot spots in time and space for disease spread. This information can be used to parameterise epidemic models and also to directly inform the design of targeted disease surveillance and control strategies.

097

Network analysis of main service providers for swine herds participating in regional PRRS control programs in Ontario, Canada

Andreia G. Arruda[1], Zvonimir Poljak[1], Robert Friendship[1], Karen J. Hand[2], Jane Carpenter[3], [1]University of Guelph, Guelph, ON, Canada; [2]Strategic Solutions Group, Puslinch, ON, Canada; [3]Ontario Swine Health Advisory Board, Stratford, ON, Canada. Contact: arrudaa@uoguelph.ca

Purpose:
The importance of networks in infectious disease epidemiology has been recognized in the last decade for several animal diseases. In Ontario, a link was established between the introduction of porcine epidemic diarrhea (PED) and the exposure to contaminated feed (Pasick et al., 2014); and swine truck networks have been linked to the occurrence of specific porcine reproductive and respiratory syndrome (PRRS) virus genotypes (Arruda et al., 2015). The current North American swine industry is characterized by a high degree of connectedness of swine sites within production systems, and a limited number of specialized service providers such as animal transporters and feed suppliers.
The objective of the current study was to describe static relationships between swine sites and their service providers, including transportation, feed, semen and boar companies.
Methods:
The source of data was a SQL Server 2008 database containing data from PRRS area control and elimination projects. Network information was collected using a standardized questionnaire. Network analysis was conducted in Gephi 0.8.2 and included measures of degree, betweeness centrality and closeness centrality. Relationships were considered undirected, both service providers and sites were considered nodes, and an edge was defined as a connection between a site and a service provider.
Results:
A total of 613 sites were enrolled in the study. These sites were connected to a total of 49 feed companies and 80 truck companies. The 202 breeding herds included in the study reported to receive semen from 14 companies and boars from 34 genetic companies.
Conclusions:
The average number of degrees and centrality parameters showed that for all networks, a few nodes had the greatest importance in the network, connecting multiple network components.
Relevance:
All parameter distributions were highly right skewed, suggesting that when the goal is to decrease disease transmission, focusing on a few nodes should yield a greater beneficial impact.
Pasick et al. 2014. Transb Emerg Dis 61(5):397-410
Arruda et al. 2015. Transb Emerg Dis doi: 10.1111/tbed.12343

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Controlling infectious disease through the targeted manipulation of contact network structure

M Carolyn Gates[1], Mark E. J. Woolhouse[2], [1]Massey University, Palmerston North, New Zealand; [2]University of Edinburgh, Edinburgh, United Kingdom. Contact: c.gates@massey.ac.nz

Purpose:
Livestock populations are linked through dynamic contact networks with characteristic structural features that drive the epidemiology of directly transmissible infectious diseases. Using movement data from the British cattle industry as a case example, this analysis explores whether disease dynamics can be altered by placing targeted restrictions on contact formation to reconfigure network topology while still allowing farmers to engage in normal trade activities.
Methods:
This was accomplished using a simple network generation algorithm that combined configuration wiring with stochastic block modelling techniques to preserve the weighted in- and out-degree of individual nodes (farms) as well as key demographic characteristics of the individual network connections (movement date, livestock market, and animal production type). We then tested a control strategy based on introducing additional constraints into the network generation algorithm to prevent farms with a high in-degree from selling cattle to farms with a high out-degree as these particular network connections are predicted to have a disproportionately strong role in spreading disease.
Results:
Results from simple dynamic disease simulation models predicted significantly lower endemic disease prevalences on the trade restricted networks compared to the baseline generated networks. As expected, the relative magnitude of the predicted changes in endemic prevalence was greater for diseases with short infectious periods and low transmission probabilities.
Conclusions:
Overall, our study findings demonstrate that there is significant potential for controlling multiple infectious diseases simultaneously by manipulating networks to have more epidemiologically favourable topological configurations. Further research is needed to determine whether the economic and social benefits of controlling disease can justify the costs of restricting contact formation.
Relevance:
Network analysis offers a promising framework for developing control strategies that do not rely on diagnostic tests, antimicrobials, or biologics to reduce the prevalence of economically important livestock pathogens.

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Research synthesis in veterinary science.

Annette O'Connor[1], Jan Sergeant[2], [1]Iowa State University, Ames, IA, [2]University of Guelph, Guelph, ON, Canada. Contact: oconnor@iastate.edu

Purpose: Reviews of the scientific literature are critically important for synthesizing the state of knowledge and are used extensively in teaching, clinical practice and public policy. Despite the importance of literature reviews, very little attention has been paid to the science of research synthesis in the veterinary sciences. In the same manner that different study designs address different research questions, different approaches to combining scientific literature serve different and valid purposes. However, again reflective of the situation in the primary research, the potential for bias in a review should be considered when interpreting the results. In this presentation, we will introduce concepts in research synthesis and discusses some of the basic forms of reviews including narrative integrative reviews, scoping reviews, systematic reviews and meta-analysis, and describe their utility for veterinary science. We also will discuss potential sources of bias and design features that can be incorporated into reviews to either reduce the potential for bias or at least acknowledge the potential for bias.

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The value of pathogen information in treating mastitis.

Elva Cha[1], Rebecca Smith[2], Anders Ringgaard Kristensen[3], Julia Hertl[1], Ynte Schukken[4], Loren Tauer[1], Frank Welcome[5], Yrjö Gröhn[1], [1]Cornell University, Ithaca, NY, [2]University of Illinois, Urbana, IL, [3]University of Copenhagen, Copenhagen, Denmark; [4]GD Animal Health, Deventer, Netherlands; [5]Quality Milk Production Services, Cornell University, Ithaca, NY, Contact: elvacha@gmail.com

Identification of cows with clinical mastitis (CM) can be performed in several ways. Usually, herdsmen observe outward signs from cows indicating they are likely suffering from CM. Another approach is to identify whether the pathogen causing CM is Gram positive, Gram negative or Other. The most detailed level of information currently available for mastitis diagnostics is obtainable by sending milk samples for culture to an external laboratory, which will identify the pathogen causing CM often within 24 hours. Knowing the exact pathogen involved will permit treatment to be specifically targeted, resulting in less discarded milk due to potentially inappropriate antibiotic use. The disadvantages, however, are the additional waiting time for receiving results which delays treating cows and the cost of culture, bringing into question the financial benefit of this method. The objective of this study was to identify the financial value of these different protocols to the farm, and ascertain exactly how much is gained or lost by additional information, while accounting for the costs in obtaining more detailed information. The economic model used was built using the Multi Level Hierarchic Markov Process software as the application program; and in order for the Net Present Value (NPV) to be comparable across the different levels of information, modifications were made programmatically to the calculation of NPV. Preliminary data demonstrate the model predicting the value of CM culture information at the pathogen specific level provides a greater NPV than other levels of information even when accounting for fluctuations in key market prices. For example, NPV was lowest for the gram decision model, was greater for the generic CM model (with an added value of information (VOI) of 2.42USD) and greatest for the pathogen specific CM model (added VOI of 3.59USD) compared with the gram CM model when milk price was increased and decisions were made based on treatment cost. Similar results were observed with fluctuations in cow replacement cost. These results quantify the extent and ircumstances under which the pathogen specific CM model provides the greatest value for optimal decision making.

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Stochastic bias analysis to adjust for misclassification of farmer-reported cases of clinical mastitis in a secondary database on the incidence risk ratio for culling

Chris W. R. Compton[1], Cord Heuer[1], Tim Carpenter[1], Scott McDougall[2], Claire V. C. Phyn[3], [1]Massey University, Palmerston North, New Zealand; [2]Anexa Animal Health, Morrinsville, New Zealand; [3]DairyNZ, Hamilton, New Zealand. Contact: ChrisComptonNZ@gmail.com

Purpose Policy-makers, advisors and farmers need accurate estimates of the ef- fects of disease on the risk of culling and mortality in dairy herds to determine total economic costs and to develop control strategies. This typically requires data sets gathered prospectively from large numbers of herds over extended time periods, with attendant high costs. Increasingly, secondary data sets are used to answer such questions, but this comes at a cost of decreased data quality and a consequent increased risk of biased results due to misclassification of risk factors. Recently available quantitative bias analysis (QBA) software provide corrected estimates in the presence of misclassification and may be used in the analysis of such data. The aim of this study was to estimate the effect of misclassification of cases of clinical mastitis (CM) on the incidence risk ratio(IRR) of culling in seasonal calving dairy cows.
MethodsA subset of farmer-reported data over 2 lactations (n=134 herds, n=171,110 cow lactations) was available from a previous study (National Herd Fer- tility Study). Graphs of causal pathway were used to define the adjustment vari- ables required in subsequent multi-level logistic regression models to estimate the total effect of CM on culling. A crude probabilistic bias analysis was undertaken using distributions for the bias parameters obtained from other published reports, assuming either differential (D) or non-differential (ND) misclassification. Data from a current validation study in a comparable population will be used to update the bias parameters and type of misclassification.
Results The crude incidence risk for culling of cows with and without recorded cases of CM was 23.6 and 14.7 cases per 100 cows in the period from calving until the end of the dairy season, respectively (naive IRR=1.6, 95% CI 1.5 to 1.7). The ND and D bias-corrected IRRs were 1.8 (95% CI 1.7 to 1.9) and 1.9 (95% CI 1.8 to 2.1), respectively.
Conclusions The adjusted IRR was increased by up to 20% using QBA methods.
Relevance Methods of QBA provided more realistic estimates of the effects of risk factors under a variety of misclassification scenarios common in secondary databases.

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A Bayesian decision-theoretic framework to evaluate the cost-effectiveness of specific dry period management interventions on clinical mastitis and somatic cell count

Peter M. Down[1], Andrew J. Bradley[2], James E. Breen[1], Chris D. Hudson[1], Martin J. Green[1], [1]University of Nottingham, Sutton Bonington, United Kingdom; [2]Quality Milk Management Services Ltd, Wells, United Kingdom. Contact: svxpd1@nottingham.ac.uk

Purpose:
The purpose of this study was to investigate the cost effectiveness of mastitis control interventions to reduce intramammary infections during the dry period.

Methods:
An integrated Bayesian cost effectiveness framework was used to construct a probabilistic decision model that could be used to inform clinical decision making. Data were collected from 77 UK dairy farms that had a diagnosed problem with 'environmental' pathogens causing intramammary infections during the dry period. The data consisted of clinical mastitis (CM) and somatic cell count (SCC) records, current herd management and a record of interventions that were actually implemented by the farmer as part of the mastitis control plan. Multiple linear regression models were developed for CM and SCC outcomes and carried forward into a Bayesian framework. A Bayesian one-step microsimulation model was constructed such that posterior predictions from the model incorporated uncertainty in all parameters. The incremental net benefit (saving - cost) over a 12-month period was calculated at each of 10000 Markov chain Monte Carlo iterations for each mastitis intervention. The resulting posterior distributions were used to make predictions about the likely return on investment in new theoretical herds.

Results:
A total of 14 interventions were carried forward into the cost-effectiveness model for the CM outcome and 12 interventions for the SCC outcome. The median values for the parameter estimates ranged from a 15%-77% reduction in the incidence rate of CM in the first 30 days after calving in the CM model and 8.0-58% reduction in the rate at which 'uninfected' cows became 'infected' (>200,000 cells/ml) in the first test day after calving in the SCC model. The probability of a net saving of at least £500 or £1000 was calculated for each intervention under different farm scenarios.

Conclusions:
The study identified specific mastitis interventions that were cost effective and which are being incorporated into a tool to optimise on-farm decision making.

Relevance:
This research provides an example of how intuitive and clinically useful the Bayesian approach can be for practical cost-effectiveness analysis.

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Does clinical mastitis in the first 100 days of first lactation predict increased mastitis occurrence and short herd life in dairy cows?

Julia A. Hertl[1], Ynte H. Schukken[2], Loren W. Tauer[3], Frank L. Welcome[1], Yrjo T. Grohn[1], [1]Cornell University, Ithaca, NY, [2]GD Animal Health, Deventer, Netherlands; [3]Cornell University, Ithaca, NY, Contact: jah12@cornell.edu

Purpose: Mastitis is a common problem in the dairy industry worldwide. It is associated with decreased milk production and reproductive performance, and increased death and culling. The study objective was to examine the effects of clinical mastitis (CM) cases occurring in early productive life (the first 100 days in a cow's first lactation) on future rate of CM and total productive lifetime. Methods: Data were available on CM cases in 55,144 lactations from 24,831 cows in 5 New York State (USA) dairy farms, from January 2004 to February 2014. A generalized linear mixed model with a Poisson distribution was fit to estimate the effect of the number of CM cases occurring during the first 100 d of Lactation 1, and other factors (calving season, farm), on the rate of total number of CM cases over a cow's lifetime. A Cox proportional hazards model was fit to estimate the effect of these factors, as well the total number of CM cases in a cow's lifetime, on a cow's lifetime (number of days from Lactation 1 calving until death/culling or end of study). Results: In the first 100 d of Lactation 1, 22,788 (91.8%) cows had no CM cases, 1801 (7.3%) cows had 1 case, 203 (0.8%) cows had 2 cases, 31 (0.1%) cows had 3 cases, and 8 (0.03%) cows had 4 cases. Over the entire lifetime, cows experienced between 0 and 25 cases of CM. The most common pathogens isolated were *Streptococcus* spp., *Escherichia coli*, and *Staphylococcus* spp. Compared with cows having no CM cases in the first 100 d of Lactation 1, cows having one CM case then had a 1.4 times higher rate of total number of CM cases in their lifetime. Cows having 2, 3, or 4 cases then had a 1.6, 2.7, and 1.6 times higher rate of total number of CM cases in their lifetime, respectively. For each additional case of CM in the first 100 d of Lactation 1, the hazard rate of culling increased by 53%. For each additional case of CM during lifetime, the hazard rate of culling decreased by 10%. Conclusions: The findings indicate that CM cases occurring early in productive life increase the rate of contracting subsequent CM cases and also shorten total productive life. Relevance: The findings may provide insight into management of dairy cows with repeated cases of CM early in productive life.

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Dairy cow activity as a potential management tool for detection of clinical mastitis

Paivi J. Rajala-Schultz, Kathryn E. McCullough, Gustavo M. Schuenemann, Paige N. Gott, The Ohio State University, Columbus, OH, Contact: paivirs@hotmail.com

Purpose: Intramammary infections cause considerable economic losses in dairy herds and clinical mastitis (CM) is also an animal welfare issue. Early detection and treatment could mitigate these consequences. Modern free-stall dairies are increasingly using activity monitoring of cows as a management tool. Dairy cows display classic sickness behavior after experimentally induced mastitis, but behavioral changes in cows with naturally occurring CM have been less frequently reported. The objective of this study was to describe activity of cows with naturally occurring CM prior to disease diagnosis by herd personnel.
Methods: Activity monitors (IceQube™) were placed on a hind leg of 100 cows during dry period and kept for 14-28 days after calving in three Ohio dairy herds. The monitors measured lying and standing time and number of lying bouts and steps. An average lying bout length was calculated. CM cases were diagnosed by farm personnel according to their standard operating procedures. Daily summaries of the different activity parameters were used as outcomes. Data were analyzed with PROC MIXED in SAS v.9.3, accounting for the correlated data structure. Cow's own activity on days 4 and 5 before diagnosis was used as the baseline in the analysis. Days with respect to CM diagnosis, days in milk, herd and parity were tested in the models.
Results: During the study period, 21 cows were diagnosed with CM; 16 of these cows had no other diseases and were included in the analysis. Cow activity was significantly altered two days prior to CM diagnosis by herd personnel. Lying bout length was significantly shorter (P=0.0405), standing time longer (P=0.0485) and cows were taking significantly fewer steps (P=0.040) starting two days prior to diagnosis.
Conclusions: These results suggest that cow activity is altered around CM occurrence and before herd personnel is able to detect and diagnose CM.
Relevance: As this type of technology becomes more readily available on farms, precision monitoring of behavioral changes could assist in early detection of CM and alert herd personnel to more careful examination of at-risk cows, ultimately improving farm profitability and cow welfare.

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Empirical evidence of no protection for a recurrent case of mastitis from a previous case of pathogen specific clinical mastitis.

Elva Cha[1], Julia Hertl[1], Ynte Schukken[2], Loren Tauer[1], Frank Welcome[3], Yrjö Gröhn[1], [1]Cornell University, Ithaca, NY, [2]GD Animal Health, Deventer, Netherlands; [3]Quality Milk Production Services, Cornell University, Ithaca, NY, Contact: elvacha@gmail.com

The objective of this study was to determine whether the occurrence of a previous case of pathogen-specific clinical mastitis (CM) protects dairy cows against a recurrent case as a means to better understand the relevance of pathogen specific mastitis treatment and vaccination. Pathogens studied were *Escherichia coli*, *Staphylococcus aureus*, *Staph.* spp., *Streptococcus* spp., *Klebsiella* spp. and *Trueperella pyogenes*. A total of 40,864 lactations (19,835 cows) were analyzed: 17,265 were primiparous and 23,599 were multiparous lactations, from 5 large, high milk producing dairy herds in New York State. We estimated the effects of parity, calving diseases, milk yield, current season and number of CM cases in the previous lactation on the risk of a 1st case of CM. Different models, accounting for the unit of analysis which was relatively short therefore diminishing the distinction between risk and rate, were explored. These included generalized linear mixed models with a log link and Poisson error distribution, zero inflated Poisson distribution models and negative binomial and logistic regression models. The aforementioned risk factors and the occurrence of previous cases of pathogen-specific CM within the current lactation were evaluated as risks for 2nd and 3rd cases of pathogen-specific CM. Cows were at greater risk of pathogen-specific CM in the current lactation if they had more CM cases in the previous lactation; e.g., multiparous cows were 5.9 times [95% CI: (3.8, 9.3)] more at risk of a 1st case of *Klebsiella* spp if in the first two weeks of lactation they had ≥ 3 cases of CM in the previous lactation, compared to cows that had no CM in the previous lactation. Multiparous cows were at greater risk of a 2nd CM case if they had suffered from a 1st case of CM that was caused by the same pathogen as the 2nd case; e.g., multipara in weeks ≥ 3 were 5.9 times [95% CI: (4.5, 7.8)] more likely to have a 2nd case of *Staph aureus* CM if the 1st case was also *Staph aureus*. In general, there is no evidence for protective immunological memory due to a previous CM case with the same pathogen; the extent of this, however, is pathogen specific and promotes closer inspection of the pathogen's mechanism of action.

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Test strategies for intramammary infections in dairy cows - comparison of PCR and bacteriological culture using latent class analysis.

Ann-Kristin J. Nyman[1], Karin Persson Waller[1], Jenny Frössling[2], Ulf Emanuelson[3], [1]National Veterinary Institute, Uppsala, Sweden; [2]National Veterinary Institute, Uppsala, Sweden; [3]Swedish University of Agricultural Sciences, Uppsala, Sweden. Contact: ann.nyman@sva.se

Real-time PCR analysis of milk samples is a fast method to find cows with bacteria in milk and have the potential to be used for routine analysis of test-day milk samples. However, the results of the PCR analysis are difficult to interpret and needs to be further evaluated. The objective of this study was to investigate the test performance of PCR analysis of composite milk samples, and of conventional bacteriological culturing (BC) of quarter milk samples, when used to identify cows with intramammary infections (IMI). Comparison of test strategies was based on three major pathogens; Staphylococcus aureus (S. aureus), Streptococcus dysgalactiae (Str. dysg.), and Streptococcus uberis (Str. uberis). The sensitivity (Se) and specificity (Sp) of real-time PCR (SePCR; SpPCR) and BC (SeBC; SpBC) was estimated using latent class analysis, studying one pathogen at the time. Milk samples from 970 dairy cows from 25 herds were included. Latent class analysis was first performed using the composite and quarter milk samples from the same test-day. In a second analysis, PCR testing of the composite milk sample was compared to the results from BC of quarter milk samples from the test-day and from the day before and after (in parallel). In the first comparison, the results showed higher estimates of Se for composite milk PCR analyses than for quarter milk BC; SePCR was 0.87 and SeBC was 0.69 for S. aureus, SePCR was 0.81 and SeBC was 0.30 for Str. dysg. and SePCR was 0.75 and SeBC was 0.73 for Str. uberis. The estimates of Sp was high (≥0.96) for both BC and PCR analyses. When using BC results from three consecutive days of quarter milk sampling compared to the composite milk sample from one day, the SeBC increased and was higher than the SePCR for findings of S. aureus (SePCR=0.76; SeBC=0.83) and Str. uberis (SePCR=0.69; SeBC=0.78), but not for Str. dysg. (SePCR=0.85; SeBC=0.42). In conclusion, PCR analysis of composite milk samples could better identify cows with IMI caused by major pathogens than BC quarter milk samples taken at the same occasion but not when 3 consecutive quarter milk samples were used in BC analyses. The results gives insight to when bacteriology or PCR could be useful depending on the purpose of milk sampling.

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The influence of the rearing period on intramammary infections in Swiss dairy heifers: A multilevel cross sectional study

Maren Jana Bludau[1], Florian Leiber[1], Ariane Maeschli[1], Peter Klocke[2], Michele Bodmer[3], **Beatriz Vidondo**[4], [1]Research Institute of Organic Agriculture, Frick, Switzerland; [2]Bovicare GmbH, Postdam, Germany; [3]University of Bern, Bern, Switzerland; [4]Veterinary Public Health Institute, Liebefeld, Switzerland. Contact: beatriz.vidondo-curras@vetsuisse.unibe.ch

Purpose: Healthy heifers are the basis of a healthy dairy herd. In the last years the frequency of heifer mastitis occurrence seemed to increase but the reasons are still poorly understood.
Methods: The occurrence of coagulase-negative staphylococci, contagious and environmental major pathogens was estimated and potential risk factors for intramammary infection were determined on quarter, animal and herd level using a multivariable and multilevel logistic regression analysis. Fifty-four dairy farms in Switzerland were enrolled. Data on housing, management and welfare level of young stock was collected by observing and interviewing the farmer using a structured questionnaire. In addition, data was collected from external rearing farms and alpine farms where young stock usually spends the summer. Foremilk samples of 1'564 quarters (391 heifers) were collected aseptically within less than 24 hours post partum for bacterial culture.
Results: In approximately 50% of the quarter samples a positive bacteriological culture result was found. At herd level stanchion barns and the breed category "Brown cattle" were risk factors for intramammary infections caused by contagious major pathogens such as Staphylococcus aureus. At quarter level teat swelling and teat lesions were highly associated with intramammary infection caused by environmental pathogens. Keeping pregnant heifers in a separate group appeared to be protective against intramammary infections by coagulase-negative staphylococci. Besides, the odds of intramammary infections by coagulase-negative staphylococci increased if weaning age was <4 months and if concentrates were fed to calves younger than 2 weeks.
Conclusions: The current study investigated the associations between risk factors related to the rearing period at the herd level, heifer level (such as breed) and quarter level and the presence of intramammary infections in first lactation heifers in Switzerland.
Relevance: Various farm management and rearing systems exist in Switzerland, providing a wide variety of factors potentially related to intramammary infections in early lactating dairy heifers that have not been addressed until now.

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Longitudinal study on usage of intramammary antimicrobials in Swiss dairy herds.

Ioannis Magouras[1], Luis Pedro Gomes do Carmo[1], Bart van den Borne[1], Gertraud Schüpbach-Regula[1], Ruth Badertscher[2], Dagmar Heim[3], Cedric Müntener[4], [1]Veterinary Public Health Institute, University of Bern, Liebefeld, Switzerland; [2]Federal Office for Agriculture (FOAG), Bern, Switzerland; [3]Federal Food Safety and Veterinary Office (FSVO), Liebefeld, Switzerland; [4]Institute for veterinary pharmacology and toxicology, University of Zurich, Zurich, Switzerland. Contact: ioannis.magouras@vetsuisse.unibe.ch

Purpose: Mastitis is economically the most important health problem in dairy cattle. While Switzerland has an excellent dairy milk quality, it is among the countries with the highest usage of intramammary antimicrobials (IMA) according to data published by the European Surveillance of Veterinary Antimicrobial Consumption (ESVAC). However, ESVAC data refers to national antimicrobial sales data, which hinders making inferences on antimicrobial consumption at herd level. The objective of this study was to analyze patterns of IMA usage in relation to milk quality and production data in Swiss dairy herds.
Methods: In this longitudinal study, IMA usage in a cohort of Swiss dairy herds (mean 177 herds per year) was analyzed for the period 2010-2013. The average herd size was 24 dairy cows. Mean number of dairy cows per year included in the study was 4177, which represents ~0.59% of the Swiss dairy cattle population. The convenience sample of herds reported electronically all medical treatments, production data and economic data.
Results: On average, IMA usage was recorded in ~90% of all herds, with 78% of herds applying dry cow treatment (DC) and 86% applying antimicrobials during lactation (LC). Annual proportion of dairy cows receiving DC varied between 30 and 37%. LC was recorded in 17-20% of all cows, with 66-71% of treated animals being treated once, 19-23% twice and the remaining cows over 2 times per year. Penicillins (particularly cloxacillin and penicillin G) represented 80-82% (DC) and 81-84% (LC) of IMA usage. Usage of aminoglycosides was 16-20% (DC) and 11-14% (LC) respectively.
Conclusion and relevance: This study identified differences in IMA usage between Swiss dairy herds, indicating that room for improvement exists. Future analysis includes linking IMA usage with somatic cell count and production data in order to identify potential associations that might prove valuable in understanding what drives IMA usage in Swiss dairy herds.

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Effect of cow and quarter level factors at dry-off on intramammary infection status at calving

Paige N. Gott, Paivi J. Rajala-Schultz, Gustavo M. Schuenemann, The Ohio State University, Columbus, OH, Contact: gott.11@buckeyemail.osu.edu

Purpose
Increased milk yield at dry-off is associated with increased risk of intramammary infection (IMI) at calving (CALV). Studies on drying off methods date back decades. Abrupt cessation of milking is widely practiced although gradual cessation significantly decreases milk yield before dry-off. **Objective:** to evaluate the effect of milk cessation method (*tx*), average daily milk yield at dry-off (*drymilk*), and milk leakage after dry-off (*leak*) on IMI at CALV.
Methods
Cows in 5 Ohio dairy herds with parlor milk meters were enrolled 7-14d before dry-off and randomly assigned to ABRUPT or GRADUAL cessation of milking. GRADUAL cows were milked 1/d the final week of lactation and ABRUPT cows kept their usual milking schedule.
Aseptic quarter foremilk samples were collected at enrollment, the final milking before dry-off (DRY), and within 7d of CALV. Milk was cultured following NMC protocols. Isolation of ≥10 colonies of like morphology was called an IMI. Cows were observed for *leak* on d1, d2, and d4 after DRY. *drymilk* was the average of d-2 and d-3 milk weights before DRY.
Quarter IMI at CALV (yes/no) was the outcome modeled in PROC GLIMMIX in SAS. Season at DRY, *tx*, *drymilk*, *leak*, DRY IMI status, farm milking frequency, and *age* (parity 1 vs parity 2+) were predictors in the model, adjusting for clustering of quarters within cows and cows within herds.
Results
Data from 971 quarters of 263 cows were analyzed. On average, GRADUAL *drymilk* was 13.4 kg/d and ABRUPT 19.1 kg/d, but *drymilk* was not associated with IMI at CALV (P=0.7803). Quarters with major IMI at DRY had 7.8 times higher odds of IMI at CALV than uninfected quarters at DRY (P=0.0001). Cows leaking post-dry had 3.3 times higher odds of IMI at CALV than cows not leaking (P=0.0227). Interaction between *tx* and *age* was significant (parity 1 cows benefitting from GRADUAL milking).
Conclusions
Gradual cessation of milking reduced *drymilk* and milk leakage post-dry increased the risk of IMI at CALV.
Relevance
Identification of optimal dry-off methods for today's dairy cows can help improve udder health, milk quality, and cow welfare. Consumers have increased interest in food animal production, so implementing best practices on-farm may ease consumer concerns.

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Streptococcus agalactiae New intramammary subclinical infections in Colombian Dairy herds

Julian Reyes Velez[1], Javier Sanchez[1], Nicolás Ramírez[2], Guillermo Palacio[2], Ofelia Arroyave[2], Juan Cerón[3], Manuel Jaramillo[3], Gregory Keefe[1], [1]University of Prince Edward Island, Charlottetown, PE, Canada; [2]Universidad de Antioquia, Medellin, Colombia; [3]Cooperativa COLANTA, Medellin, Colombia. Contact: jreyes@upei.ca

Purpose*: Streptococcus agalactiae* (*S. agalactiae*) is an important cause of contagious mastitis for the dairy industry in South America. The objective of the study was to determine the incidence of new intramammary infections (NIMIs) for *S. agalactiae* and to explore the influence of specific predictors over the NIMI in dairy herds from Antioquia, Colombia.
Methods: A total of 542 cows in 31 dairy herds from 6 municipalities monitored over a 24 month period (January-2009 to December-2010) were included in the analysis (Multilevel Poisson regression model). Quarters were classified as having a NIMI if they were California mastitis test (CMT) positive, had SCC >200,000 cells/mL and were *S. agalactiae* culture positive and did not meet these criteria on the previous test. Only cows with two consecutive records for *S. agalactiae* and complete days in milk (DIM) information were used. Specific predictors were DIM and age (years), pre-dipping, post-dipping and milking type. The days at risk (DAR) were calculated using the DIM between two tests in the same quarter and lactation period.
Results: From a total of 5,089 observations, 447 were considered NIMIs. The cow average DIM was 234.7 DIM (SD: 128.3). The average cow age was 6.6 years (SD: 2.3). Milking by hand was performed in 68.0% and 32.0% were machine milked. Pre-dipping was practiced in 33.8 % of the herds and Post-dipping in 60.5%. The quadratic effect of age was significant (P<0.05). A 30 days increase in DIM was associated with a 6% reduction of NIMI's per month (0.99^{30}= 0.93) (P <0.01). The IR for hand milking was 2.97 times than the IR for machine milked herds (P<0.01). The IR for not pre-dipping was 1.96 (P<0.05) and for not post–dipping was 1.32 but not significant (P=0.158). Herd and Cow Random effects variances were 0.07 (SE: 0.07) 0.32 (SE: 0.13), respectively.
Conclusions: As preliminary conclusions, NIMIs were more frequent in older cows and at the beginning of the lactation. Hand milking and not pre-dipping were risk factors for *S. agalactiae* NIMIs.
Relevance: This study provides relevant information for the development of more effective control measures against *S. agalactiae* in similar production systems in the Antioquia region in Colombia.

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Intramammary infections with different coagulase-negative staphylococci species in dairy cows

Ann-Kristin J. Nyman, Karin Persson Waller, National Veterinary Institute, Uppsala, Sweden. Contact: ann.nyman@sva.se

Subclinical mastitis (SCM) causes an increase in milk somatic cell count (SCC), and can lead to reduced milk production and early culling. In many countries, coagulase-negative staphylococci (CNS) are the most common bacterial finding at SCM in dairy cows. New methodology (MALDI-TOF) makes it possible to identify different CNS species, but the knowledge on the epidemiology of these species is limited. The objective of this project was to improve advisory services on how to control mastitis caused by different CNS species, by evaluating effects on SCC, milk production, number of cases of clinical mastitis (CM) and culling. Farmers that had sent milk samples positive for CNS to the National Veterinary Institute were asked to participate. Participating farmers took new udder quarter milk samples from the cow of interest within one month after the initial sampling, and at dry-off or after calving. So far, 344 cows from 174 herds have been enrolled in the study, and 17 different CNS species have been identified. The four most common CNS species were Staphylococcus epidermidis (S. epidermidis), S. simulans, S. chromogenes, and S haemolyticus. Differences in daily milk yield and cow composite SCC between these four species were evaluated using data from the test milking closest in time to the initial sampling. The preliminary results shows that the composite SCC tends to be lower for S. chromogenes positive cows compared to cows positive for other CNS ($p=0.07$). However, the milk yield did not differ significantly between cows having different CNS. So far, only 5 cows have had a registered case of CM and 8 cows have been culled due to mastitis. A total of 135 follow-up samples taken within 35 days after initial sampling of CNS positive quarters have been received. In 87% of those samples the same CNS species as at the first sampling was found. Cows will continue to be enrolled until May 2015 and the follow up period will last until April 2016. The final results will hopefully give better insight into how the most common CNS species affects the cow, and will improve the advisory services on how to control mastitis caused by different CNS species.

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Antimicrobial susceptibility patterns of environmental streptococci recovered from bovine milk samples in the Maritime Provinces of Canada

Marguerite Cameron[1], Javier Sanchez[1], J. McClure[1], Luke Heider[1], Matthew Saab[1], Natasha Robinson[1], Juan Carlos Rodriguez-Lecompte[2], Greg Keefe[1], [1]University of Prince Edward Island, Charlottetown, PE, Canada; [2]University of Prince Edward Island, Charlottetown, PE, Canada. Contact: mcameron@upei.ca

Purpose:
Environmental streptococci are ubiquitous in the farm environment and are a frequent cause of mastitis in dairy cows. Antimicrobial susceptibility patterns of environmental streptococci associated with bovine intramammary infection in Canada have not been well defined. The aim of the current study is to determine the patterns of antimicrobial resistance among different species of environmental streptococci isolated in milk samples collected from dairy cows in the Maritime Provinces of Canada.
Methods:
The isolates were sourced from the Canadian Bovine Mastitis Research Network and comprise 79 S. uberis, 38 S. dysgalactiae, and 192 other streptococci species identified in 307 milk samples collected from 252 cows originating from 18 dairy herds. Isolates classified as other streptococci will be characterized further using Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry. Just over half of the isolates (186/309) were recovered in samples collected from randomly selected healthy lactating mammary quarters and the remainder were isolated from quarters that had been previously infused with antimicrobials as either a treatment for mastitis or as prophylaxis upon entry into the non-lactating period.
Results:
To date, 57 S. uberis isolates have been analyzed using the Sensititre microdilution system and mastitis plate format (Trek Diagnostic Systems Inc., Cleveland, OH) which contains 10 antimicrobials commonly used for mastitis prevention and control. Resistance was most commonly observed to erythromycin (19.3%; 11/57), followed by penicillin (8.8%; 5/57), and penicillin/novobiocin (1.8%; 1/57); 75.4% (43/57) of the isolates were pansusceptible. The 11 isolates resistant to erythromycin originated from 4 farms and 8 cows; the 5 penicillin resistant isolates were recovered on different farms.
Conclusions:
While resistance to penicillin in the current study is low, these early results suggest the possibility of an emergence of resistant streptococci and support the need for further investigation. Initial results also indicate that erythromycin should not be used for the treatment of mastitis caused by S. uberis.

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Prevalence of coagulase-negative staphylococci from bovine milk in Canadian dairy herds

Larissa A. Z. Condas, Jeroen De Buck, Diego B. Nóbrega, Domonique Carson, **Herman W. Barkema**, University of Calgary, Calgary, AB, Canada. Contact: barkema@ucalgary.ca

Purpose: Coagulase-negative staphylococci (CNS) are the most frequently isolated pathogens from intramammary infections (IMI) in dairy cattle worldwide. Many studies report their importance as a group; however, inconsistent epidemiologic findings may be due to species heterogeneity. Therefore, more accurate identification and distribution estimates are needed. The objective was to determine regional prevalence of CNS species from bovine milk in Canada. Additionally, associations between species-specific prevalence of CNS IMI with bulk tank somatic cell count (BTSCC), barn type, parity, and DIM were also determined.
Methods: Data and milk samples were obtained from the National Cohort of Dairy Farms, with 98,232 quarter-milk samples collected in 91 herds across Canada. In total, 5,447 CNS isolates from 5,149 cows were characterized (using molecular techniques). Prevalence (quarter-level, with correction factors) was estimated using mixed effects logistic regression.
Results: Overall prevalence of CNS was 10.13%. 26 CNS species were identified, the 5 most prevalent being S. chromogenes (7.8%), S. simulans (2.3%), S. xylosus (0.52%), S. haemolyticus (0.46%), and S. epidermidis (0.11%). Prevalence varied considerably across provinces, BTSCC strata, and barn type. For example, S. chromogenes was associated with higher BTSCC, and prevalence was higher in free-stall and bedded-pack barns. However, S. xylosus was most frequently isolated from Ontario and Québec (mostly tie-stall barns). Additionally, prevalence of most CNS species was higher in heifers and at calving, with S. simulans being one of the most commonly isolated species in this period, whereas S. epidermidis, S. haemolyticus and S. xylosus had increasing prevalence over later periods in lactation and in multiparous cows.
Conclusions: Epidemiology of CNS differs considerably among species.
Relevance: Identification of the most common CNS species and their prevalence according to various characteristics of dairy production should promote development of specific management strategies to address increasing prevalence of CNS in herds across Canada.

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Randomized clinical trial on impacts of dairy meal feeding interventions on early lactation milk production in smallholder dairy farms of Central Kenya

Shauna Richards[1], John Vanleeuwen[1], Getrude Shepelo[2], George Karuoya Gitau[2], Collins Kamunde[3], Fabienne Uehlinger[4], Jeff Wichtel[1], [1]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada; [2]Faculty of Veterinary Medicine, University of Nairobi, Nairobi, Kenya; [3]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada; [4]Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, Canada. Contact: srichards@upei.ca

Purpose: There is limited field-based research and recommendations on the effect of cattle feeding management on smallholder dairy farms for the growing dairy industry in Kenya. This clinical trial aimed to determine the effect of feeding locally produced dairy meal (DM) on early lactation daily milk production (DMP) on Kenyan smallholder dairy farms, controlling for other factors associated with DMP.
Methods: Privately owned, recently calved cows (n=111) were randomly assigned to one of three groups of feeding recommendations for DM (meeting predicted DM requirements by 1) 100%; 2) 50%; or 3) whatever DM the farmer normally fed). DM was provided for free to groups 1 and 2 to ensure they had sufficient DM to feed to the recommendations. Farm data collection occurred biweekly for a 60-day period post-calving in June 2013. A repeated measures multivariable linear regression model was used on the DMP outcome variable. With variability in DM consumption within feeding groups due to variability in DMP, actual DM fed was assessed as an independent variable rather than assigned feeding groups.
Results: DMP was positively associated with each kg/day of DM fed (0.52 kg/day), cow weight, feeding DM in the month prior to calving, and feeding high protein forage, and was negatively associated with having mastitis. Taller cows had higher DMP than shorter cows, whereas heifers had similar DMP regardless of height. Thin cows (score < 2.5) produced less milk than cows in better condition, whereas thin heifers produced more milk than heifers in better body condition (possibly due to small sample size of heifers).
Conclusions: Feeding DM in the month prior to calving, improving body condition prior to calving, and enhancing DM and high protein forage can lead to substantially more DMP in early lactation. In addition, taller cows had higher DMP, indicating the importance of educating farmers on good genetic selection and heifer management.
Relevance: These findings will help with future management recommendations for higher DMP on smallholder dairy farms.

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Multivariate syndromic surveillance to detect West Nile Virus outbreaks

Céline Faverjon[1], Gunnar M. Anderson[2], Jackie Tapprest[3], Carole Sala[4], Anouk Decors[5], Pierre Tritz[6], Orsolya Kutasi[7], Alain Sandoz[8], Agnès Leblond[1], [1]INRA, Lyon, France; [2]SVA, Uppsala, Sweden; [3]ANSES, Dozulé, France; [4]ANSES, Lyon, France; [5]ONCSF, Auffargis, France; [6]AVEF, Faulquemont, France; [7]Szent Istvan University, Ullo, Hungary; [8]UFR Aix-Marseille, Marseille, France. Contact: celine.faverjon@vetagro-sup.fr

Purpose:
West Nile Virus (WNV), a vector-borne disease which mainly affects birds, has complex interactions which can lead to the infection of horses and humans. Various methods are already used for the early detection of WNV but their output is either not quantitative or does not take into account all available information. Our study aimed to test the use of three time series (i.e. nervous syndrome in horses and wild bird mortalities collected respectively by the French networks RESPE, SAGIR and horse mortalities recorded in FSDI) combined with prior knowledge on WNV seasonality to improve WNV surveillance.
Methods:
WNV seasonality was estimated based on historical outbreaks data in Europe. The baselines of the three time series were fitted and used to simulate 100 years where simulated WNV outbreaks were inserted. Two outbreaks detection algorithms were tested: one based on a multiple of the standard error of the prediction and another on likelihood ratio [1]. The information were combined using the Bayesian framework assuming the independence of time series. The performance criteria used to compare the algorithms included sensitivity, specificity, ROC curves and Area under the curve (AUC).
Results:
When data sources were considered separately, the ROC curve from nervous symptoms in horses were the most relevant for WNV detection. Adding information on WNV seasonality improves the detection performances compared to an algorithm based on a multiple of the standard error of the prediction (nervous symptoms AUC = 0.835 vs 0.822; bird mortalities 0.825 vs 0.632 ; horses mortalities 0.650 vs 0.50). The combination of the three time series provided the best results (AUC = 0.90) mainly due to nervous symptoms in horses and bird deaths.
Conclusions:
Using the Bayesian framework to combine information on disease seasonality with evidence from nervous syndrome in horses and wild bird mortality improves WNV early detection. This approach can be used for other diseases involving multiple sources of evidence.
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Use of cattle mortality data for syndromic surveillance: simulation-based assessment of the performances of an anomaly detection algorithm

Viviane Hénaux[1], Jean-Baptiste Perrin[2], Benoît Durand[3], Emilie Gay[1], Christian Ducrot[4], Pascal Hendrikx[1], Didier Calavas[1], [1]ANSES, Lyon, France; [2]Direction Générale de l'Alimentation, Paris, France; [3]ANSES, Maisons-Alfort, France; [4]INRA, St Genès Champanelle, France. Contact: viviane.henaux@anses.fr

Purpose: In the context of limited resources, the development of efficient methods to prospectively analyze the continuous flow of syndromic data and rapidly detect anomalies is a priority for animal disease surveillance. We performed a simulation study to evaluate the performances of an anomaly detection algorithm considered for automated surveillance of cattle mortality. **Methods:** First, we simulated 1,000 outbreaks of a disease causing extra deaths in the network of French cattle farms according to an epizootic model, and injected these disease-related extra deaths in a 5-year authentic mortality dataset (representing about 20 millions of cattle). Second, we applied our algorithm (based on temporal regression analysis and spatial cluster detection) on each of the 1,000 semi-synthetic datasets to identify clusters of spatial units showing an excess of deaths in comparison with their own historical fluctuations. Third, we verified if the clusters identified by the algorithm did contain simulated extra deaths in order to evaluate the ability of the algorithm to detect unusual mortality clusters caused by an outbreak. This evaluation was replicated using different disease patterns to investigate how the sensitivity (proportion of detected outbreaks) varied according to epidemiologic parameters (basic reproductive number (R_0) ranging from 3 to 9 and daily mortality rates from 1 to 5%). **Results:** Median sensitivity increased from 54 to 80% with increasing R_0 and mortality rate, and about one in three alarms was a true alarm (positive predictive value). Overall, outbreak detection occurred 1 to 2 weeks after the first simulated death. The median number of deaths per infected herd increased with mortality rate, with up to 8 dead cattle per infected herd at first alarm for high R_0 and mortality rate. **Conclusions:** Our results confirmed that automated algorithms could help identifying abnormal cattle mortality increases related to unidentified health events. **Relevance:** Such a syndromic surveillance system could facilitate the rapid implementation of adapted investigation and control measures by animal health services.

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The comparison of three statistical methods to assess the potential of syndromic surveillance for early detection of emerging vector-borne diseases in cattle.

Wim Swart, **Anouk Veldhuis**, Henriëtte Brouwer-Middelesch, Gerdien van Schaik, GD Animal Health, Deventer, Netherlands. Contact: a.veldhuis@gdanimalhealth.com

Purpose: Emerging diseases are difficult to detect at the early onset of the disease when they result in non-specific symptoms. They may go unnoticed as such symptoms can be misinterpreted as the result of an endemic disease, environmental conditions or reduced feed quality. Recent examples in the field of cattle health surveillance illustrate the potential of non-specific herd productivity data for veterinary syndromic surveillance. This study presents the comparison of three statistical methods to retrospectively detect the emerging vector-borne Bluetongue virus (BTV-8) and Schmallenberg virus (SBV) in the Netherlands using routinely collected milk production records.
Methods: Time series of milk production records were constructed for 2005-2011 to generate a historical baseline and a prediction for years with known disease outbreaks (BTV in 2006 and 2007 and SBV in 2011). Model residuals were analysed using 1) Bayesian Disease Mapping (BDM), 2) Prospective space-time cluster analysis (ST-CA) and 3) a cumulative sum (CUSUM) algorithm. Each method aimed at sensing an unexpected reduction in milk production based on aberrations in model residuals.
Results: The expected time of introduction of BTV and SBV in the Netherlands is narrowed down to August 2006 (BTV; with re-emergence in July 2007) and August 2011 (SBV). BDM and CUSUM detected a drop in milk production in June 2007, in a geographical gradient that resembles the known spread of BTV based on previous studies. CUSUM and ST-CA detected clusters of decreased milk production in August 2011 that could be associated with the SBV outbreak, in which ST-CA was most timely.
Conclusion and relevance:
In veterinary health, the application of syndromic surveillance is often based on clinical and diagnostic data although a number of other data sources are being explored. This study confirmed the potential of syndromic surveillance based on non-specific herd data. The comparison of three statistical methods revealed benefits and drawbacks within each method. Practical implications of each method (e.g. calibration of parameter settings) and agreement in results between the methods will be discussed in more detail during the presentation.

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Evaluation of an innovative biosurveillance system as an informative tool for conducting syndromic surveillance of equine health based on a pilot study in Colorado, USA.

Lina Mur[1], Lindsey Holmstrom[1], Austin Riddle[2], Keith Biggers[2], Tammy Beckham[1], [1]Institute for Infectious Animal Diseases, Texas A&M University System, College Station, TX, [2]Texas Center for Applied Technology, Texas A&M University System, College Station, TX, Contact: lina.mur@ag.tamu.edu

Collection of quality, real-time data is an important challenge of animal health surveillance. Syndromic surveillance systems are becoming more popular in veterinary medicine, but they strongly depend on the collection and submission of near real-time data in standardized formats.
The objectives of this study were to develop a mobile application for collecting information during clinical visits by veterinarians to equine herds and evaluate the utility of collected data for the syndromic surveillance of equine health status.
Beginning in August 2013, the developed mobile application is being piloted in Colorado, USA by seven equine veterinarians and information from their clinical visits is being recorded. Data collected during the first year (August 2013-2014) were evaluated based on the frequency, amount, completeness and information included in submitted reports. In addition, temporal trends were evaluated and used to create preliminary baselines that will be used for future anomaly detection methods within the system. Each veterinarian submitted an average of 35 reports of per month, although strong differences were found among them (sd: 36.8). Syndromic reports represented 47.5% of the total reports. Based on the pilot data collected, daily analysis was possible for the musculoskeletal reports, whereas weekly analysis was possible for digestive, oral, respiratory, and “other” syndromic categories. There was not enough data to evaluate the other syndromic categories. Although strong differences were observed in report submissions and frequency between veterinarians, common factors such as the day of the week, month of the year, and time since enrollment into the pilot strongly influence reporting activities. These factors should be considered for modeling baselines for future anomaly detections.
The use of the mobile application during the pilot provided a considerably high amount of valuable data that would be employed as a preliminary baseline for monitoring 5 equine health syndromes. The results obtained from this study, and lessons learned, will be critical for the future implementation of a real-time syndromic surveillance system for equine health in the US.

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A Case Series Investigation of Bovine Tuberculosis on California, USA dairies

Brian McCluskey, Jason Lombard, USDA, APHIS, VS, Fort Collins, CO, Contact: brian.j.mccluskey@aphis.usda.gov

Purpose: The purpose of this study was to investigate potential pathways of introduction of M. bovis onto California dairies. Methods: A case series design was used to investigate the epidemiology of bovine tuberculosis (bTB) on California, USA dairies. From 2002 to 2013, bTB was detected on 12 dairies in California, all of which are included in this case series. A description of these recent outbreaks and potential pathways of introduction are included in this study. Pathways included purchasing cattle, use of heifer-raising operations, commingling of cattle at greater risk of exposure to infected cattle with cattle destined for California dairies, contact with infected wildlife, exposure to humans with bTB infections, and others. Initial phylogenetic analysis included spoligotyping and 24 loci MIRU-VNTR approaches. Whole genome sequencing of available isolates from 11 of the dairies was also conducted. Results: Epidemiologic and phylogenetic analysis confirmed the source of infection in 3 herds and probable sources of infection in 2 herds. In the 7 remaining herds an epidemiologic link to a source could not be determined and phylogenetic analysis results did not associate M. bovis isolates acquired from these herds with another specific U.S. herd or U.S.-born animal. Conclusions: The root cause(s) of bTB on California dairies is certainly multifactorial with complex interactions of herd management practices, importation of cattle at greater risk of exposure to infected cattle, and the potential of human M. bovis exposure. Relevance: Preventing new introductions of M. bovis onto California dairies will require rigorous epidemiologic investigation of all the potential pathways of introduction discussed here. The extensive use of phylogenetic analysis has improved epidemiologists' ability to narrow the scope of potential sources.

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Role of cattle trade in infectious disease spread, application to bovine Tuberculosis in France

Aurore Palisson[1], Aurélie Courcoul[2], Benoît Durand[2], [1]Paris Sud University, Villejuif, France; [2]Paris Est University, Anses, Maisons-Alfort, France. Contact: aurore.palisson@anses.fr

Purpose: Trade of live animals and local transmission on pastures are the two major modes of infectious disease spread in cattle. Analysing their respective weights is necessary to adapt and target infection control measures. Despite the fact that France is officially free of bovine tuberculosis (bTB), there are still about 100 outbreaks per year in France. In order to allow targeting bTB control measures, our objective was to quantify the weight of cattle trade in disease spread.
Methods: We developed a stochastic individual-based model in discrete time with a monthly time step. It incorporates an explicit within-herd model that extends a previously validated compartmental model (Bekara *et al.*). The between-herd model simulates the movements of infected animals between herds, based on retrospective field data from the French Cattle Tracing System database. Thus our model mimics the spread of bTB in real herds with real animals. The main model output was the incidence per year and per county. Simulated data were compared with observed data. Initial conditions were based on likely herd bTB states on the 1st of July, 2005.
Results: We ran 500 simulations from the 1st of July, 2005 to the 30th of June, 2014 or until disease eradication. Half of the simulations ended before May 2009, and disease eradication was always obtained before June 2014, whereas about 100 outbreaks were reported in France in 2014. The median of the cumulated number of infected herds was 199 herds [179 - 218], far below the 860 outbreaks reported in France between July 2005 and June 2014. Nevertheless, 57% [50 - 64] of the infected herds were beef herds which is consistent with the observed data.
Conclusions: Our results show that cattle trade had little impact on bTB spread in France between 2005 and 2014. The weight of cattle trade in bTB spread is probably much lower than the weight of local transmission. The next step for this work will be to accurately quantify its weight in bTB spread.
Relevance: According to our results, control measures should be focused on local transmission in France.
Bekara M.E.A, Courcoul A., Bénet J.J., Durand B. Modeling Tuberculosis Dynamics, Detection and Control in Cattle Herds. *Plos ONE*, **9**, 1-17 (2014)

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Variability in the response to the single intradermal tuberculin test in tuberculosis-infected and non-infected cattle.

Julio Alvarez[1], Carmen Casal[2], **Maria Luisa de la Cruz**[3], Harrison Quick[4], Alberto Diez-Guerrier[5], Javier Bezos[5], Beatriz Romero[2], Jose Luis Saez[6], Nuria Sanchez[2], Alvaro Roy[2], Emmanouil Liandris[2], Alejandro Navarro[2], Andres Perez[1], Lucia de Juan[2], Lucas Dominguez[2], [1]University of Minnesota, St Paul, MN, [2]Centro VISAVET, Universidad Complutense, Madrid, Spain; [3]Universidad Complutense, Madrid, Spain; [4]Centers for Disease Control and Prevention, Atlanta, GA, [5]MAEVA SERVET SL, Alameda del Valle, Spain; [6]Ministerio de Agricultura, Alimentacion y Medio Ambiente, Madrid, Spain. Contact: ml.cruz@ucm.es

Purpose:
The intradermal tuberculin test (ITT) is the basis of all control and eradication programs against bovine tuberculosis worldwide. Among factors influencing the response to the intradermal inoculation of the antigens, location has been largely deemed as a significant one. However, quantitative evidence on the variation of the test accuracy associated to changes in the site of inoculation is limited. The objective of this study was how to improve the tuberculin test by determining if the response elicited 72 hours after the intradermal inoculation of a bovine PPD antigen was site-dependent.
Methods:
Up to 1,066 animals from infected and non-infected herds were tested with a modified ITT so that each animal received eight inoculations in the neck (four in each side). Qualitative (positive/negative) and quantitative (increase in mm) responses were recorded and analyzed using a hierarchical Bayesian logistic regression model
Results:
A significant effect of the inoculation site was observed in animals from tuberculosis-infected cattle, with sites located in the most cranial region of the neck showing an increased probability of yielding a positive response. In contrast, no effect was observed in animals from tuberculosis-free herds.
Conclusions:
The probability of detecting a reactor in a tuberculosis-infected herd was largely affected by the position in which the bovine PPD was inoculated, being highest in the anterior neck area compared with the other neck areas studied.
Relevance:
Our results suggest that inoculation of the PPD in cranial positions may contribute to the maximization of the sensitivity of the tuberculin test when used in infected populations, while specificity would not be affected in tuberculosis-free populations.

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Physiological stress is associated with false negative outcome in tuberculin skin test in cattle

Siben Li, Paul Bessell, Ian Handel, Mark Bronsvoort, Roslin Institute, Edinburgh, United Kingdom.
Contact: siben.li@roslin.ed.ac.uk

Purpose: Stress can influence immune responses and depending on duration, can suppress cell-mediated immunity. Bovine tuberculosis (bTB) caused by Mycobacterium bovis is mainly diagnosed using the single intra-dermal comparative cervical tuberculin (SICCT) test in Great Britain and Ireland. The test compares immune response of individual cattle to two antigens (bovine and avian tuberculin). Experimental studies suggest that stress and physiological changes can have marked effects on the innate and acquired immune responses in animals affected by mycobacteria infections. The stresses of handling, testing, movement and calving may affect diagnostic test performance, but data are sparse and few analyses have been carried out to estimate their effects. Here we have evaluated various stresses using a case-case approach.
Methods: Animals with identified gross pathology (TB-like lesion and/or bacteria culture) that were SICCT negative within 60 days prior to slaughter (false negatives) were matched with confirmed test positives (true positives). A list of stress-related risk factors was defined from available data for each animal and an unconditional multivariate logistic regression model was fitted to explore their effects.
Results: The probability of a false negative outcome increases with age and male cattle have higher odds of being a false negative compared to females. Repetitive skin tests within 60 and 120 days as well as recent movement and parturition were all statistically associated with being a false negative (a missed infection).
Conclusions: This suggests that the recent life history of the animal may affect the tuberculin test response and this may be partially responsible for the poor test sensitivity. Veterinary health authorities could look to adjust the timings of testing relative to calving, movements and previous test occasions in order to minimise the risks of false negative test.
Relevance: Our results suggest that physiological stress suppresses the SICCT response of bTB-infected cattle, and there is potential for substantial degree of missed infection as a result. Infection missed by SICCT is likely to contribute to persistent and recurrent herd breakdowns.

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Quantitative evaluation of the effectiveness of bovine tuberculosis surveillance in free-ranging wildlife in France using scenario tree modelling

Julie RIVIERE[1], Yann LE STRAT[2], Barbara DUFOUR[1], Pascal HENDRIKX[3], [1]Alfort National Veterinary School, Maisons-Alfort, France; [2]French Institute for Public Health Surveillance, Saint-Maurice, France; [3]French Agency for Food, Environment and Occupational Health and Safety, Maisons-Alfort, France. Contact: julie.riviere@vet-alfort.fr

Purpose and Methods: The surveillance of bovine tuberculosis (bTB) in wildlife is of growing importance as wildlife reservoir can hinder the eradication of bTB in cattle and as surveillance of wild species, not regulated by EU legislation, is constrained by practical difficulties. The sensitivity of the French bTB surveillance system in free-ranging wildlife, implemented in 2011, was assessed for the first time using scenario tree modeling. It relies on three components applied according to geographical risk levels: (i) passive surveillance on hunted wild boar, red and roe deer by carcass examination in all areas, (ii) passive surveillance on animals found dead, moribund or with abnormal behaviour on wild boar, red deer, roe deer and badger in all areas and (iii) active surveillance on wild boar and badger in medium and high risk areas.We developed three scenario trees in which various detection nodes were identified and estimated from the ongoing surveillance data supplemented by experts' opinion when needed (for example the accuracy of hunters for the detection of tuberculosis like-lesions, according to their training, experience and the local situation).
Results: In high risk areas, the probability of detecting at least one infected animal over 100 processed, with a given design prevalence, was estimated at 30% for red deer and roe deer and 60% for wild boar for the carcass examination; from 4% (red deer) to 15% (wild boar and badger) for the surveillance on dead or moribund animals; and about 85% for wild boar and badger for the active surveillance. The hunter's awareness has an impact on the sensitivity of the surveillance varying from 45.9% to 60.9% in wild boar in high risk areas for an untrained and a trained hunter respectively.
Conclusions and Relevance: The results are relevant for hunters and veterinary authorities aiming at knowing the actual efficacy of wildlife bTB surveillance, and could support decision-making processes regarding enhancement of surveillance strategies. Furthermore, the comparison of the cost-effectiveness ratio of each surveillance component allows the identification of the most efficient component's combination according to geographical areas and species.

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Spatial clustering of bovine tuberculosis outbreaks in Uruguay (2011-2013)

Catalina Picasso[1], Julio Alvarez[1], Scott Wells[1], Federico Fernandez[2], Andres Gil[3], Andres Perez[1], [1]University of Minnesota, Saint Paul, MN, [2]Ministry of Livestock, Agriculture and Fisheries, Montevideo, Uruguay; [3]Universidad de la Republica, Montevideo, Uruguay. Contact: picas001@umn.edu

Bovine tuberculosis (BTb) is a chronic disease of cattle caused by Mycobacterium bovis infection. BTb prevalence in Uruguay (Uy) has been traditionally low as a consequence of an active surveillance program in slaughterhouses and dairy farms. Between 2011 and 2013, however, BTb incidence increased, raising concern among farmers, industry, veterinarians, and government authorities.
The goal of this study was to assess the spatial dynamics of BTb outbreaks reported in Uy between 2011 and 2013.
Data provided by the Ministry of Livestock Agriculture and Fisheries in Uy included geolocation, status (positive, negative), and date of detection of the outbreak, for every cattle farm in the country. Fifteen, 26, and 16 outbreaks were reported in 42,759, 43,213, and 42,186 susceptible dairy farms in 2011, 2012, and 2013, respectively. The spatial distribution of new farm-cases, referred to as incident outbreaks, was analyzed using the spatial scan statistic and Cuzick-Edwards (CE) test, realized in SatScan and Cluster Seer software, respectively.
Spatial scan statistics results showed significant (P=0.05) spatial clustering in the three years at the southwestern (2011, 2012, 2013), northwestern and southeastern (2012) Uy. Using CE test, significant clustering at the first and second order of neighborhoods was detected in 2012; however, no significant clustering was identified in the other two years studied. Spatial aggregation of cases in southwestern Uy in 2011 suggests an initial distribution of outbreaks in that specific area, with subsequent local dissemination. BTb introduction into different regions of the country suggests a role for live animal movements on disease spread. A likely consequence of the control measures applied during the epidemic is the retraction of cases in 2013, when a residual aggregation of cases was detected in the northwestern area of Uy.
Results demonstrate the spatial dynamics of BTb in Uy during an extended period of high disease incidence and consequent reduction in the number of farm-cases. These results will help to understand the mechanisms for disease in the country and ultimately, the design and implementation of effective control programs for the disease.

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A phylogeographic analysis of whole genome sequenced *Mycobacterium bovis* isolates sampled in New Zealand.

Joseph Crisp[1], Marian Price-Carter[2], Geoffrey de Lisle[2], Desmond M. Collins[2], Ruth Zadoks[1], Rowland Kao[1], [1]University of Glasgow, Glasgow, United Kingdom; [2]AgResearch, Palmerston North, New Zealand. Contact: j.crisp.1@research.gla.ac.uk

Purpose:
Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, is an important livestock disease raising public health and economic concerns around the world. In New Zealand routine surveillance in domestic cattle and deer herds acts to greatly reduce the prevalence of this pathogen in livestock but at a considerable social and economic cost. In addition the presence of wildlife bTB vectors hampers eradication campaigns.

Methods:
Whole Genome Sequencing (WGS) techniques were used to provide high resolution genetic information to inform a phylogeographic analysis. This research aimed to describe the sampled bTB system in order to better understand the mechanisms of spread and persistence of *M. bovis* in New Zealand. A further aim was to examine the practicality of WGS methods as a molecular typing tool. A Bayesian phylogenetic analysis platform, BEAST, was used to find a representative model of the sampled system. Within this platform, analyses were conducted to estimate the mutation rate, spatial diffusion rate and most likely ancestral host states of the sampled *M. bovis* population.

Results:
The WGS techniques employed added increased resolution in comparison to Restriction Endonuclease Analysis (REA) – a molecular typing tool. A mean mutation rate of 1.05 (95% CI: 0.70-1.43) events per genome per year was estimated. The spatial diffusion rate estimation gave a mean of 1.54 (95% CI: 1.05-2.06) km/year. For the majority of ancestors to the sampled *M. bovis* population, the most likely host state was non-cattle. In addition a dominant direction of *M. bovis* spread from non-cattle populations into cattle populations was observed.

Conclusions:
WGS techniques in combination with powerful Bayesian phylogenetic analyses platforms provide an informative and descriptive picture of the sampled *M. bovis* population. The mutation rate observed was high, relative to those previously estimated for *Mycobacterium* systems. Non-cattle reservoirs were heavily implicated in the maintenance of the sampled *M. bovis* population.

Relevance:
WGS methods are becoming increasingly feasible as an epidemiological tool and add a much improved and needed resolution to epidemiological analyses.

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Risk Evaluation of Farms Neighboring Bovine Tuberculosis Free Farms in Southern Chile

Carla Rosenfeld[1], **Matias Fischer**[2], Luis Paredes[2], Rafael Tamayo[3], Bibiana Benavides[4], Enrique Paredes[5], Edison Alves[2], [1]Universidad Austral de Chile, Valdivia, Chile; [2]Servicio Agrícola y Ganadero, Valdivia, Chile; [3]Universidad Austral de Chile, Valdivia, Chile; [4]Universidad de Nariño, Pasto, Colombia; [5]Universidad Austral de Chile, Valdivia, Chile. Contact: matias.fischer.wilhelm@gmail.com

Purpose:
The Bovine Tuberculosis (bTB) epidemiologic surveillance program in Chile is focused in the risk to bTB-free dairy farms.
The objective of this study was to conduct a qualitative evaluation of the bTB transmission risk from neighboring farms (NF) to bTB-free farms that supply milk to a dairy plant in Southern Chile.
Methods:
We carried out a cross-sectional study that included an epidemiologic survey of both the NF and the bTB-free farms, and an assessment of the bTB status of the NF's cattle done through the application of tuberculin tests.
The survey addressed two issues: the entry to the farms of new animals with unknown bTB status, and the movement of animals in and out the farms due to poor condition of the fences. In both cases, frequency and origin of animals were considered. Farms were classified as medium risk when animals entered the farm with unknown bTB status and/or when fences were in bad condition. Tuberculin tests were only applied in NF classified as medium risk. NF were classified as high risk when they had at least one individual with a bTB-positive test.
Results:
Surveys were conducted in 378 NF and in 112 bTB-free farms. The number of NF for each bTB-free farm ranged from 1 to 20, with an average of 3. NF harbored a total of 77,658 cattle and 91 NF did not have cattle.
77 NF were classified as medium risk due to animals entering the farm with unknown bTB status, and 50 due to fences in bad condition. 18 bTB-free farms were allowing animals entering the farm with unknown bTB status, and 25 had fences in bad condition. 286 farms (both NF and bTB-free) were allowing the entry of animals with unknown bTB status. 175 NF tested negative for tuberculin, and only one farms were infected (prevalence 0.56%).
Conclusions:
We concluded that NF have a low bTB prevalence and that they do not represent risk for milk-supplier bTB-free farms. The bTB surveillance system should focus on milk-supplier bTB-free farms, since they are still allowing the entrance of animals with unknown bTB status. We also concluded that qualitative risk evaluation is a good decision-making tool for risk management in an eradication program. **Relevance:** Generate information to improve decision-making in the control of bTB in Chile.

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Risk factors for bovine tuberculosis - a case-control study in three French departments

Maud Marsot[1], Benoit Durand[1], Axelle Scoizec[2], Marina Béral[3], Yoann Mathevon[4], Ariane Payne[5], Aurélie Courcoul[1], [1]ANSES, Maisons-Alfort, France; [2]DRAAF Aquitaine, InterRegional Epidemiological Veterinary Cell (CIREV), Bordeaux, France; [3]DRAAF Bourgogne, InterRegional Epidemiological Veterinary Cell (CIREV), Dijon, France; [4]Livestock Health Protection Group of Dordogne (GDS Dordogne), Périgueux, France; [5]INRA, UMR Agroécologie Pôle Microbiologie Environnementale et Risque Sanitaire, Dijon, France. Contact: maud.marsot@anses.fr

Purpose:
Although France is officially free of bovine tuberculosis (bTB), the country is experiencing for some years a slight increase in the incidence and geographical spread of the infection. To eradicate bTB from low incidence regions, it is essential to accurately know the infection risk factors. Although several studies identifying bTB risk factors were conducted in the United Kingdom and Spain, no information is available in France up to date. The objective of this work was to study the factors associated with the risk of bTB in cattle herds in the three most affected French departments (Dordogne, Côte-d'Or and the Ardennes).
Methods:
A case-control study was conducting to compare herds having experienced a bTB breakdown between 2012 and early 2014 with randomly selected control herds in the three considered departments. A questionnaire on farming practices, direct and indirect contact between herds (e.g. on pastures or by vehicles or materials), and presence of other domestic species was performed in the selected herds. Other variables of interest related to animal movements between farms and to contacts between herds and wildlife (e.g. wild boar densities) were collected. A conditional logistic regression was then implemented to assess risk factors related to bTB.
Results:
A total of 225 herds (75 cases and 150 controls) were investigated. So far, the univariate analysis revealed a significant effect in 24 factors of 65. These preliminary results highlighted the influence of animal movements between farms, direct and indirect contacts between herds and densities of wildlife on bTB infection of herds.
Conclusions:
Preliminary results illustrate the multifactorial perspective associated with the bTB problem. Further analysis will provide us with information on the multivariate analysis of bTB risk factors.
Relevance:
The identification of the main risk factors will increase the understanding of bTB dynamics and help the decision-makers to implement adapted and targeted surveillance, biosecurity and control measures in France.

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Whole genome sequencing in multi-host pathogen systems: A description of analytical approaches for bovine Tuberculosis in GB, US and NZ.

Rowland R. Kao[1], Richard J. Delahay[2], Daniel J. O'Brien[3], Anthony O'Hare[4], Marian Price-Carter[5], Suelee Robbe-Austermann[6], Liliana Salvador[1], Robin Skuce[7], [1]University of Glasgow, Glasgow, United Kingdom; [2]APHA, Woochchester Park, United Kingdom; [3]Michigan Dept. of Natural Resources, East Lansing, MI, [4]Stirling University, Stirling, United Kingdom; [5]AgResearch, Wellington, New Zealand; [6]USDA, Ames, IA, [7]Agri-food and Biosciences Institute, Belfast, United Kingdom. Contact: rowland.kao@glasgow.ac.uk

Purpose: Multi-host pathogen systems present particular challenges to disease control paradigms. One exemplar of this is Bovine Tuberculosis (bTB) in cattle, with the role of infected wildlife (e.g. badgers in GB, deer in the US and possums in NZ) usually at best only partially understood. However, whole genome sequencing (WGS) of the causative agent, Mycobacterium bovis, is generating exciting new insights into the role of wildlife in disease persistence and spread. Here, we describe a range of quantitative approaches to analyzing these data, highlighting opportunities and pitfalls associated with their interpretation.
Methods: Three different analytical approaches (i) statistical analyses relating genetic distance to known epidemiological risk factors (ii) statistical analyses based on Bayesian evolutionary analyses using the 'molecular clock' of the pathogen population, and (iii) mathematical models jointly estimating epidemiological and genetic processes are used to analyse sequence data for M. bovis from GB, the US, and NZ.
Results: Our analyses of WGS data have identifed transition rates between species (NZ), estimated rates of spatial spread (UK/NZ), identified spatio-temporal correlations between bacteria extracted from cattle and wildlife (UK/US/NZ), and been used to determine species transmission rates (UK), with additional data generation and analysis ongoing.
Conclusions: Using analyses based on WGS, we identify several important features of bTB transmission from wildlife, illustrating as well how an appropriate consideration of the density of available data, the potential for data biases, and the transmission scale determine the most appropriate type of analyses and influence our interpretation of their outcome.
Relevance: WGS is becoming an increasingly common tool for analysis of host-pathogen interactions. By describing the pros and cons (with examples) of various analytical tools, we aim to provide insights into the potential for these data to transform our epidemiological understanding of these challenging problems.

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Effectiveness of risk-based testing of imported animals for bovine tuberculosis in the Netherlands

Clazien J. de Vos, Jeanet A. van der Goot, Fred G. van Zijderveld, Manon Swanenburg, Armin R. W. Elbers, Central Veterinary Institute, part of Wageningen UR, Lelystad, Netherlands. Contact: clazien.devos@wur.nl

Purpose
The Netherlands are officially free from bovine tuberculosis (bTB) since 1999. However, frequent reintroductions occurred in the past 15 years due to importation of infected cattle. Currently, cattle are not tested after importation into the Netherlands. Additional testing (AT) would, however, enhance the probability of detecting an imported bTB infection in an early stage. The goal of this study was to evaluate the effectiveness of risk-based AT for bTB in cattle imported into the Netherlands.
Methods
A generic stochastic import risk model was developed that simulates disease introduction by importation of live animals on an annual basis. Main output parameters are the number of infected animals that is imported (N_{inf}), the number of infected animals that is detected by testing (N_{det}), and the economic loss incurred by importing infected animals (*Loss*). The model was parameterized for bTB. Model calculations were optimized to either maximize N_{det} or to minimize *Loss*.
Results
Model results indicate that the risk of bTB introduction into the Netherlands is very high with N_{inf} = 99 (median) per annum. Random testing of 8% of all imported cattle results in N_{det} = 7 (median), while the median N_{det} = 75 if the sampling strategy for AT is optimized to maximize N_{det}. However, in this scenario, *Loss* is more than doubled if compared to the current situation without AT, because only calves are tested for which cost of detection is higher than the expected gain of preventing a possible outbreak. When optimizing the sampling strategy for AT to minimize *Loss*, only breeding and production cattle are selected for AT resulting in N_{det} = 1 (median). *Loss* is, however, reduced with 75% if compared to the current situation.
Conclusions
We conclude that the effectiveness of AT can greatly be improved by risk-based sampling. The optimal sampling strategy for risk-based AT for bTB depends on the objective of AT. To minimize *Loss*, AT should focus on breeding and production cattle.
Relevance
The model used in this study is a generic import risk model that can be used to evaluate the import risk and the optimal sampling strategy for AT for any livestock disease.

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Comparing output-based surveillance models to substantiate the tuberculosis free status of the Danish cattle population

Alessandro Foddai[1], Liza Rosenbaum Nielsen[2], Preben Willeberg[3], Lis Alban[1], [1]Danish Agriculture & Food Council, Copenhagen, Denmark; [2]University of Copenhagen, Copenhagen, Denmark; [3]National Veterinary Institute, Technical University of Denmark, Copenhagen, Denmark. Contact: afo@lf.dk

We compared two published studies on models used to assess the performance of the surveillance system to substantiate freedom from bovine tuberculosis (bTB) in Denmark, if meat inspection were to be changed from the current meat inspection methods (CMI) to visual-only inspection (VOI). In one study, the surveillance system sensitivity (SSe) was estimated to substantiate confidence in bTB detection and in bTB free status. In the other study, the SSe was part of the estimation of the negative predictive value (NPV) of the system to substantiate the confidence in bTB free status. Both studies found that changing from CMI to VOI would decrease the SSe. However, the two studies reported diverging conclusions regarding the effect on the substantiation of Denmark as a bTB free country.The study objectives were: a) to investigate why the conclusions differed, and b) to create a hybrid model based on elements from both studies to evaluate the impact of a change from CMI to VOI of slaughtered cattle on the confidence in bTB freedom.The hybrid model was based on a stochastic scenario tree using the NPV approach. The NPV was updated on an annual basis for each of 42 years of test-negative surveillance data considered (1995-2037), while assuming a low (<1%) annual probability of introduction of bTB into the Danish cattle population.
The most important reasons for the diverging conclusions were: the output-based surveillance standard chosen to substantiate the bTB free status (SSe vs. NPV) and the number of years of surveillance data considered. With the hybrid model the NPV reached a level ≥ 95% after the first year of surveillance and remained ≥ 97% with both CMI and VOI until the end of the analyzed period.It is appropriate to use the NPV of the surveillance system to substantiate bTB free status using documented test-negative surveillance results over an extended period of time while maintaining a low probability of introduction of bTB into a cattle population. In Denmark, the probability of introduction of bTB should be kept < 1% on an annual basis.These results could be considered when deciding if the CMI can be replaced by VOI in cattle abattoirs in countries for which a high confidence in bTB freedom can be demonstrated.

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Estimating the Impact of potential Changes to Meat Inspection on the Sensitivity of Abattoir Surveillance for bovine Tuberculosis in Ireland

Preben Willeberg[1], Isabella Higgins[2], Erik Houtsma[2], Simon More[2], [1]DTU Vet, Copenhagen, Denmark; [2]UCD School of Veterinary Medicine, University College Dublin, Dublin, Ireland. Contact: prwil@vet.dtu.dk

The European Food Safety Authority (EFSA) has recently published a series of opinions to assess the impact of changing from the current meat inspection procedures (CMI) to alternative visual-only inspection (VOI) procedures. The aim of the proposed changes is to increase the safety of products from the main meat-producing species by minimizing the risk of microbiological cross-contamination, e.g. caused by palpation and incision of carcasses. Potential negative effects of these changes for animal health surveillance have also been evaluated.
Some EU countries, including Ireland, do not have OTF (Official Tuberculosis Freedom) status, and field-testing and routine meat inspection (MI) are both used to detect cases of bovine tuberculosis (bTB). Concern has been raised that changes from CMI to VOI will adversely affect the effectiveness of bTB surveillance in these countries.
Purpose: We estimate the impact of proposed changes from CMI to VOI on the probability of detecting one or more animals with a confirmed bTB lesion in non-restricted herds in Ireland.
Methods: An @Risk simulation model was developed for the estimation, using the assumed changes in the inspection sensitivity as described by EFSA in their 2013 bovine opinion. Slaughterhouse data from Ireland during 2010 - 2012, with > 4 million cattle from > 86,000 herds, were used to characterise the distributions of number of cattle slaughtered from, and within-herd bTB prevalence of, non-restricted herds.
Results: The model estimates for average herd-sensitivity were 84 - 87% for CMI, and 58 - 60% and 48 - 49%, for VOI, assuming a three-fold and five-fold decrease, respectively, in inspection sensitivity of VOI relative to that of CMI.
Conclusions: If VOI were introduced in EU cattle abattoirs without alternative surveillance means to compensate for the decrease in abattoir surveillance sensitivity, such changes might jeopardise bTB control and eradication programs in non-OTF countries, including Ireland.
Relevance: MI has a dual purpose of contributing to secure public health and food safety, as well as to enable surveillance of animal health and welfare, and both aims should be supported by MI procedures applied at any time.

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A bovine tuberculosis model for England and Wales (BoTMEW) allows investigation of control options

Colin P. D. Birch, Oliver Tearne, Anthony Goodchild, Animal and Plant Health Agency, Addlestone, United Kingdom. Contact: colin.birch@apha.gsi.gov.uk

Purpose:
During recent decades, bovine tuberculosis (bTB) has increased in Great Britain until it now dominates animal health interventions by the public sector. Its dynamics and control are complicated by the strong association of infection in cattle with infection in badgers. Controls have escalated so that many measures are being applied together. This model was developed at farm level resolution to allow analysis of the impacts of these multiple control measures in England and Wales.
Methods:
To represent specific surveillance regimes, as well as allowing direct comparison of model outputs with detailed records of herd level cases (´breakdowns´), the model explicitly estimates the numbers of breakdowns detected by five surveillance streams: regular herd tests, post breakdown tests(tests detecting recurrence in herds recently cleared of infection), other targeted herd tests, pre-movement tests and surveillance at slaughter. Parameters for a baseline model were established, then local and widespread modifications to parameters were used to represent new control measures introduced since 2012, to project their future impacts. The potential impacts of future control options, including cattle vacination and expanded culling and vaccination of badgers, were also compared.
Results:
By assuming persistent local wildlife reservoirs of infection in high incidence areas, a short term run of the baseline model (2008-2010) could be fitted close to the distribution of breakdowns among surveillance streams and major control regions in 2010, including the observed low number of breakdowns in low incidence areas, which other models have exceeded.
Conclusions:
Current measures were found to be sufficient to maintain bTB in low incidence areas at low levels and further reduce it. Substantial reductions within high incidence areas depend on processes about which there is limited knowledge, especially the persistence of bTB in badger populations and the impact of culling and vaccination
Relevance:
The model has provided a detailed description of the state of bTB in England and Wales, which is consistent with disease records and current understanding.

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Long-term drivers of bovine tuberculosis at the country level: reconstructing the impacts of herd structures and of control programs in France, 1965-2000

Mohammed el Amine Bekara[1], **Aurélie Courcoul**[1], Jean-Jacques Bénet[2], Benoit Durand[1], [1]University Paris Est - Anses, Maisons-Alfort, France; [2]University Paris Est - ENVA, Maisons-Alfort, France. Contact: aurelie.courcoul@anses.fr

Purpose. The application of mandatory control programs from 1965 allowed France to obtain the bovine tuberculosis (bTB) free status in 2000. However, the disease was not eradicated, and an upsurge of cases is observed since 2004 in some areas. Three surveillance and control programs were successively applied between 1965 and 2000, and herd structures have simultaneously undergone major changes. The objectives of this study were to reconstruct the dynamics of the within-herd bTB transmission between 1965 and 2000 and to analyze the respective weights of herd structures and of control programs on the bTB transmission.
Methods. A stochastic dynamic model allowed reconstructing the within-herd bTB dynamic in average French herds in 1965, 1980 and 2000. A simulation protocol was defined and a sensitivity analysis was performed.
Results. Most simulation outputs were consistent with field data collected between 1965 and 2000.
Conclusions. According to our model, the evolution of herd structures turned out to have a stronger effect on between-herd bTB transmission on pastures, than changes in the control programs.
Relevance. Eradicating the disease in France is likely to be complex as the ability of veterinary services to steer the evolution of herd structures and husbandry practices is limited.

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An evidence informed evaluation of *M. paratuberculosis*, a controversial public health issue

Lisa Waddell[1], Andrijana Rajic[2], Katharina Staerk[3], Scott McEwen[4], [1]Public Health Agency of Canada, Guelph, ON, Canada; [2]Food and Agricultural Organisation, Rome, Italy; [3]Royal Veterinary College, London, United Kingdom; [4]University of Guelph, Guelph, ON, Canada. Contact: lisa.waddell@phac-aspc.gc.ca

Purpose:
Canada has one of the highest reported prevalence estimates (161- 319/ 100 000) of Crohn's disease. The multi-factorial etiology of Crohn's is not well understood; *Mycobacterium avium* subsp. *paratuberculosis* is the leading infectious disease candidate. To evaluate the zoonotic potential of *M. paratuberculosis* and human exposures to *M. paratuberculosis* using a mixed method approach.
Methods:
Research was evaluated and summarized using a stakeholder-engaged scoping review and systematic review-meta-analysis. Additional insights were solicited through administration of an international expert survey.
Results:
The evidence from 128 studies on the zoonotic potential of *M. Paratuberculosis* and 251 studies examining human exposure to *M. paratuberculosis* will be presented, along with the results from 171 completed expert surveys (54% response rate). The stakeholders were instrumental in defining the many sources of human exposure to *M. paratuberculosis*; ruminants, environment, water and food whose relative contributions will be presented.
Conclusions / Relevance:
After 30 years there are still important knowledge gaps including uncertainty about *M. paratuberculosis'* role in Crohn's disease and poor sensitivity of diagnostic tests. In agreement with the experts, evidence and knowledge gaps, *M. paratuberculosis* remain a low priority public health issue globally. This project provides transparent, contextualized evidence informed inputs for our stakeholders and public health decision makers.

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Prevalence and risk factors for bovine tuberculosis in the state of Santa Catarina using design-based models

Flávio P. Veloso[1], Ana Lourdes A. A. Mota[2], Karina D. Baumgarten[1], Fernando Ferreira[3], José S. Ferreira Neto[3], José H. H. Grisi Filho[3], Ricardo Dias[3], Marcos Amaku[3], Evelise O. Telles[3], **Vitor S. P. Gonçalves**[2], [1]CIDASC, Florianópolis, Brazil; [2]Universidade de Brasília, Brasília, Brazil; [3]Universidade de São Paulo, São Paulo, Brazil. Contact: vitorspg@unb.br

Several Brazilian states have recently carried out major epidemiological studies to underpin the planning of the national programme for control and eradication of bovine brucellosis and tuberculosis. In Santa Catarina, a random sample survey was carried out in 2012 to estimate the prevalence and investigate risk factors for bovine tuberculosis (BTB). The state was divided in five geographical regions and in each one of them was taken a simple random sample of bovine herds with adult females. In each selected herd a sample of adult females (> 2 years) was tested for bovine tuberculosis and it was administered a questionnaire to collect data on animal production and management practices that could be associated to the presence of the disease at the herd-level. The prevalence of herds with test-positive animals at estimated at 0.50% [IC 95%: 0.074%; 0.93%], whereas the prevalence for adult females was 0.06% [IC 95%: 0%; 0.12%]. After a preliminary univariable analysis, a standard model-based logistic regression was used to test for confounding and to assess the goodness-of-fit and the discriminatory performance of the predictive model. Then, the same variables were used to develop a design-based model, taking into account the sampling weights of each herd, considering the regions as a sampling strata, which is more appropriate for population inference. Both models gave results of the same magnitude, but the standard errors were wider in the design-based logistic regression, as expected: the Odds Ratio for herds with more than 18 adult females (3rd quartile of the herd-size) was 7.68 [IC 95%: 1.22%; 48.39%] and the dairy farms showed an Odds Ratio of 10.43 [IC 95%: 2.00%; 54.25%] compared to the beef or dual-purpose herds. These results confirm that dairy herds, where animals are kept in partial or full confinement, and larger herds, that tend to be more production intensive, have higher risk for BTB. Although the design-based model is more appropriate for estimating population parameters using a complex sample survey, the methods for model building are not fully developed.

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The risk of Bovine Tuberculosis test failure in cattle post movement in Ireland.

Elizabeth A. Lane, Peter K. Maher, **Margaret Good**, Department of Agriculture, Food and the Marine, Dublin, Ireland. Contact: margaret.good@agriculture.gov.ie

Purpose:
Over a three-year period, 7.8M cattle movements onto farms resulted in 402,365 (5.2%) movements into a herd that subsequently experienced a Bovine Tuberculosis (bTB) breakdown. The aim was to estimate 1) the risk of bTB test failure after movement; 2) the proportion likely infected before moving; and 3) the effect of test interval prior to the move on the likelihood of test failure.

Methods:
Data were gathered on cattle movements (402,365) into herds that subsequently had a bTB breakdown. A backwards stepwise multivariable logistic model was utilised to develop models to evaluate the independent factors, test-type, year, interval from movement to breakdown, accounting for herd structure, on the risk of becoming positive to test.

Results:
0.8 % of animals moved into herds with a subsequent bTB breakdown are skin test positive, within two months.
2.7 % of animals that moved herds within a year subsequently are bTB skin test positive.
The porportion of animals with a positive test increases ($P > 0.01$) with each time category.
The odds ratio for bTB positive skin test increases ($P > 0.01$) with increasing length of time in herd.
Animals 4.3 (CI 3.2 - 5.6) times greater risk of positive skin test one year after movement compared to those tested within 60 days of movement (referent category).
Higher risk test-types (e.g. reactor, contiguous, factory lesion) were more likely to have an animal bTB test positive compared with lower risk test-types - risk category 2 and risk category 3 were 3.2 (CI 2.3 - 4.5) and 2.6 (CI 1.7 - 4.2) times, respectively, more likely to have positive skin test compared with lower risk test-types.
There was a significant effect of year on the outcome and this was accounted for in the logistic regression models.

Conclusions:
The risk of bTB was greater the longer the moved animal is in the new herd and the higher risk category the next test type scheduled for that herd.
Based on our findings, in excess of 2.6 million individual pre-movement tests would be required to find an additional 1000 skin test positive animals in each given year.

Relevance:
The results of this study have been used to determine the need to reintroduce a pre-movement bTB test requirement for high-risk herds.

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Modeling within- and between-farm transmission of bovine tuberculosis using dynamic cattle movement networks in Uruguay

Kimberly VanderWaal[1], Eva Enns[2], Catalina Picasso[1], Julio Alvarez[1], Andres Perez[1], Federico Fernandez[3], Andres Gil[4], Meggan Craft[1], Scott Wells[1], [1]University of Minnesota, St. Paul, MN, [2]University of Minnesota, St. Paul, MN, [3]Ministry of Livestock Agriculture and Fisheries, Montevideo, Uruguay; [4]Universidad de la Republica, St. Paul, Uruguay. Contact: kvw@umn.edu

Bovine tuberculosis (bTB) causes great economic losses due to costly surveillance, culling of infected herds, and imposition of movement restrictions in affected regions, while also posing a public health concern. Although network models of epidemiological processes are often useful for understanding between-farm transmission of livestock diseases, these approaches are difficult in bTB in part due to the chronic nature of the disease characterized by long latent periods, low within-farm transmission rates, and limitations of diagnostic tests. Thus, between-farm transmission models must run over long time periods and incorporate within-farm dynamics in order to characterize the between-farm spread of bTB and identify efficient surveillance strategies. We developed an integrated within- and between-farm stochastic transmission model that simulates the spread of bTB in a network of cattle farms. Due to the slow nature of bTB spread, a dynamic network of movements was used to allow connections to change over time. Transmission between farms occurred via movements or local spatial spread. We developed this model utilizing data on cattle movements and bTB incidence from Uruguay, a country with comprehensive animal traceability. We investigated how the size and spatial extent of an epidemic, in the absence of surveillance or control, was influenced by characteristics of the index farm. We found that in our network, epidemics originating in dairy farms resulted in significantly larger epidemics with greater spatial extents than epidemics originating from other production types. Epidemics originating in farms with <5 cattle resulted in epidemics with smaller spatial extents. Network position and geographic location of the index case were also correlated with epidemic size and extent. Applications to risk-based surveillance and control are discussed. The model used in this work unites within-herd, between-herd and spatial transmission dynamics to provide a unique and realistic representation of the spread of bTB, and will provide a modeling framework that can be applied to other livestock systems.

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Linking bovine tuberculosis in badgers to environmental variables using Bayesian hierarchical analysis

Aurélie Courcoul[1], Asma Saidouni[1], Edouard Réveillaud[2], Marina Béral[3], Ariane Payne[4], Benoit Durand[1], Maud Marsot[1], Céline Richomme[5], [1]Anses, Maisons-Alfort, France; [2]Anses, Maisons-Alfort, France; [3]DRAAF Bourgogne, Dijon, France; [4]INRA, Dijon, France; [5]Anses, Malzéville, France. Contact: aurelie.courcoul@anses.fr

Purpose. Although France is officially free of bovine tuberculosis (bTB), the infection is not eradicated. The country is experiencing an increase in bTB incidence and in some areas, wildlife has been reported infected. A surveillance network of bTB in badgers, wild boar and red deer (Sylvatub programme) is currently implemented but the spatial context of bTB epidemiology in badgers has not been investigated so far. The objective of this work was to identify the highest risk areas of bTB in badgers in the French department of Côte-d'Or and the factors associated with this risk.
Methods. Using the number of badgers analyzed and the number of badgers bTB positive in each administrative unit of Côte-d'Or, we implemented a hierarchical Bayesian model to assess the Standard Incidence Ratio (SIR) of bTB in badgers in each of these administrative units and to link it to variables of interest. The model took into account the spatial correlation between the spatial units. Variables of interest were related to cattle farming (e.g. farm or animal densities), bTB in cattle (e.g. incidence), landscape (e.g. wood or edge density) and wildlife characteristics (e.g. wild boar or red deer densities approximated by hunting bags) in each spatial unit.
Results. Over the 2,147 badgers analyzed in Côte d'Or between 2009 and 2014, 93 were bTB positive. We highlighted an excess risk of bTB in badgers in some administrative units of the west of the department. Besides, some variables related to bTB in cattle, landscape diversity and wildlife densities were identified as associated with bTB in badgers.
Conclusions. The relationship between bTB in badgers and bTB in cattle was expected. However, our findings also support the premise that landscape and wild game factors are associated with bTB in badgers. bTB infection in Côte-d'Or is therefore a complex multi-host system where both ecological and epidemiological considerations have to be taken into account.
Relevance. This work is a step of an analysis of surveillance data which aim to help French decision-makers to better design control measures against bTB, targeting the high-risk administrative units and addressing the bTB problem in a comprehensive way.

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Impact of routine hormone treatments for the reproductive management of dairy herds on reproductive efficiency and methane emissions

Simon Archer[1], Chris Hudson[1], Jude Roberts[2], Martin Green[1], [1]University of Nottingham, Sutton Bonington, United Kingdom; [2]Zoetis UK Ltd, Tadworth, United Kingdom. Contact: simon.archer@nottingham.ac.uk

Purpose: The aim of this study was to evaluate variation between herds in the change in cost and methane emissions associated with 3 simple interventions to manage breeding in early lactation.
Methods: Data for 10,000 herds of 200 cows were simulated. Probability of conception was predicted daily from the start of the study (at a calving) for each cow up to day 300 of lactation. Four scenarios of differing first insemination management were simulated for each herd using the same theoretical cows: A baseline scenario based on breeding from observed oestrous events only, synchronisation of oestrous for fixed time first insemination using 2 methods, and a regime using prostaglandin treatments followed by first insemination to observed oestrous events. Cows that did not conceive to first insemination were re-inseminated following detection of oestrous. For cows that conceived, gestation length was 280 days with cessation of milking 60 days before calving. Those cows not pregnant after 300 days of lactation were culled and replaced by a heifer. Daily milk yield was calculated for 730 days from the start of the study for each cow. Change in mean reproductive and economic outputs were summarised for each herd following each intervention. For each scenario, methane emissions were determined by daily forage dry matter intake, forage quality, and cow replacement risk.
Results: Improvement in herd fertility using the programmes investigated was associated with reduced cost and methane emissions.
Conclusions: Economic and environmental improvements associated with reduced methane emissions could occur if farmers can be persuaded to adopt programmes to improve the first service management of dairy cows.
Relevance: Controversial management interventions for dairy cows, such as routine exogenous hormone treatments increasingly require robust justification for their use, and this study provides the framework for decision support tools.

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Food systems approach to zoonotic disease interventions: a case study of brucellosis in Albania

Mieghan Bruce[1], Toni Kirandjiski[2], Jonathan Rushton[1], Ylli Pema[2], Javier Guitian[1], Nigel Poole[3], [1]Royal Veterinary College, London, United Kingdom; [2]"Improving consumer Protection Against Zoonotic diseases – Albania" EuropeAid/128304/C/SER/AL, Tirana, Albania; [3]School of Oriental and African Studies, London, United Kingdom. Contact: mbruce@rvc.ac.uk

Purpose: Successful and sustainable control of zoonoses has proven to be elusive in many countries, despite the recognition that effective technical solutions are available. Although control policies have been implemented in Albania for over sixty years, brucellosis persists in people and livestock. The food system encompasses the activities and interactions of people involved in production to consumption and disposal of agricultural goods, within the broader social, political, and economic environment. We argue that positioning the analyses of zoonoses within the food system will provide new insights for effective control.
Methods: Using brucellosis as an example, a framework for conceptualizing zoonotic disease dynamics in the food system was developed. The framework is composed of seven components and the interactions between them: (i) the aetiological pathogens, (ii) the host species, (iii) infectious material (iii) places of risk, (iv) people at risk, (v) intervention options and (vi) the social, economic and political settings within the system. Data on the food system and brucellosis in Albania were collected from farmer interviews, focus groups, direct observation and relevant literature.
Results: In Albania, brucellosis is both an occupational and food-borne disease and intervention strategies need to target both forms at multiple levels. People can take measures to protect themselves against exposure, for example heat-treating milk. However other farm-level interventions require an enabling institutional structure such as provision of practical waste-disposal sites. Targeting roadside butchers as high-risk groups, will require a nuanced approach because of the regulatory environment that makes these activities nominally illegal. Finally, the national policy prescribes livestock vaccination but government budget constraints threaten its success.
Conclusions: An understanding of the multiple determinants of brucellosis is required for successful control.
Relevance: The food systems framework can be used to identify context specific areas to combat zoonoses and help anticipate factors that may threaten the success of control policies.

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Importance of improving productivity in motivating animal health risk management

Russell D. Bush[1], James R. Young[1], Sonevilay Nampanya[1], Sothoeun Suon[2], Syseng Khounsy[3], **Peter A. Windsor**[1], [1]University of Sydney, Narellan NSW, Australia; [2]Department of Animal Health and Production, Phnom Penh, Cambodia; [3]Department of Livestock and Fisheries, Luang Prabang, Lao People's Democratic Republic. Contact: peter.windsor@sydney.edu.au

Background
Improvements in animal health risk management require appropriate incentives for farmers to alter practices. Identification of 'entry points' for initial farmer engagement provides an effective platform for promotion of health, welfare and production interventions capable of improving enterprise productivity and profitability.
Methods
Research conducted in Cambodia and Lao PDR (2007-2014) utilized paired villages, High Intervention (HI) receiving health and production interventions and Low Intervention (LI) receiving minimal disease control interventions to act as a control. Initial engagement provided free vaccination against foot and mouth disease (FMD) and haemorrhagic septicaemia (HS). In HI villages, participatory training in forage feeding, providing ad libitum water and risk management through village level biosecurity was provided.
Results
Feeding forages for 4-months achieved gains of 0.32 and 0.22 kg/day respectively compared to 0.04 and 0.09 kg/day for free-grazing to provide an estimated increase in cattle value in Cambodia of US$ 61.29 and US$ 78.00 in Lao PDR. The gains would increase if farmers supplied the recommended 15% of liveweight per day instead of 8%. By project end HI farmers disease knowledge scores were 97.5% compared to LI farmers at 47.2% ($P<0.001$).
Discussion
Although similar constraints applied in each country, the 'entry point' to engage farmers was very different. Forage growing (from 2.7 ha to 45 ha in four years) and feeding providing the best incentive for farmers in Cambodia due to rice straw being the year-round staple feedstuff of cattle. However, in northern Lao PDR where native rangeland grasses were sufficient to increase liveweights during the wet season, freedom from livestock disease through vaccination gained greater success. Avoiding endemic disease losses from FMD and HS was highly valued by farmers in both countries as both diseases were active in neighbouring sites.
Conclusion
The strategy of identifying key project entry points provided a superior platform for uptake and adoption of health and production interventions, leading to increased animal values and improved smallholder livelihoods and food security.

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Assessing and understanding the food safety and zoonosis risk practices of the beef, sheep and goat Nairobi food systems using value chain analysis.

Pablo Alarcon[1], Patrick Muinde[2], Maurice Karani[2], James Akoko[2], Eric M. Fèvre[3], Paula Dominguez-Salas[1], Stella Kiambi[4], Barbara Häsler[1], Jonathan Rushton[1], [1]Royal Veterinary College, London, United Kingdom; [2]International Livestock Research Institute, Nairobi, Kenya; [3]Institute for Infection and Global Health, Liverpool, United Kingdom; [4]University of Nairobi, Nairobi, Kenya. Contact: palarcon@rvc.ac.uk

Purpose

Beef, sheep and goat food systems are thought to be important sources of pathogens in Nairobi. This study aimed to use value chain (VC) analysis to investigate food safety and zoonotic risk practices of these systems.

Methods

VC analysis is commonly used to assess market structures yet its potential to investigate food safety and zoonotic risks is unexplored. In a cross-sectional study of people in Nairobi's beef, sheep and goat food systems (farmers to consumers), data were collected through 75 focus groups and 571 interviews. Data were obtained on movement of people, animals and products (chain mapping), power groups, rules, incentives and enforcement (governance), barriers, distribution of benefits and food safety and zoonoses risk practices. Data were analysed to produce chain profiles and quantify commodity flows and gross margins. Qualitative analysis identified food safety, zoonosis and VC themes.

Results

Eight chain profiles were identified, with the 'less integrated terminal markets' representing three quarters of the city's ruminant meat supply. Main food safety and zoonotic risk practices related to: water and equipment contamination; poor cold chain; human contact contamination; animal movements; and lack of hygiene. Poor governance enhanced these risks such as: inadequate market business models; enforcement failures; control gaps; and power group pressures. Barriers identified to corrective actions were: lack of infrastructure; limited financial capacity; poor training and services. Furthermore, unequal distribution of benefits in low cost markets provided a negative incentive for the perpetuation of risks.

Conclusions

This study identified main food safety and zoonoses risk practices, people and VC factors involved in risk-taking activities to help future control programmes in the Nairobi beef, sheep and goat system.

Relevance

Food safety risks and diseases can be effectively controlled and understood when these are investigated using a food system approach which considers chain governance, barriers and inequalities. The methods used provide a clear guideline and way forward for epidemiologists to investigate these risks using a VC approach.

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Host Mobility and Foot-and-Mouth Disease Transmission

Hyeyoung Kim[1], Ningchuan Xiao[1], Mark Moritz[2], Rebecca Garabed[3], [1]The Ohio State University, Columbus, OH, [2]The Ohio State University, Columbus, OH, [3]The Ohio State University, Columbus, OH, Contact: kim.3594@osu.edu

Purpose: Animal and human movements have a fundamental impact on disease transmission over time and across regions. However, the exact role of different types of movement in transmission of infectious diseases is likely specific to the disease and setting. To address this issue, we developed agent-based models of foot-and-mouth disease (FMD) transmission in the Far North Region of Cameroon.
Methods: We modeled the dynamic pattern of host herds' daily and seasonal movements for three management systems: mobile, sedentary, and trans-boundary trade based on population data collected over a five-year period (2008-2012). By isolating and removing different management types, we can simulate theoretical disease dynamics and better understand the role of each type of movement in disease transmission. We then compare the simulation results from all considered scenarios with an empirical data set of reported outbreaks from 2010-2014.
Results: Simulation results of mobile herds alone demonstrate that after a year an FMD outbreak ceases, implying that mobile herds cannot produce a completely endemic situation without the presence of other management types. On the other hand, simulations including all types of the management systems produce an endemic situation or repeated epidemics.
Conclusions: Our model provides an effective methodological framework to represent daily and annual movement of herds and to explore their impact on FMD transmission. By employing an ABM model, we successfully incorporate individual herd movements in the simulations and bring the model closer to the data. Our results are in line with the empirical evidence that we obtain from herder reports of clinical sign of disease.
Relevance: With more simulation and estimation, this model will provide new insights into FMD transmission in the Far North of Cameroon and other, similar systems.

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Impacts of land use and biodiversity changes on the risk of selected zoonotic diseases: observations from a case study in an arid/semi-arid area in Kenya

Bernard K. B. Bett[1], Said Mohammed[2], Rosemary Sang[3], Salome Bukachi[4], Johanna Lindahl[1], Salome Wanyoike[5], Ian Njeru[6], Delia Grace[1], [1]ILRI, Nairobi, Kenya; [2]ILRI, Nairobi, Kenya; [3]KEMRI, Nairobi, Kenya; [4]University of Nairobi, Nairobi, Kenya; [5]Ministry of Agriculture, Nairobi, Kenya; [6]Ministry of Health, Nairobi, Kenya. Contact: b.bett@cgiar.org

Purpose:
We carried out a study in irrigated and pastoral areas in a semi-arid region in Kenya to investigate linkages between land use and biodiversity changes and the risk of selected zoonotic pathogens including Rift Valley fever virus (RVFV), West Nile virus (WNV), dengue fever virus, *Leptospira* spp, *Brucella* spp and *Coxiella burnetti*. The study tested the hypothesis that disease regulation as an ecosystem service is affected by changes in biodiversity, climate and land use, with differential impacts on peoples' health and wellbeing.
Methods:
The study was implemented between 2012 - 2014 and the activities conducted included: ecological analyses to quantify changes in land use and their effects on ecosystem services; entomological surveys to characterise mosquito species by habitat and season; and livestock and human sampling to determine the prevalence of the pathogens listed above. Data collected were analysed using multiple models including ecological niche models to predict the distribution of the various mosquito species in the area and a stochastic partial differential equation model (SPDE geostatistical model) to predict the risk of these pathogens in space.
Results:
Irrigated areas have had a drastic decline in biodiversity and are infested with a large variety of mosquito species that are capable of transmitting multiple arboviruses. Outputs from the SPDE model used to analyse sero-prevalences of these pathogens in people suggest a significant variation in their distribution as follows: WNV and dengue fever virus are more prevalent in irrigated and riverine areas compared to pastoral rangelands; *leptospira* spp and *brucella* spp are more prevalent in pastoral areas and RVFV and *C. burnetti* occur in equal proportions across the areas.
Conclusions:
We observe that irrigation has had significant impact on biodiversity and the distribution of important zoonotic pathogens. The distribution of these diseases across the sites closely mirrors those of the key reservoir hosts and the livelihood practices by area.
Relevance: The information generated would inform the on-going debate on the linkages between biodiversity and the occurrence of emerging infectious diseases.

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Saving Lives in Paradise: Rabies Control Program in Bali, Indonesia

Pebi P. Suseno[1], Ratna V. Ekowati[1], Ernawati R[1], James McGrane[2], I. P. Sumantra[3], Mardiatmi M[1], Pudjiatmoko P[1], [1]Directorate of Animal Health, Jakarta Selatan, Indonesia; [2]FAO ECTAD, Jakarta Selatan, Indonesia; [3]Livestock and Animal Health Services, Denpasar, Indonesia. Contact: pebi212@yahoo.com

Purpose:
Rabies was confirmed in southern Bali in late 2008. Initial dog vaccination and culling of unconfined dogs was not successful to control the disease and by June 2010 rabies has spread to all nine districts in Bali with 149 human deaths recorded until end of 2014. Integrated rabies control program was implemented to reduce cases in both human and animal.
Methods:
Starting In 2010, an island-wide dog vaccination campaign was implemented, the strategy in all vaccination campaigns focused on achieving at least 70% vaccination coverage in each sub-village in Bali by using vaccination teams with specially-trained dog catchers. These teams enabled vaccination of the roaming dog population. Vaccination campaign was planned and managed from the provincial level.
A well-managed campaign implementation system was put in place with the following key components: 1) SMS and paper reporting system, 2) scheduled coordination meetings, and 3) development of campaign-specific SOPs. Key people in the campaign management and field staff were trained based on their responsibilities in the SOP such as dog catching and handling, vaccination, cold chain and logistics management, rapid response, communication, surveillance and integrated human bite case management. The best vaccination teams was selected and assigned to conduct sweeping vaccination for all unvaccinated dogs in the island. The progress of the vaccination campaign was monitored using the RVC database.
Results:
Using this well-managed and coordinated control strategy more than 70% of dogs were vaccinated (estimated dog population around 350.000) in 4297 sub-villages within a three month period annually. This simple strategy successfully reduced the human cases by 98% in 2013 compared to 2010 and animal cases by 77% in 2011 compared to 2010.
Conclusions:
This experience in Bali shows that dog vaccination strategy with monitoring and management of vaccination activities can effectively reduce rabies in both animals and humans.
Relevance:
The work of animal health staff to vaccinate dogs and coordination with human health staff to conduct integrated bite cases management is a real example of one health concept in action.

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Potential sources and transmission of Salmonella and antimicrobial resistance in Kampala, Uganda

Josephine A. Afema[1], Denis K. Byarugaba[2], Devendra Shah[1], Esther Atukwase[2], Maria Nambi[2], William M. Sischo[1], [1]Washington State University, Pullman, WA, [2]Makerere University, Kampala, Uganda. Contact: jaafema@vetmed.wsu.edu

Purpose: In sub-Saharan Africa, non-typhoidal Salmonella serovars cause invasive disease, but the sources of infection and transmission pathways are poorly understood.
Methods: Salmonella from various sources in Kampala were serotyped, screened for antimicrobial resistance, and common serovars were genotyped using multiple locus variable number tandem repeat analysis or pulsed-field gel electrophoresis.
Results: Salmonella was detected in 6/10 influent and 6/10 effluent samples from a wastewater treatment plant (WTP); 16/30 influent from 3 waste stabilization ponds (WSP); 13/24 storm/wastewater from a channel draining the city; and 9/22 flush-water from two abattoirs that process cattle, sheep and goats. Salmonella was only detected in effluent of one WSP (3/10). Overall, 6.6% of poultry fecal samples from four live bird markets, and 4% of swine fecal samples at slaughter were Salmonella positive. We obtained 774 isolates from all sources, identified 32 serovars, and 61.2% were susceptible to a panel of 15 antimicrobials. Salmonella from cattle, goats, sheep and swine were mostly pan-susceptible (95%), whereas 19.3% poultry isolates were resistant to 10 antimicrobials (deca-resistant), and were associated with Salmonella Kentucky. Similar genotypes and resistance phenotypes were found in common serovars from various sources and historical isolates.
Conclusions: Our results indicate some Salmonella clones have disseminated and persisted amongst humans, livestock and the environment.
Relevance. Concurrent detection of similar strains in the abattoirs or WTP and the channel suggests environmental pollution, and could be mitigated by regulation and enforcement. Restriction of deca-resistant S. Kentucky to poultry, while less resistant S. Kentucky occurred in poultry, human and environmental sources suggests host or management factors could be responsible. Unlike S. Kentucky, other serovars in poultry were not associated with extensive drug-resistance; a plausible explanation is that S. Kentucky is prone to acquiring resistance; however, the mechanisms and factors driving resistance remain undetermined and need to be investigated.

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Population impact of leptospirosis on public health and livestock production

Juan M. Sanhueza, Cord Heuer, Emilie Vallée, Peter R. Wilson, Jackie Benschop, Julie M. Collins-Emerson, Massey University, Palmerston North, New Zealand. Contact: j.m.sanhueza@massey.ac.nz

Purpose:
In New Zealand, leptospirosis in humans is caused primarily by occupational exposure to animals (abattoir workers, farmers, veterinarians, etc.). Disease notification rates are thought to underestimate the true incidence, especially of mild cases. Disease burden has not been quantified to date. The objective of this study was to estimate the public health burden, the production loss in beef cattle, sheep, deer and the overall economic cost of leptospirosis.
Methods:
Five independent studies were used to estimate disease burden: I) a one year prospective cohort study in meat workers; II) two cross-sectional studies in farmers and veterinarians, and III) two longitudinal studies of disease-specific production loss in livestock. The studies in humans estimated the risk of influenza-like illness due to Leptospira exposure in the population (population attributable risk [PAR]). Census data on occupations and PAR information were subjected to stochastic simulation to estimate the expected number of leptospirosis cases for these occupations. Health insurance data provided the cost associated with clinical reported cases. The public health burden of leptospirosis was measured by Disability Adjusted Life Years (DALYs).
Results:
The expected number of human leptospirosis cases was 13-fold higher than the notified number. Livestock production loss was higher than economic loss due to DALYs. The stochastic distribution of DALYs and economic loss will be presented at the conference.
Conclusions:
Leptospirosis is substantially underreported in New Zealand. Results from livestock studies suggest that vaccination (as a means to protect humans) may be profitable in a proportion of beef cattle and deer herds.
Relevance:
Findings of the economic impact inform livestock industries about the feasibility of propagating vaccination of specific livestock sub-populations to reduce the public health burden of leptospirosis.

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Value chain analysis for products and by-products of egg laying birds in peri-urban areas of Nairobi City

Joshua O. Onono[1], Pablo A. Lopez[2], Maurice Karani[3], Patrick Muinde[3], James Akoko[3], Carron Maud[2], Eric Ferve[4], Barbara Haesler[2], Jonathan Rushton[2], [1]University of Nairobi, Nairobi, Kenya; [2]Royal Veterinary College, UK, London, United Kingdom; [3]International Livestock Research Institute, Kenya, Nairobi, Kenya; [4]International Livestock Research Institute,Kenya; University of Liverpool, UK, Liverpool, United Kingdom. Contact: jonono@rvc.ac.uk

Livestock keeping in urban areas is a source of livelihoods for poor urban families, but it also poses public health challenges.

Purpose

This included mapping of value chains for products from commercial layers (CL) and indigenous layers (IL) kept in peri-urban areas of Nairobi City, prioritization of barriers to entry into layer farming and assessment of disease and food safety management.

Methods

Data on interaction between people and poultry products, barriers to entry and disease and food safety management were collected through key informant interviews, focus group discussions (FGD) and administration of questionnaires. Twelve FGD were conducted and 250 questionnaires administered to individual farmers. Additional data was obtained from retailers of poultry products and government officers.

Results

The CL farms kept between 100 and 1,000 birds per flock while for IL farms, flock sizes were between 1 and 50 birds. CL farms obtained day old chicks from distributors of large and small-scale hatcheries and from hawkers, while IL farms obtained chicks from small-scale hatcheries and neighbouring farms. Products from these farms were eggs, spent hens and poultry manure. Eggs from CL farms were sold to shops, consumers and hawkers, while those from IL farms were sold to neighbours, bakeries and restaurants, while some were consumed at home. Spent layers were sold to brokers, neighbours and households. Poultry manure was used on crop farms and as feed for dairy cattle. The barriers to entry included poor quality feeds, poultry diseases, seasonality and scarcity of water and land. The diseases included coccidiosis, Newcastle disease and respiratory problems and these were managed by personnel from “agrovets”, while in slums sick birds were slaughtered and consumed. Furthermore, hawkers and personnel from restaurants and shops were reported to lack training in food safety.

Conclusion and relevance

Risk for zoonoses exists along poultry value chains and hence with increasing urbanization in developing countries, investigation of food systems in cities should adopt this framework to better understand public health risks.

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Elimination of rabies from an endemic area by targeting strategic key points

Johann L. Kotzé[1], Geoffry T. Fosgate[2], [1]Government, Malelane, South Africa; [2]University of Pretoria, Pretoria, South Africa. Contact: johann.vet@gmail.com

Purpose:
Canine rabies is controlled mainly through the vaccination of dogs. It is generally accepted that a herd immunity of 70% would result in its elimination but is seldom achieved due to poor resource allocation. The objective of this study was to determine if the strategic application of vaccinations could eliminate rabies from an endemic area since the 1950's.
Methods:
Beginning in 2009, rabies vaccinations were focused at strategic points along the borders between sub-populations of the study area. The rationale was to prevent the spread of infection between the sub-populations and allowing natural extinction of the virus in the smaller sub-populations. Phylogeographic analysis of rabies virus have shown that regional variants arise and disappear with time. In 2012 the last positive case was diagnosed in the study area whilst a maximum of only 45% population immunity was achieved. To determine if the strategy was responsible for the success, a logistic regression model was developed using data from 2002 to 2014. The strategic application of vaccinations and the total number of vaccinations were included as determinant variables with elimination as the response variable.
Results:
The model showed the strongest association in two areas of the meta-population that were amenable to strategic application due to their specific topography. These had p-values lower than 0.001 associated with the strategy and no significant association with the number of vaccinations. Another two areas of commercial farmland showed no significant association with any of the study variables.
Conclusions and Relevance:
It is concluded that strategic placement of rabies vaccination campaigns can isolate sub-populations and assist to eliminate rabies within a meta-population. This requires fewer resources and could help resource poor countries to achieve elimination.

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Cephalosporinase-producing enteric bacteria recovered from patients at the OSU Medical Center, 2013: Microbiologically, are we what we eat?

Dixie Mollenkopf[1], Roger Faubel[2], Preeti Pancholi[2], Timothy Landers[3], Matthew Erdman[4], Joshua Daniels[5], Thomas Wittum[1], [1]Ohio State University, Columbus, OH, [2]Ohio State University Medical Center, Columbus, OH, [3]Ohio State University, Columbus, OH, [4]National Veterinary Services Laboratories, Ames, IA, [5]Ohio State University, Columbus, OH, Contact: mollenkopf.12@osu.edu

Purpose:
The dissemination of Enterobacteriaceae expressing resistance to β-lactam antimicrobials, which are therapeutically used in both human and veterinary medicine, is of critical concern. The normal commensal flora of food animals may serve as an important reservoir for the zoonotic food-borne transmission of Enterobacteriaceae harboring β-lactam resistance. We hypothesized that the predominant β-lactamase genes reported in US livestock and fresh retail meat products, $bla_{\text{CMY-2}}$ and $bla_{\text{CTX-M}}$, would also be predominant in human enteric flora.

Methods:
We recovered enteric flora from a convenience sample of OSUMC patients included in the hospital *Clostridium difficle* surveillance program in order to screen for and estimate the frequency of carriage of AmpC, ESBL, and CRE resistance genes. In- and outpatient diarrheic submissions (n=692) received for *C. difficle* culture at the OSUMC clinical diagnostic laboratory from July to December, 2013 were included. Aliquoted to a transport swab, each submission was inoculated to MacConkey broth with cefotaxime and incubated at 37°C. This broth was inoculated to MacConkey agars supplemented with cefepime, cefoxitin, and meropenem to select for the ESBL, AmpC, and CRE phenotypes.

Results:
Our selective culture yielded 196 isolates (28 %) with reduced susceptibility to cefotaxime. Of these, 21 (3.0%) samples harbored *E. coli* isolates carrying the AmpC bla_{CMY}. Another 21 (3.0%) samples produced isolates harboring the ESBL $bla_{\text{CTX-M}}$: 19 carrying CTX-M-15 and 2 with CTX-M-27. Two (0.3%) samples produced *Klebsiella pneumoniae* isolates expressing carbapenem resistance. Of these, 1 *K. pneumoniae* carried a plasmid mediated NDM-1 while the second isolate harbored KPC-3.

Conclusion:
Our results indicate that β-lactamase resistance genes likely acquired through zoonotic food-borne transmission are present in the enteric flora of this hospital-associated population at lower levels than reported in livestock and fresh food products.

Relevance:
The zoonotic food-borne transmission of resistant enteric bacteria may not produce an important reservoir of bacterial resistance genes in human enteric flora.

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Knowledge Attitudes and Practices (KAPs) of livestock owners toward brucellosis in Jordan

Imadidden I. M. Musallam, Mahmoud N. Abo-Shehada, Javier F. Guitian, Royal Veterinary college, Herts, United Kingdom. Contact: Imusallam@RVC.AC.UK

ABSTRACT

Purpose: To evaluated livestock owners' knowledge, attitudes and practices with regard to brucellosis in Jordan.

Methods: Between May and October 2013, 537 livestock-keeping households were selected across the whole country by means of stratified random sampling. In each household, someone with animal husbandry responsibilities and someone regularly involved in elaboration of dairy products, were administered a questionnaire during face-to-face interviews.

Results: The results show that livestock keepers across Jordan are highly aware of brucellosis and of the risk of infection if raw milk is consumed. Awareness of the risk of infection through direct contact with infected livestock or via consumption of dairy products made from unpasteurized milk is considerably lower. These knowledge gaps manifest in a high frequency of high-risk practices such as assisting in animal parturition or disposing aborted foetuses without protective gloves or masks and not boiling milk before preparation of dairy products. When brucellosis is suspected, basic hygiene practices are often disregarded and suspect animals are freely traded.

Conclusions and Relevance: In the short-term, public health education should be enhanced as the disease is likely to remain endemic in the ruminant reservoir as long as a suitable compensation program is not established and trust on available vaccines regained.

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Estimates of the Relative Contributions to the Burden of Disease due to Selected Foodborne Hazards: a World Health Organization Expert Elicitation.

Tine Hald[1], Willy Aspinall[2,3], Brecht Devleesschauwer[4,5,6], Roger M. Cooke[7], Timothy Corrigan[8], Arie H. Havelaar[9,10,11], Herman Gibb[12], Paul R. Torgerson[13], Martyn D. Kirk[14], Fred J. Angulo[15], Robin Lake[16], Niko Speybroeck[5], Sandra Hoffmann[17], [1]National Food Institute, Technical University of Denmark, Søborg, Denmark; [2]Bristol University, Bristol, United Kingdom; [3]Aspinall & Associates, Tisbury, United Kingdom; [4]Ghent Univeristy, Merelbeke, Belgium; [5]Université catholique de Louvain, Brussels, Belgium; [6]Institute of Tropical Medicine, Antwerp, Belgium; [7]Risk Analysis Resources for the Future, Washington, DC, [8]GAVI Alliance, Geneva, Switzerland; [9]University of Florida, Gainesville, FL, [10]National Institute for Public Health and the Environment (RIVM), Bilthoven, Netherlands; [11]Utrecht University, Utrecht, Netherlands; [12]Gibb Epidemiology Consulting LLC, Arlington, VA, [13]University of Zurich, Zurich, Switzerland; [14]The Australian National University, Canberra, Australia; [15]Centers for Disease Control and Prevention, Atlanta, GA, [16]Institute of Environmental Science and Research, Christchurch, New Zealand; [17]U.S. Dept. of Agriculture, Washington, DC, Contact: tiha@food.dtu.dk

Purpose: The Foodborne Disease Burden Epidemiology Reference Group (FERG) was established in 2007 by the World Health Organization (WHO) to estimate the global burden of foodborne diseases (FBDs). This estimation is complicated because most hazards causing FBD are not transmitted solely by food, but have several transmission routes including transmission from animals, humans, and environmental sources. In 2014, we conducted an expert elicitation study to estimate the relative contribution of food to the global burden of diseases commonly transmitted through the consumption of food.
Methods: Structured expert judgment using Cooke's Classical Model was applied to obtain food attribution estimates for 19 hazards in 14 WHO subregions. Experts were identified by professional network sampling and selected based on experience. Experts were scored on their ability to judge uncertainty accurately and informatively using subject relevant "seed" questions whose answers were unknown to the experts at the time of interview. The 5th, 50th and 95th percentile responses to the seed questions were used to weight and aggregate the expert responses to the "target" questions regarding transmission routes.
Results: A total of 72 experts were enrolled. Pathogens with one or more animal reservoirs (e.g. *Salmonella* spp. and *Toxoplasma gondii*) were assessed by the experts to have a higher proportion of illnesses attributable to food than pathogens with a human reservoir, where human-to-human transmission (e.g. *Shigella* spp. and Norovirus) or waterborne transmission (e.g. *Salmonella Typhi* and *Vibrio cholerae*) were judged to dominate. For many of the pathogens, the foodborne route was assessed relatively more important in developed subregions than in developing subregions.
Conclusions: For the first time, we present worldwide estimates of the proportion of specific diseases attributable to food and other major transmission routes.
Relevance: The findings are essential for estimating the global burden of FBDs. While gaps were identified, we believe the estimates are the best current source of guidance to support decision makers when allocating resources for intervention, and for future research.

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Raw milk vendors are here to stay-how to decrease the public health risks?

Pamela Woods[1], Joan Burumu[2], Susan Richardson-Kageler[3], Pious Makaya[2], [1]University of Zimbabwe, Harare, Zimbabwe; [2]Ministry of Agriculture, Mechanisation and Irrigation Development, Harare, Zimbabwe; [3]University of Zimbabwe, Harare, Zimbabwe. Contact: pwoods.zim@gmail.com

Purpose

Informal roadside milk markets have appeared in Zimbabwe in the last decade with smallholder and resettled farmers also selling milk locally. These "illegal" milk sales occur parallel to existing formal milk marketing and public health systems. Vendor distribution, milk suppliers, and potential hazards posed by informal milk sales in Zimbabwe are not known.

Methods

All informal milk vendors found long the 7 major roads going into the capital Harare from 110 km radius were interviewed with structured questionnaires about their raw milk sources, management and sales during January to March 2014 and 2015. Purchased milk and vendor's site water samples were cultured at Central Veterinary Laboratories, Harare

Results

75 informal milk vendors selling raw milk were interviewed and milk and their water supplies sampled. The average milk volume for sale was 17L +/- SD= 9.7 and was sold in Coke bottles. Most vendors purchased milk for resale, only 28% sold milk from their own farms. 57% of milk samples had TBC > 300 cfu/ml, while "milk from own farm" related to safe TBC levels ($\chi 2=10.27$, $p=0.001$). Coliform levels (mean ±SD) of 2±2.11 differed between categories of selling points ($F=4.961$ $DF=5$ $p<0.001$) unrelated to water source type. "Raw milk transport from source by bicycle" was associated with E.coli ($\chi 2=8.46$, $p=0.01$) (prevalence 4%), and "by foot" together with "volume milk for sale" were associated with S.aureus (44%) ($\beta=4.807$ $p=0.001$, $\beta=0.264$ $p=0.003$). Vendors' knowledge of milk hygiene was low but their income from milk sales was important, especially for women.

Conclusions

The milk sold by vendors grouped in two categories, either "risky" or "possibly safe". Health education of vendors and consumers would increase public safety.

Relevance

National efforts to increase milk supply have also resulted in entrepreneurial vendors and public health risks. Public health policies should include this emerging sector that provides low priced milk and livelihoods.

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Use of mixed logistic regression to evaluate the correlation of hygiene levels and the presence of Salmonella in large swine slaughterhouses.

Luis G. Corbellini[1], Alfredo Bianco Júnior[2], Eduardo de Freitas Costa[1], Ana Sofia Ribeiro Duarte[3], Elenita R. Albuquerque[2], Jalusa D. Kich[4], Marisa Cardoso[1], Maarten J. Nauta[3], [1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil; [2]Ministério da Agricultura, Florianópolis, Brazil; [3]National Food Institute, Søborg, Denmark; [4]Embrapa Suínos e Aves, Concórdia, Brazil. Contact: luis.corbellini@ufrgs.br

Purpose: Pork is an important source of Salmonella to humans. Abattoir hygiene is a key factor to avoid carcass contamination and microbial indicators such as Enterobacteriaceae, which are found in the environment and in the intestine of animals, can be used to assess the safety of food processing. It can be hypothesized that Salmonella occurrence is associated with Enterobacteriaceae counts (EC) on the carcass surface. However, the extent of this association requires investigation, as many factors such as variation provided by slaughterhouse and day of sampling can influence this relationship.
Methods: Mixed logistic regressions with random effects were performed to assess the change in the log of EC and its correlation with Salmonella using two data sets. The first describes the EC and Salmonella isolation in 60 pork carcasses sampled at 11 slaughter steps, including the carcass as a random effect. The second describes the EC and Salmonella isolation on 1,150 pre-chill carcasses sampled in 13 slaughterhouses over 230 sampling days, and the model combined two random intercepts, slaughterhouse and date of sampling nested with slaughterhouse.
Results: Significant associations ($p < 0.0001$) between EC and Salmonella occurrence were found in both models. Nevertheless, although strong associations were found, they were not constant, given that there was a high variation in the probability of a carcass being positive for Salmonella according to the EC mainly between days of samples. The effect of the day of sampling on the Salmonella prevalence was so large that the predictive value of the EC count for Salmonella isolation in a daily basis was compromised.
Conclusion: It is possible that in some days, batches with a high prevalence of Salmonella carriers shedding a high number of Salmonella were slaughtered. In these days, the hazard of contamination/cross-contamination of carcasses will be so high that even a hygienic slaughter, confirmed by the low EC on carcasses, will not be able to avoid the presence of Salmonella on some carcasses.
Relevance: The results of this study demonstrate that it may be difficult to predict when hygiene failure measured via EC actually indicates Salmonella contamination.

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A collaborative cross-sectional study of brucellosis and Q fever in humans and livestock in village households in Afghanistan

Joanna McKenzie[1], Zarif Akbarian[2], Ghulam Ziay[3], Bashir Noormal[2], Islam Saeed[4], Abul Hussain[5], Zabiullah Shahab[2], Tania Dennison[6], Ron Jackson[1], **Roger Morris**[1], [1]Massey University, Palmerston North, New Zealand; [2]Afghan National Public Health Institute, Kabul, Afghanistan; [3]3Central Veterinary Diagnostic & Research Laboratory, Kabul, Afghanistan; [4]Afghan National Public Health Institute, Kabhul, Afghanistan; [5]General Directorate of Animal Health and Production, Kabul, Afghanistan; [6]Animal Health Development Project, Kabul, Afghanistan. Contact: roger.morris@morvet.co.nz

Little information is available on zoonotic diseases of ruminants and their effect on associated householders under different ecological and husbandry settings in Afghanistan. Objectives of the study were to:

1. Determine seroprevalence of brucellosis in humans, small ruminants and cattle.
2. Identify risk factors for brucellosis sero-positivity in humans.
3. Determine seroprevalence of *Coxiella burnetti* (Q fever) in the sample populations.

Methods

A cross sectional survey was implemented in six secure districts in Herat Province in December 2012 and January 2013, including 20 random households in 10 random villages. In each household a blood sample was collected from up to 5 people, up to 10 female sheep and goats of breeding age and up to 5 female cattle of breeding age. A questionnaire on knowledge, attitudes and practices associated with brucellosis was collected from each household. Serum samples were tested for brucellosis using the Rose Bengal Test and a competitive ELISA in series, and for Q fever using an indirect ELISA. Ethics approval was obtained from the Afghan Institutional Review Board.

Results

Blood samples were collected from 1017 humans, 876 goats, 1143 sheep and 344 cattle in 204 households from 11 villages (6 Kuchi (nomadic) and 5 sedentary). Brucellosis seroprevalence in people was 5%, with at least one seropositive person in 16% of households. Brucellosis seroprevalence in animals was 1.6% in goats, 0.6% in sheep, and 0.3% in cattle, with 12% of households having at least one seropositive animal. Q fever seroprevalence in humans was 64%, with at least one seropositive person in 97% of households. Q fever seroprevalence in animals was 43% in sheep, 53% in goats, 5% in cattle, with at least one seropositive animal in 99% of households.

Conclusions

Brucellosis results were broadly consistent with other Asian countries with comparable husbandry systems, but the extremely high Q fever prevalence was unexpected.

Relevance

The study provided baseline information for planning and monitoring future interventions and greatly strengthened collaboration, coordination and capability of veterinary and public health professionals from government, NGOs and donor funded projects.

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The effect of wind on Q fever transmission: a mechanistic approach

Francois Beaudeau[1], Thierry Hoch[1], Mohamed-Lemine Brahim[1], Alain Joly[2], Simon Nusinovici[1], [1]INRA - ONIRIS (Nantes-Atlantic National College of Veterinary Medicine), Nantes, France; [2]GDS Bretagne, Vannes, France. Contact: francois.beaudeau@oniris-nantes.fr

• Purpose: There is a consensus on the main role of the wind in the transmission of C. burnetii, the agent of Q fever, between ruminants and from ruminants to humans. However, no study so far has focused on the mechanisms associated with this airborne transmission. The objective of the present study was, using a mechanistic epidemiological approach, to investigate the processes underlying the so-called wind effect and to assess its influence on the incidence risk for C. burnetii infection. This approach was here applied to the transmission process between dairy cattle herds.
• Methods: Ninety-five dairy cattle herds located in the Finistère department (western France) were subjected to samplings of bulk tank milk and indoor dust every 4 months over a one-year period, in order to determine their C. burnetii status using PCR tests. A total of 27 incident herd-periods (negative-tested on both PCR tests and becoming positive-tested at least once on the subsequent sampling time) and 71 negative herd-periods (negative-tested on both PCR tests over two consecutive sampling time) were retained for analysis. For a given herd, the effect of (i) the cumulated number of bacteria in herds located under the main wind direction (BW), and (ii) the mean wind speed in this area (WI) on its risk of becoming incident was assessed using logistic regression.
• Results: Compared to herds in areas with low WI (≤5.5 m/s), the risk was significantly higher (OR = 4.76; CI: [1.42-16.0]) in herds in areas with high WI (>5.5 m/s) and high BW (>20); whereas the risk was not significantly different from unity in other situations.
• Conclusions: In agreement with our assumptions, C. burnetii transmission to a free herd occurs only in case (i) the wind itself transporting from infected sources, and (ii) the load of the contaminated particles/aerosols generated, are high enough to act jointly.
• Relevance: These results provide decision makers with relevant basis for orienting preventive actions (eg. vaccination) in rural and peri-urbans areas, in order to lower the C. burnetii burden in the environment, and hence to limit both the transmission between ruminant farms and the zoonotic risk, in areas that are particularly at risk.

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Q fever infection in dairy cattle herds: increased risk with high wind speed and low precipitations

Simon Nusinovici[1], Jenny Frössling[2], Stephan Widgren[2], Francois Beaudeau[1], **Ann Lindberg**[2], [1]INRA - ONIRIS (Nantes-Atlantic National College of Veterinary Medicine), Nantes, France; [2]Swedish National Veterinary Institute (SVA), Uppsala, Sweden. Contact: ann.lindberg@sva.se

• Purpose: The propagation of the bacteria between ruminant herds may either result from its passive transport through wind and/or the introduction of infected shedder animals into free herds. However, the impact on C. burnetii spread between farms of the air-borne dispersion relatively to movements of possibly infected domestic cattle has not been yet quantified. This information would help to make relevant decisions on the control measures to implement against C. burnetii spread. The objectives of this study were (i) to describe the spatial distribution of Q fever infected dairy cattle herds in Sweden, (ii) to quantify the respective contributions of wind and animal movements on the risk of infection, while accounting for other sources of variation and (iii) to investigate the possible protective effect of precipitation.
• Methods: A total of 1,537 bulk milk samples were collected and tested for presence of C. burnetii antibodies. Putative clusters of positive-tested herds were detected by spatial statistical analysis using SaTScan. The contribution of the investigated factors was quantified using multivariable logistic regression.
• Results: The prevalence of positive-tested herds was higher in the south of Sweden. For herds located in areas with high wind speed, open landscape, high animal densities and high temperature, the risk of being infected reached very high values. Compared to climatic and environmental factors, the contribution of animal movements to the risk of infection was limited. Finally, the cumulated precipitations over one year were identified as a protective factor.
• Conclusions: Meteorological factors highly impact the risk of C. burnetii infection.
• Relevance: Because these factors are not controllable, vaccination could be an appropriate control measure. In windy areas with open landscape, high animal densities and high temperature, the vaccination of cattle in both infected and still free herds may contribute to limit both the risk of transmission between cattle herds and also the zoonotic risk.

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Leptospirosis and Q fever in slaughterhouse workers in western Kenya

Elizabeth A. J. Cook[1], Lian F. Thomas[1], William A. de Glanville[1], Barend M. deC. Bronsvoort[2], Njeri Wamae[3], Sam Kariuki[3], Eric M. Fèvre[4,1], [1]International Livestock Research Institute, Nairobi, Kenya; [2]University of Edinburgh, Edinburgh, United Kingdom; [3]Kenya Medical Research Institute, Nairobi, Kenya; [4]University of Liverpool, Liverpool, United Kingdom. Contact: annievet1@gmail.com

Purpose:
Zoonotic diseases are underreported and often misdiagnosed; thus the true prevalence of these pathogens in Kenya and elsewhere is unknown. Slaughterhouse workers are considered a high risk group for exposure to zoonoses due to their intimate contact with animals and animal products. This study examined slaughterhouse workers in Kenya for zoonotic diseases, identified risk factors for exposure and compared rates of exposure to that of the wider community.
Methods:
The study was conducted in rural western Kenya between February and October 2012. In total 142 slaughterhouses and 738 workers participated. A comprehensive questionnaire was administered to participants. Blood samples were tested by ELISA for exposure to leptospirosis and Q fever. Risk factor analyses for zoonotic disease exposure in slaughterhouse workers were conducted using multivariable logistic regression.
Results:
The unadjusted seroprevalence of leptospirosis in slaughterhouse workers in western Kenya was 13.4% (CI95 11.1-16.1) and Q fever was 4.5% (CI95 3.2-6.2). This is compared to the unadjusted seroprevalence of leptospirosis in the community of 6.5% (CI95 5.1-8.3) and Q fever 1.5% (CI95 0.9-2.5). The odds ratio for leptospirosis seropositivity in slaughterhouse workers was 2.3 (CI95 1.6-3.4) and for Q fever was 1.9 (CI95 1.0-3.8) times that of the community.
Risk factors associated with exposure to leptospirosis in slaughterhouse workers included: having wounds (OR 2.7; CI95 1.4-5.3); smoking at work (OR 1.8; CI95 1.1-3.0); eating at work (OR 2.1; CI95 1.2-3.6); and cleaning the intestines (OR 3.8; CI95 1.8-8.2). The risk factors significantly associated with exposure to Q fever included: being intoxicated at work (OR 3.2; CI95 1.1-9.4).
Conclusions:
This is the first report of these zoonoses in slaughterhouse workers in Kenya. The study quantified the rates of exposure in slaughterhouse workers compared to the community. Potential risk factors for zoonotic disease exposure in slaughterhouses were identified.
Relevance:
Information will be used to recommend targeted training for slaughterhouse workers, managers and inspectors regarding the risks and methods to reduce disease transmission.

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Intercontinental dissemination of salmon bacterial kidney disease (BKD) through fish trade and movement.

Ola B. Brynildsrud[1], Edward J. Feil[2], Jon Bohlin[3], Santiago Castillo-Ramirez[2], Duncan Colquhoun[4], Una McCarthy[5], Iveta M. Matejusova[5], Linda D. Rhodes[6], Gregory D. Wiens[7], David W. Verner-Jeffreys[8], [1]NMBU, Oslo, Norway; [2]U of Bath, Bath, United Kingdom; [3]Public Health Institute, Oslo, Norway; [4]NVI, Oslo, Norway; [5]Marine Scotland, Aberdeen, United Kingdom; [6]NOAA, Seattle, WA, [7]USDA, Leetown, WV, [8]CEFAS, Weymouth, United Kingdom. Contact: ola.brynildsrud@nmbu.no

Purpose:
Salmon aquaculture goes back at least to the 18th century, and have since developed into the fastest-growing food production sector on the planet. Through efforts of pioneers, salmon and ova have been extensively moved, traded and used for stocking purposes across much of the world. Unfortunately, this has in some cases contributed to propagation of disease. The present study examines the transmission history of *Renibacterium salmoninarum*, causative agent of the important bacterial kidney disease (BKD) in salmonid fish.
Methods:
Using Next-Generation Sequencing, we explore single nucleotide polymorphisms (SNPs) between 68 strains isolated 1960-2009 from a worldwide range of locations. We use Bayesian evolutionary analyses for phylogenetic inference, phylogeographics as well as population parameter estimates.
Results:
We robustly delineate two major lineages to the *R. salmoninarum* phylogenetic structure, diverging prior to modern aquaculture. The data suggests intercontinental spread of the major lineage, lineage 1, concurrent with anthropogenic movements of fish, feed and ova.
Conclusions:
Globalization and aquaculture expansion contributed to the dissemination of *R. salmoninarum*, although the disease was likely endemic to some areas prior to this.
Relevance:
The findings demonstrate the need for strict biosecurity measures in an increasingly globalized world. It represents a landmark in using advanced methodology for the study of aquaculture pathogens.

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Case definitions applied to clinical and subclinical Bacterial Kidney Disease (BKD) in salmonid aquaculture in Atlantic Canada

Annette S. Boerlage, Javier Sanchez, Henrik Stryhn, K. Larry Hammell, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada. Contact: aboerlage@upei.ca

Purpose: Bacterial Kidney Disease (BKD) causes loss in salmonid aquaculture in Atlantic Canada. Causative agent of BKD is the Gram-positive bacteria *Renibacterium salmoninarum*. Infected salmon are often asymptomatic (subclinical infection) and the disease is considered chronic. One of the challenges in quantifying information from farm production and health records is the application of a standardized case definition.
Methods: We explored case definitions for farm-level and cage-level clinical and subclinical BKD in a retrospective longitudinal study in Atlantic Canada combining: 1) industry records of weekly production data like growth and mortalities, 2) passive syndromic surveillance for BKD using reports of veterinarians and aquatic health workers on fish sampling during routine mortality dives (y/n/not done), 3) diagnostic submissions and test results (+/-/not done), and 4) treatments to control BKD (y/not done). Classification trees were used to characterize BKD events. Alternative definitions were explored such as: varying mortality threshold, varying signs for a BKD event, and integrating farm-level status (parallel with cages) into the definition for a subclinical infected cage. Accuracy of clinical test definitions were assessed as sensitivity and specificity relative to less and more restrictive gold standard definitions, combined with individual assessment of records around the events.
Results and Conclusion: Cages were regarded 'susceptible' (uninfected) by default and become 'subclinically infected' upon a BKD event, defined by the presence of BKD in a report, positive test result for BKD, or treatment for BKD. 'Clinical infection' was designated when a cumulative mortality ≥5% occurred during a rolling 4-week period within a fixed number of weeks of a BKD event. 'Clinical infection' reverted to 'subclinical infection' when the rolling 4-week cumulative mortality fell below the 5% threshold.
Relevance: This study shows how industry data can be used to standardize case definitions for BKD, a required component of risk factor investigations associated with *R. salmoninarum* transmission and the impact of infections on productivity.

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Pathogen surveys of imported ornamental fish to assess biosecurity risk to Australia

Joy A. Becker[1], Paul Hick[1], Kate Hutson[2], Alison Tweedie[1], Terrence Miller[2], Richard Whittington[1], [1]University of Sydney, Camden, Australia; [2]James Cook University, Townsville, Australia. Contact: joy.becker@sydney.edu.au

Purpose:
In Australia, 18 million ornamental fish are imported annually under a policy based on an import risk analysis (IRA) published in 1999. Recently, it was demonstrated that pre-export biosecurity measures, health certification provided by exporting country authorities and post-arrival quarantining of fish in Australia were insufficient to prevent entry of fish with subclinical infections of exotic pathogens. Of particular interest was gourami iridovirus, which was the subject of an IRA published in 2014. The objective of this project is to provide scientific data to underpin disease risk minimization for imported ornamental fish.
Methods:
Repeated cross sectional surveys were undertaken in imported ornamental fish under quarantine prior to entry into Australia for the presence of nationally listed aquatic pathogens and to identify parasite assemblages. Freshwater fish were tested to the OIE standard to detect 2% prevalence with 95% confidence assuming a test of 100% sensitivity and specificity. Marine fish were tested for specific viral pathogens with a design prevalence of 10%.
Results:
Fish hosts were prioritised based on prior knowledge of infection with the listed pathogens, volumes of importation to Australia and current import conditions. Testing of quarterly samples identified pathogens of biosecurity concern. Few external parasites were detected on any of the fish examined and typically were limited to ciliate infestations. Internal parasite fauna included members of protozoa, myxozoa, trematoda, cestoda and nematoda.
Conclusions and relevance:
From March 2016, Australia will require health certification for families of gourami, cichlid and poeciliid to be declared free of gourami iridovirus. Concurrently, Australia is trialing a new system for managing biosecurity risks associated with imported ornamental fish by shifting the emphasis of risk management off-shore. The results of this project will be used to inform national biosecurity policy and the current trial using a random surveillance model to manage the biosecurity risks of imported ornamental fish.

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Spatial epidemiology of infectious Piscirickettsia salmonis affecting farmed salmon in Chile

Fernando O. Mardones[1], Rolando Ibarra[2], Alfredo Tello[2], Matias Medina[2], Matias Medina[2], Gustavo Monti[1], [1]Universidad Austral de Chile, Santiago, Chile; [2]Instituto Tecnológico del Salmon, Puerto Montt, Chile. Contact: fomardones@uach.cl

Purpose:
We investigated the spatio-temporal distribution of SRS and risk factors associated with SRS-mortalities, emphasizing the role of density-dependency indicators such as the distance between farms and number of stocked fish.
Methods:
A longitudinal study was carried out collecting retrospective information for cohorts of farmed salmon that were transferred to the sea after Dec. 2010 and harvested before Jan. 2014, and that were held on the same farm for at least 6 months (mo). Analyses included mixed effects Cox regression models and the use of the scan statistic test for the detection of spatio-temporal clusters of SRS.
Results:
Overall, 83% of the cohorts reported mortalities attributable to SRS, with median time-to-first SRS-mortalities of 4, 5 and 6 mo post transfer for Atlantic salmon, rainbow trout and Coho salmon, respectively. Four variables were retained in the final fitted model: reported mortalities caused by infectious pancreatic necrosis virus (IPNV) (hazard ratio [HR] = 1.7), and salmon stocked on summer compared to fall (HR = 1.32) were associated with reduced time to disease; whereas time-to-first SRS-mortalities was longer for farms located at the 11th region compared to the 10th region (HR = 0.69), and Coho salmon compared to Atlantic salmon (HR = 0.49). Factors used as proxies for density-dependency processes were insignificant here. 6 spatio-temporal clusters were identified mostly during summer at the 10th (n=3) and 11th (n=3) regions.
Conclusions:
SRS is widely distributed, affecting all farmed salmon species and most areas. The association between IPNV and SRS is a key finding that demonstrates the need for an integrated management of infectious diseases. Reporting clusters may suggest that passive transmission in seawater from SRS-infected farms (proximity) could be, in part, a critical factor in controlling disease, however, the occurrence of such clusters, mostly during summer, may indicate that increased water temperatures together with some stocking or harvesting practices may exacerbate this disease.
Relevance:
SRS has an estimated annual cost of USD 770 million, and our results are useful for the design of more cost-effective strategies.

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Risk factors associated with Piscirickettsia Salmonis (SRS) outbreaks in salmonids during their marine phase, in Chilean production sites

Gustavo Monti[1], Adriana Mendoza[2], Marilyn Wolter[2], [1]Universidad Austral de Chile, Valdivia, Chile; [2]SGS Chile Ltda., Puerto Varas, Chile. Contact: gustavomonti@uach.cl

Purpose
To assess risk factors associated with SRS mortality outbreaks in Atlantic Salmon (AS) and Rainbow Trout (RT) that started their marine phase between 2010 - 2013.
Methods
A retrospective study design was used using all complete production cycles that started between 01/01/2010 and 31/12/2011. A case was considered when the daily specific mortality rate for a cage exceeded 0,02 % and there was presence of fishes with clinical signs associated with SRS and confirmed by PCR. Data was available from 4 companies that contributed with 61 sites that included 1,186 cages located in the XI Region. Information was obtained from the company's databases and by a questionnaire to the responsible veterinarians or technician after a training session.
The association between risk factors and SRS status was evaluated using a mixed Cox model using R. The space-time analysis was performed by SaTScan, using a Poisson model for space clustering.
Results:
The overall prevalence during the study for AS was 48.7% and 48.6% for RT. The median time for the first outbreak was 295 ds IQR (165; 364) for AS and 164 ds IQR (129; 188) for RT.
Risk factors associated with an increased risk to -be-a case- cage, for AS were:
−Year when smolts were introduced
−Area where the site is located
−IPN outbreak during marine phase
−# oral antiparasite treatments 30 ds previous to SRS outbreak or censoring date
−# injected antimicrobial treatments 30 ds previous to SRS outbreak or censoring date; and those associated with a decreased risk were:
−Type of smolts rearing system
Risk factors associated with an increased risk to -be-a case- cage, for RT were:
−Fish-Density when smolts were introduced (kg/m3); and those associated with a decreased risk were:
−# oral antiparasite treatments 60 ds previous to SRS outbreak or censoring date
−Average weight of smolts when they were introduced;
−Sealice total load 8 wks. previous to SRS outbreak or censoring date
A space-time cluster of sites was detected that involved both species.
Conclusions:
Several risk factors were identified that will allow to adjust management for controlling this disease.
Relevance:
Health situation could be improved.

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Agent-based models: A powerful, underutilized tool for understanding resistance to chemical controls in aquatic parasites

Maya L. Groner, **Gregor McEwan**, Crawford Revie, University of Prince Edward Island, Charlottetown, PE, Canada. Contact: gmcewan@upei.ca

Purpose: Effectively controlling parasites while preventing the evolution of resistance to chemical controls is a challenge for agri- and aquaculture. Numerous processes influence the evolution of chemical resistance in parasites including environmental conditions, host and parasite metapopulation structure, chemical treatment regimens and genetic mechanisms of resistance. Quantifying the impacts and interactions of these factors is challenging. Many unresolved questions remain regarding how to optimize practices for specific situations. For example, many 'standard practices', such as the use of chemical refugia often rely on poorly characterized assumptions about the genetic architecture of resistance genes and the existence of associated fitness costs. This is particularly true in marine environments where issues of resistance are more recent.
Agent-based models (ABMs) are a powerful tool for understanding resistance evolution. ABMs can estimate resistance evolution even in the absence of complete information on influential processes while sensitivity analyses can prioritize areas for future work. Unlike compartmental models, which focus on population-level dynamics, ABMs incorporate information from multiple levels of biological organization. Complex patterns (e.g. resistance or population growth) emerge from simple actions of individuals.
Methods: We use an ABM of salmon lice on wild and farmed hosts to explore how interactions between environmental factors, population structure and treatment strategies influence resistance evolution.
Results: We show that chemical refugia, in the form of migratory wild salmon hosts can retard the evolution of resistance. In contrast to terrestrial systems where refugia are effective at one tenth the size of treated populations, wild and farmed salmon populations must be of similar magnitude to alter evolutionary trajectories. This occurs because wild salmon refugia are ephemeral and transmission between-populations is lower than among-populations.
Conclusions & Relevance: This model demonstrates that ABMs are a valuable and underutilized tool for evaluating management strategies for pests.

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Risk of disease transfer by wellboats in Norway

Helga R. Høgåsen, Trude M. Lyngstad, Mona D. Jansen, Arve Nilsen, Norwegian Veterinary Institute, Oslo, Norway. Contact: helga.hogasen@vetinst.no

Purpose: The transport of live aquaculture animals is known to play a significant role in the long-distance spread of diseases. Whereas the risk of introducing infected fish into a non-infected area is obvious, the risk associated with contaminated vehicles (wellboats) is unknown and challenging to assess. Wellboats in Norway have a complex activity and use a variety of biosecurity measures. Moreover, several compartments, more or less interrelated, may be involved in spreading disease - transport water, ballast water, and contaminated surfaces within or outside the boat. Transport water may or may not be exchanged during transport, creating additional complexities related to the boat's route.
The aim of this research was to help risk managers choose the most adequate measures to reduce the risk of disease transfer by wellboats.
Methods: The risk assessment was structured according to the OIE guidelines for import risk assessment, adapted to our purpose. Information was gathered from the literature, the industry, and visits to fish farms, wellboats, and slaughterhouses.
Pancreas disease (PD) is considered the most important viral infection in Norwegian aquaculture. PD-specific data were applied to the generic model, to provide a qualitative risk assessment for the spread of PD by wellboats in Norway.
Results: Results include a visual representation of the different pathways involved and their likelihood for spreading PD. They show the complexity of the system, the biosecurity in place, and the most vulnerable steps and pathways leading to the possible spread of PD.
Conclusions: Major findings are the paucity of measures related to ballast water, the importance of direct delivery to the slaughterhouse, the risk associated with combining open and closed transports, and the data gaps relating to well boat disinfection and infection pressure in water.
Relevance: Our approach provides risk managers with an accessible overview of different infection pathways, and clear indications about further research and regulatory needs.

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Predicting pathogen transmission between aquaculture sites in coastal waters of eastern Canada.

Raphaël Vanderstichel[1], Fred Page[2], Larry Hammell[1], Crawford Revie[1], Sophie St-Hilaire[1], Ian Gardner[1], [1]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada; [2]St Andrews Biological Station, Fisheries and Oceans Canada, St Andrews, NB, Canada. Contact: rvanderstich@upei.ca

Background. Effective control measures to minimize transmission of pathogens between marine farms are essential to reduce infectious disease mortality, production costs, and environmental impact from therapeutic treatments. The sea louse, a parasitic copepod of Atlantic salmon, is detrimental to aquaculture in Canada and has become a concern globally. Although distance is known to affect farm-to-farm spread, the impact of coastal water movements on pathogen diffusion and transmission is poorly understood. A centralized data management system (Fish-iTrends) has been used for industry sea lice counts and treatments in eastern Canada since 2009, while expert oceanographers in Fisheries and Oceans Canada have developed ocean circulation models (Finite-Volume Community Ocean Model; FVCOM) since the early 2000s.

Objective. Assess the impact of coastal water movements on the diffusion and transmission of pathogens by combining ocean circulation models, environmental data, and aquaculture surveillance records.

Methods. Linear mixed models are used to identify within-farm risk factors using Fish-iTrends records and satellite remote sensing environmental data. FVCOM hydrodynamic models are used to simulate particle movement in coastal waters, as a proxy for pathogen diffusion amongst aquaculture farms. Particle tracks are summarized into kernel density surfaces and connectivity matrices amongst farms to estimate predictors of transmission by comparing them with actual surveillance data.

Results and Conclusions. A total of 650 cages from 40 sites met the inclusion criteria for within-farm modeling. Significant predictors of infestation included pathogen life stage, water temperature, and year. Seaway distance between all farms in our study region has been calculated and locations matched to remote sensing data to estimate amongst-farm diffusion and transmission. Initial kernel density modeling of particle tracks appears promising.

Relevance. Our methods will be applicable to aquaculture areas with hydrodynamic and disease surveillance data, and will benefit decision makers in establishing protocols for effective management.

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Economics in decision making for control of first incursion of exotic aquatic animal diseases

Birgit C. Oidtmann[1], Clemens Matt[2], Kevin Denham[3], Mark A. Thrush[1], Edmund J. Peeler[4], Jeo Lee[5], [1]Centre for Environment, Fisheries and Aquaculture Science, Weymouth, United Kingdom; [2]Government Economic Service, London, United Kingdom; [3]Centre for Environment, Fisheries and Aquaculture Science, Weymouth, United Kingdom; [4]Centre for Environment, Fisheries and Aquaculture Science, Weymouth, United Kingdom; [5]Centre for Environment, Fisheries and Aquaculture Science, Lowestoft, United Kingdom. Contact: Birgit.Oidtmann@cefas.co.uk

Purpose:
Understanding the costs and benefits of alternative control measures compared to no intervention is crucial to inform decision-making in the face of an outbreak of an aquatic animal (AA) disease.
This study compares the direct costs of alternative strategies to control an exotic notifiable fish disease outbreak in England and Wales (E&W). This is different from studies presented previously on the economics of AA diseases, where either the benefits of an improved surveillance system were compared to less efficient surveillance, or where the consequences of a disease incursion were assessed without an evaluation of alternative control strategies.
Methods:
We developed a deterministic spreadsheet model to assess the impact of control strategies (i.e. culling and movement restrictions) was assessed at the farm (and national) level and thus took account of the scale and type of farm operation (e.g. hatchery, production for human consumption, restocking, or combinations of these). The model was used to calculate the direct costs of two hypothetical outbreak scenarios for infectious haematopoietic necrosis and includes production data from every salmonid farm in E&W.
Results:
Preliminary results show that culling incurs the largest costs to individual farms; however, movements of live fish from farms located in the same river catchment as infected farms are restricted until disease freedom is reinstated, leading to impact on their farming operations over 2 years or more (2006/88/EC). The economic impact can vary substantially depending on affected river catchment(s).
Conclusions:
Farmers may need to change their business models (e.g. switch from production for restocking to production for human consumption) to be able to continue to operate a financially viable business while movement restrictions remain in place.
It will be important to evaluate the effectiveness of alternative control strategies that may have less severe consequences for the farming industry.
Relevance:
The model provides a valuable tool to government for decision making in the event of an AA disease outbreak and allows exploring the costs and benefits of alternative control strategies *ex ante*.

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Survival analysis and spatial epidemiology of White Spot Syndrome (WSS) in the shrimp farming industry of Sinaloa, Mexico, from 2005 to 2011.

Ana Muniesa[1], Fernando Mardones[2], Mª Cristina Chávez[3], Leobardo Montoya[3], Julio Adalberto Cabanillas[4], Ignacio de Blas[1], **Beatriz Martínez-López**[2], [1]Universidad de Zaragoza, Zaragoza, Spain; [2]Center for Animal Disease Modeling and Surveillance (CADMS), VM: Medicine and Epidemiology, University of California, Davis, CA, [3]Unidad Mazatlán en Acuicultura y Manejo Ambiental del CIAD, A.C., Mazatlán, Mexico; [4]Comité Estatal de Sanidad Acuícola de Sinaloa, Culiacán, Mexico. Contact: beamartinezlopez@ucdavis.edu

Purpose: White spot disease (WSD), caused by white spot syndrome virus, leads to high mortality and economic losses to the shrimp farming industry. In Mexico, the shrimp production is one of the most important primary activities generating an annual income of USD 711 million. However, since WSD was reported in 1999, Mexican shrimp industry has been severely affected. The aim of this study was to characterize the WSD spatiotemporal patterns and to identify the primary risk factors contributing to WSD occurrence from 2005 to 2011 in one of the most important shrimp production states of Mexico, Sinaloa.
Methods: We used longitudinal data collected by the "Comité Estatal de Sanidad Acuícola de Sinaloa" from 2005 to 2012 regarding WSD outbreaks, spatial information, environmental, production and husbandry factors at farm level. The spatio-temporal patterns of WSD were described using space-time scan statistics. The effect of 52 variables on time to WSSV outbreak occurrence was estimated using a multivariable Cox proportional hazards model.
Results: Risk of WSD was not homogeneously distributed as suggested by the 8 significant clusters found in Sinaloa. The Cox model reveal that lower survival was mostly associated to the first production cycle (HR=11.31), changes from 1.4 to 1°C of temperature oscillation caused by El Niño/La Niña events (HR=1.44) and high average daily growths (HR=1.26). Conversely, factors leading to higher survival were shrimp weight at the moment of the outbreak (HR=0.159), changes from -0.9 to -0.5°C of temperature oscillation caused by El Niño/La Niña events (HR=0.540), superficial water temperature during the pound stocking (HR=0.823) and high (>100) number of days of culture (HR= 0.830).
Conclusions and Relevance: Results would allow the design of risk-based, more cost-effective, surveillance and control strategies to minimize the economic impact of WSD in Mexico.

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Sea lice bath treatment: when should you count for reliable assessment of treatment efficacy?

Raju Gautam, Raphael Vanderstichel, Annette Boerlage, Larry Hammell, University of Prince Edward Island, Charlottetown, PE, Canada. Contact: rgautam@upei.ca

Purpose: Control of sea lice (Lepeophtheirus salmonis), an important ectoparasite of farmed salmon, frequently requires the use of bath treatments using chemotherapeutants. The clinical effectiveness of treatment is determined by comparing sea lice numbers before and after treatment. However, counts are seldom taken at the same intervals before and after treatment. To provide a more reliable measure of treatment effect, we determined the most appropriate day(s) for counting lice before and after treatment.
Methods: Bath treatment data from January 2010 to December 2014 were derived from the Fish-iTrends sea lice monitoring program at the Atlantic Veterinary College. Observed counts (pre- and post-treatment) were aggregated at the cage level and grouped into two life stage categories: (i) Pre-adult Males and Females and Adult Males (PAAM) and (ii) Adult Females (AF). Counts were log transformed and mean counts by day of count relative to treatment day were computed and compared separately, using linear mixed models, for PAAM and AF as outcomes.
Results: There were 2,167 observations for pre-treatment counts from 60 sites of which 585 observations in 48 sites had unambiguous records of post-treatment counts within 14 days over a 5 year period. Tarping with Salmosan (Azamethiphos) performed better at higher water temperatures (≥ 10.5 C). At lower temperatures, wellboat using Paramove (hydrogen peroxide) or Salmosan performed similarly, but better than tarp using Salmosan. Average counts for both PAAM and AF were not different if counted within 2 days before treatment, but were significantly lower (PAAM, $P < 0.01$ and AF, $P < 0.06$) when counted 3 or more days before treatment. Post-treatment counts were lowest for PAAM and AF after 1 day, significantly less than the day of treatment ($P = 0.005$). Counts increased from day 2 to day 8.
Conclusions: The best time to count for a more reliable treatment assessment is not greater than 2 days prior to treatment and exactly one day after treatment, and treatment method and drug type generated different responses based on water temperature.
Relevance: Findings have the potential to inform industry practices, but will require a longitudinal study for validation.

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Evaluation of active surveillance for Infectious Salmon Anaemia virus in Newfoundland and Labrador

Evan Sergeant[1], **Nicole O'Brien**[2], [1]AusVet Animal Health Services, Orange, Australia; [2]NL DFA, St. John's, NL, Canada. Contact: nicoleobrien@gov.nl.ca

Infectious salmon anaemia virus (ISAv) is a viral infection of salmon, resulting in systemic disease causing varying degrees of morbidity and mortality depending on the genotype. ISA virus occurs in most salmonid-producing countries, with periodic or regular outbreaks reported in Scotland, Norway, Canada, USA, Faroe Islands and Chile. ISAv outbreaks have occurred in Canada previously and the first ISAv events for Newfoundland and Labrador (NL) occurred in 2012 and 2013. The purpose of this study was to evaluate the active ISAv surveillance program in NL. Active surveillance for ISAv in NL is based on a program of regular site evaluations overseen by a veterinarian every 30-45 days (weather and logistics dependent). A stochastic simulation model was used to simulate the pathway for detection of ISAv through the active surveillance, should ISAv occur on one or more sites at a defined prevalence. This model was then used to analyse data for ISAv active surveillance for 2013-2014 and to estimate the probability of detecting ISAv on a monthly basis and the probability of population freedom from ISAv over time. From the available data, the mean probability of population freedom exceeded 95% by April 2013 (i.e. after 4 months). After an ISAv incursion and consequent ISAv events in the second half of 2013, probability of freedom was 0 until the ISAv events were resolved. After this, probability of freedom again reached >95% after about four months and remained high until the end of the analysis period. This type of evaluation will assist in policy and developing future surveillance programs.

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Routine clinical inspections in marine salmonid farms have a high capability of detecting viral haemorrhagic septicaemia (VHS) and play a key role in surveillance for freedom

Trude Marie Lyngstad[1], Hege Hellberg[1], Hildegunn Viljugrein[1], Britt Bang Jensen[1], Edgar Brun[1], Evan Sergeant[2], Saraya Tavornpanich[1], [1]Norwegian Veterinary Intitute, Oslo, Norway; [2]AusVet, Toowoomba, Australia. Contact: trude.lyngstad@vetinst.no

Due to the increasing demand for more cost-effective surveillance strategies, and in order to comply with the requirements in the Council directive 2006/88/EC, the Norwegian surveillance programme for viral haemorrhagic septicaemia (VHS) has been modified towards a risk-based approach. The core activity is clinical inspections carried out on a regular basis by authorized veterinarians and fish health biologists working in independent or industry owned fish health services (FHS) and laboratory investigation of suspicious samples. The aims of this study are to evaluate the impact of FHS and to estimate the probability of freedom from VHS in marine farmed salmonids in Norway based on analysis of clinical inspection data. Probabilities of fish being submitted and tested given that the population is infected, the estimates on effective probability of infection (EPI), sensitivity of the laboratory test and numbers of samples tested were included in site-sensitivity estimates. The population of farmed salmonids in Norway was divided in four risk groups (species, region, area production density and level of biosecurity) based on knowledge of VHS risk factors. Population sensitivity (SeP) and probability of freedom (PFree) were estimated on a monthly basis over a 12 month period using a hypergeometric approximation. The model estimates of site sensitivity, SeP and PFree indicate that the surveillance system based on routine inspections by the FHS has a high capability for detecting VHS. The results also show that there is a high probability of freedom from VHS in Norwegian marine farmed salmonids. A PFree of 95 % is achieved within 6-12 months depending on the assumptions given in the model. The model provides a supporting tool for evaluation of potential changes in the surveillance strategy. The current model can be viewed as generic for similar exotic viral infectious diseases in marine salmonid farming in Norway, as they share similar risk factors.

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Using industry earnings data to simplify the economic modelling of diseases affecting salmon aquaculture

Alexander G. Murray, Malcolm Hall, Marine Scotland Science, Aberdeen, United Kingdom. Contact: Sandy.Murray@scotland.gsi.gov.uk

Purpose: Salmon production suffers substantial loss to diseases, which need to be cost-effectively controlled at both farm and large scales. Costs and benefits must be balanced, often with limited data availability.
Methods: Here two applications of an economic modelling approach from Scotland are described: national controls on Bacterial Kidney Disease and farm level actions tomitigate Pancreas Disease. Costs of inspections (time and diagnostic costs) are obtained from fish health inspectors. Losses of fish due to disease are assessed for alternative controls using epidemiological modelling and analyses of observed mortality patterns.The costs of these losses are assessed under a simplified approach using Earnings Before Interest and Taxes (EBIT). EBIT allows losses, in kg, to be transformed into financial costs without a detailed assessment of production costs. Observed variation in EBIT over years is incorporated into the analysis. Additional costs of disposal and reduced quality are included. BKD is a rare disease in Scottish Atlantic salmon sites and the EBIT is simply applied to the losses under alternative control strategies. PD is more widespread and the EBIT approach was adjusted to incorporate increases in costs due to mortality, discards and reduced growth rate, and reductions in price due to reduced flesh quality.
Results: For BKD, the modelling identified a moderate control policy to be more cost effective than either laissez faire (more cases) or eradication (costs of control) policies. A relative cost benefit of treatment depends on the probability of PD, the severity (dependent on viral strain) of outbreaks, the efficacy and cost of treatment and the underlying EBIT. The model can identify conditions when different treatments are likely to be cost effective.
Conclusions: A combination of epidemiological and economic modelling is able to provide information supporting optimisation of both large-scale and farm-scale disease control strategies in Scottish aquaculture.
Relevance: This modelling has been directly applied in the development of BKD control policy and will be used to provide information to allow farmers to select approriate PD controls.

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Evaluation of PCR methods used by an Indonesian laboratory network to test for aquatic pathogens

Paul M. Hick[1], Alison Tweedie[1], Murwantoko Murwantoko[2], Toha Tosihadi[3], Mike Rimmer[1], Richard J. Whittington[1], [1]University of Sydney, Camden, Australia; [2]Gadjah Mada University, Yogyakarta, Indonesia; [3]Centre for Fish Disease and Environment Investigation, Serang, Indonesia. Contact: paul.hick@sydney.edu.au

Purpose:
Viral pathogens limit the production of food fish and access to export markets. Accurate laboratory tests can reduce the impact of viral disease by providing correct diagnoses and enabling disease control strategies based on certification of freedom from infection. Consequently, there has been a rapid increase in demand for high-throughput polymerase chain reaction (PCR) tests used according to laboratory accreditation standards. The aim of this study was to enable fish health laboratories in Indonesia to identify factors impacting the accuracy of PCR tests and develop opportunities for improved collaborative networks.

Methods:
A ring-test was designed for Nervous necrosis virus and Epizootic Haematopoietic Necrosis Virus, ensuring that laboratories needed to implement familiar and unfamiliar tests. A panel of samples containing a measured quantity of heat inactivated virus spiked into a matrix of fish tissue was prepared. This format was amenable to a free choice of assay and equipment. Identical aliquots of the panel were distributed in a freeze dried form to 20 laboratories overseen by the Directorate General of Aquaculture. Instructions were provided in two languages during a PCR training workshop hosted by the Centre for Fish Disease and Environment Investigation, Serang.

Results:
Test results and descriptions of methods were provided by 18 / 20 laboratories. The participants correctly classified 73.1% (n=238) of positive and negative samples under blind testing conditions. Results included laboratories which failed to implement a new assay, as well as 11 panels that were tested with 100% specificity and sensitivity. Conventional and real-time PCR methods performed equally. Previous experience with a test protocol predicted a correct result better than assay choice or the type of equipment.

Conclusions and relevance: The ring-test was less prescriptive and more challenging than a proficiency test. This permitted anonymity of laboratories whilst encouraging critical evaluation and collegial discussion, a format that was well received by participants. This study will guide future training and supports the establishment of reference laboratories.

Integrating macroscopic findings when evaluating diagnostic test accuracy: case study of the detection of *Mikrocytos mackini* in Pacific oysters (*Crassostrea gigas*)

Charles Caraguel[1], Nils Toft[2], Geoff Lowe[3], Gary Meyer[3], Mark Polinski[3], Cathryn Abbott[3], [1]The University of Adelaide, Roseworthy, Australia; [2]National Veterinary Institute, Copenhagen, Denmark; [3]Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo, BC, Canada. Contact: charles.caraguel@adelaide.edu.au

Purpose: *Mikrocytos mackini* is an intracellular rhizarian parasite responsible for Denman Island disease of Pacific oysters (*Crassostrea gigas*) on the northwest coast of North America. Although *M. mackini* was delisted by the OIE in 2007, it remains regulated by the Canadian National Aquatic Animal Health Program (NAAHP) and EU, and requires that laboratory tests used for its surveillance be validated to demonstrate freedom from the parasite in Canadian oyster populations.
Methods: In this study, a total of 802 Pacific oysters were sampled from 9 different populations during the spring and fall and each oyster was tested using a recently designed real-time qPCR, a conventional PCR, and histopathology. There is no recognised 'gold standard' reference test for *M. mackini* and a latent class model (LCM) analysis was used to compare the diagnostic sensitivity and specificity (Se & Sp) of the 3 tests. Whole oysters were sampled from the field, transferred live to the laboratory, and examined macroscopically for the presence of lesions prior to tissue sampling. Each oyster was categorized as: '0': no lesions, '1': questionable or suspect lesions, '2': typical lesions. A LCM was built to allow distinct test Se for each of the lesion scores while the Sp was kept constant.
Results: Oysters with typical lesions had a higher Se than oysters with suspect lesions and oysters with no lesions. Between tests used, regardless of lesion score; qPCR had the highest Se, then conventional PCR, then histopathology. Conversely, conventional PCR and histopathology had a similar Sp, higher than qPCR.
Conclusions: With a positive result providing the strongest evidence (highest likelihood ratio) among the 3 tests, conventional PCR is the method of choice to demonstrate freedom from *M. mackini* in Canadian oyster populations.
Relevance: Access to macroscopic findings refines the evaluation of diagnostic test accuracy and their application. Regardless of the test, detailed instructions on how to collect and record specimens according to the presence, location, and severity of lesions should be included in any sampling protocol to ensure optimal test accuracy and precision.

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Evaluating and identifying the best protocol to detect abalone herpesvirus when screening apparently healthy populations of Australian abalones

Charles Caraguel[1], Kevin Ellard[2], Nick Moody[3], Lynette Williams[3], Mark Crane[3], [1]The University of Adelaide, Roseworthy, Australia; [2]Department of Primary Industries, Parks, Water and Environment, Launceston, Australia; [3]CSIRO Australian Animal Health Laboratory, Geelong, Australia. Contact: charles.caraguel@adelaide.edu.au

Purpose: Abalone herpesvirus (AbHV) has been responsible for sporadic abalone viral ganglioneuritis (AVG) outbreaks in Australian greenlip abalone (*Haliotis laevigata*), blacklip abalone (*H. rubra*), and in hybrids of these two species (*H. laevigata* x *H. rubra*) in Victoria and Tasmania. Since the original outbreak in 2005, new AbHV genotypes emerged which could not be detected by the originally designed, and OIE validated, qPCR. In an effort to demonstrate freedom from AbHV, new sets of primers/probe were designed and evaluated for fitness-for-purpose.
Methods: A total of 1459 preserved abalone specimens were selected from 5 source populations with no evidence of AVG. Each abalone was screened using histopathology and 3 different sets of qPCR primers/probe: ORF49 (original set), ORF66, ORF77. In the absence of a gold standard, a latent class model analysis was used to compare the diagnostic sensitivity and specificity (Se & Sp) of the assays, accounting for conditional dependence among tests. Combinations of tests were also explored to improve the accuracy of the detection protocol.
Results: Individually, the tests showed poor to moderate Se with close to perfect Sp. Significant dependence was found between all qPCR assays. Prevalence of infection across the 5 source populations ranged from 1% to 13%. In combination, the interpretation in parallel of ORF49 and ORF66 provided the best Se (86.0%) and still a high Sp (98.2%).
Conclusions: Based on the currently known AbHV genotypes, ORF49/66 interpreted in parallel is the protocol of choice to demonstrate freedom from AbHV in a population of Australian abalones.
Relevance: AbHV detection in apparently healthy abalone populations is challenging because of low prevalence of infection, low pathogen load, and new emerging genotypes. Coupled with a wise sampling strategy, the combination of multiple tests may improve detection where individual tests do not fit.

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Prediction of PCR inhibition and its effect on performance of direct fecal PCR test for the diagnosis of Mycobacterium avium subspecies paratuberculosis infection in cattle

Kamal R. Acharya, Karren M. Plain, Richard J. Whittington, Navneet K. Dhand, The University of Sydney, Camden, Australia. Contact: kach8080@uni.sydney.edu.au

Purpose:
Johne's disease control depends on a reliable diagnosis of subclinical infection. In Australia results from faecal culture, serum antibody ELISA and a direct faecal PCR test (HT-J) are used to inform decision making. PCR inhibition is a recognised phenomenon but its impact on the performance of HT-J PCR is not well understood. This study thus aimed to compare HT-J PCR, faecal culture and serum ELISA results for investigating the effect of PCR inhibition on performance of HT-J PCR and to assess the predictability of PCR inhibition.
Methods:
A total of 296 matched serum and DNA extracts from faecal samples of an endemically infected beef herd were accessed. Sensitivity of ELISA and HT-J PCR, with and without PCR inhibition, was assessed against faecal culture (BACTEC 12B liquid media) results. Furthermore, 125 faecal samples were sub sampled, DNA extracted, optical density measured, and DNA and protein content quantified. Logistic regression was performed to study the relationship of PCR Inhibition with DNA quantity, protein concentration and protein contamination of the DNA extract.
Results:
Considering faecal culture as a gold standard, HTJ PCR had an apparent sensitivity of 58.75%. PCR inhibition was evident in 21% of the samples. A 1-in-5 dilution partially restored the sensitivity of HTJ PCR. An A260/A280 ratio of<1.8 of the DNA extract was found to increase the odds of inhibition by 13.88 (95% CI: 3.96, 48.45; P<0.05). DNA extracts with high content of protein and DNA had 19.33(95% CI: 6.25, 59.76) and 10.94 (95% CI: 4.12, 29.06) times odds of PCR inhibition, compared to extracts with low content of protein and DNA.
Conclusions:
PCR inhibition can undermine the performance of HT-J PCR. High DNA and high protein content of DNA extract can be useful predictors of PCR inhibition.
Relevance:
Effective prediction of PCR inhibition using spectrophotometric readings may improve the performance of molecular techniques like HT-J PCR and aid rapid diagnosis.

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Comparing pooling schemes for infectious disease surveillance

Syed S. U. Ahmed, Tariq Halasa, Nils Toft, Kaare Græsbøll, Technical University Denmark, Frederiksberg, Denmark. Contact: sayah@vet.dtu.dk

Background:
Examining laboratory samples for pathogens, antibodies or antigens is a central component of infectious disease surveillance. Pooling combines multiple samples together for testing, which can reduce the number of tests required compared to individual testing. This may reduce costs of surveillance. In 1943, Dorfman first proposed a pooling scheme, and since then several other pooling schemes have been developed and practiced. Despite having the potential to reduce costs and testing time, application of pooling in infectious disease surveillance remain limited due to the mathematical complexity of some schemes. Moreover, most schemes were developed and tested for samples with a low prevalence. Importantly, the efficiency gain in terms of reduced number of tested samples has not been systematically examined earlier.
Objective:
The present work surveyed various pooling schemes with the aim to make simplified description of the schemes and to examine their performances in different pool size and prevalence.
Methods:
Visual descriptions of the one and two dimensional pooling schemes with variants, three dimensional pooling scheme and more sophisticated shifted transversal design (STD) schemes were made to make them readily understandable to the infectious disease audience. Furthermore, the various pooling schemes were simulated to compare their in-silico performance using different pool sizes and prevalence.
Results:
Results of the simulation study demonstrate that a larger pool size maximizes pooling efficiency at low prevalence, whereas a smaller pool size maximizes efficiency at higher prevalence. In general, none of the pooling schemes can improve the efficiency at prevalences above 30%. The STD scheme provides the highest efficiency for different pool size and prevalence.
Conclusion:
Overall, this study helps to understand the pooling schemes better, and provide information on optimum pool size at different prevalence to gain maximum efficiency required for infectious disease surveillance.
Relevance:
Application of pooling would be advantageous and highly relevant to infectious disease surveillance of animal and human.

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Probability of seroconversion against low pathogenic avian influenza virus infections in chickens and time to antibody detection in sera and eggs samples.

Jose L. Gonzales[1], Armin A. R. W. Elbers[1], Arjan Stegeman[2], Willem G. Buist[3], Guus Koch[1], Sjaak de Wit[4], Baas Engel[3], [1]Central Veterinary Institute, WUR, Lelystad, Netherlands; [2]Utrecht University, Utrecht, Netherlands; [3]Wageningen University and Research Centre, Wageningen, Netherlands; [4]Animal Health Service (AHS), Deventer, Netherlands. Contact: jose.gonzalesrojas@wur.nl

Purpose:
Experimental evidence suggests that not all chickens infected with a low pathogenic avian influenza virus (LPAIv) develop antibodies (seroconverts) against the virus. Knowledge of the probability for seroconversion would be relevant for diagnosis and surveillance of LPAI infections. The objectives of this study were to evaluate occurrence of seroconversion in time upon a LPAIv infection and asses the diagnostic performance of a commercial ELISA test using sera or egg samples.
Methods:
Swab, sera and egg samples used in this study came from a paired-transmission experiment using an H7N7 LPAIv in chicken layers. Swab samples were tested by RT-PCR and the results used to define 'true' disease status of the chickens. In the absence of a 'gold standard', Elisa results of sera and egg samples were analyzed using Bayesian statistics.
Results:
The probability of an infected chicken to seroconvert was 0.87 (95% credible intervals (CI): 0.80 - 0.91) and the median time to detect this in serum was 4.2 (95% CI: 4.0 - 4.5) days after infection. In eggs, seronconversion could be detected on average 8.8 (95% CI: 6.9 - 10.3) days later than in serum. Upon seroconversion the sensitivity of the ELISA was 0.99 (95% CI: 0.96 - 1.00), in serum as well as in egg-yolk. The specificity of the test was 0.99 (95% CI: 096 - 1.00), both in serum and egg-yolk.
Conclusions:
Not all infected chickens seroconvert post-infection and in those which seroconvert, the sensitivity of antibody detection using sera or egg samples is similar.
Relevance:
The estimated seroconversion and test parameters are useful for the design of surveillance programmes.

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Rabies simulation in a non-endemic environment: development and application of a novel model

Salome Dürr[1], Michael P. Ward[2], [1]Veterinary Public Health Institute, Liebefeld, Switzerland; [2]The University of Sydney, Camden, Australia. Contact: salome.duerr@vetsuisse.unibe.ch

Purpose

Domestic dog rabies is an endemic disease in large parts of the world and also epidemic in previously free regions. For example, it continues to spread in eastern Indonesia and currently threatens adjacent rabies-free regions, including remote northern Australia. Disease spread models are useful tools to provide evidence on most effective disease control strategies and to inform policy decision. Existing rabies models typically focus on long-term control programs in endemic countries. However, for a region in which rabies is exotic, predictions of the effectiveness of different interventions following the initial detection of rabies are more relevant, and such models are lacking.

Methods

We here describe a stochastic, spatially explicit rabies simulation model, which was developed within a rabies free region. It is based on individual dogs in Indigenous communities in northern Australia, informed by dog census data and incorporates three types of rabies spread: within household, between households (based on a distance kernel fitted to field collected GPS data on the roaming behaviour of dogs) and between communities. Three types of control strategy are implemented in the model: a) dog vaccination (pre-emptive or reactive), b) culling (targeted or random) and c) movement ban between and within communities, with definable dog owner compliance.

Results

Outcomes suggest that vaccination with 70% coverage would significantly reduce the outbreak size while the other strategies only show a slightly positive effect when applied at high levels (50% culling and 80% ban compliance). Importantly in these Indigenous communities, culling of dogs is unlikely to be successful. Also, movement bans (which culturally would be difficult to implement) would have minor impact unless there was high compliance. The mean R0 was found to be 1.7 with epidemic peaks after 97 days post-incursion.

Conclusions/Relevance

This is, to the best of our knowledge, the first time a rabies model has been applied to compare control strategies for an epidemic situation with absence of rabies prior to the simulated incursion. It provides evidence on which to base preparedness plans and also to manage recent incursions.

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The spatial distribution of antibodies against bovine respiratory syncytial virus in bulk tank milk from two counties in Norway

Ingrid Toftaker[1], Javier Sanchez[2], Maria Stokstad[3], Ane Nødtvedt[1], [1]Norwegian University of Life Sciences, Fetsund, Norway; [2]University of Prince Edward Island, Charlottetown, PE, Canada; [3]Norwegian University of Life Sciences, Oslo, Norway. Contact: ingrid.toftaker@nmbu.no

Purpose
A cross-sectional study was conducted to investigate the association between herd level risk factors and the spatial distribution of bovine respiratory syncytial virus (BRSV).
Methods
From December 2012 to June 2013, bulk tank milk (BTM) samples were collected from 1347 herds in two Norwegian counties, and were analyzed for antibodies against BRSV and Bovine coronavirus (BCoV). Health and production data were obtained from the Norwegian Dairy Herd Recording System. Risk surface maps were made to show the spatial variation in herd level prevalence. Two spatial models were developed in SaTScan™. The first was of the test result (+/-) using a Bernoulli model, and the second was a normal model fit using the deviance residuals from a logistic regression model accounting for the main herd level risk factors. Overall predictive ability of the logistic model was assessed through ROC-analysis.
Results
The prevalence of BRSV positive herds in this study was 46%. Predictors in the logistic model were: herd size, in cows (OR 1.04, 95% CI 1.03-1.05), average milk production, in 100kg (OR 0.98, 95% CI 0.98-1.00), longitude (OR: 0.61, 95% CI 0.50-0.74), latitude (OR 2.84, 95% CI 2.04-3.94), mean distance to 5 nearest dairy herds, in km (OR 0.79, 95% CI 0.72-0.87) and BCoV tank milk positivity (OR 2.99, 95% CI 2.16-4.12). Area under ROC-curve was 0.77. The risk surface maps showed large variation in prevalence across the study area. Four significant spatial clusters of BRSV positive herds were detected ($p<0.05$). Spatial clustering of the residuals was similar to the initial clusters of positive herds.
Conclusions
Herd level risk factors for BRSV antibody positivity were herd size, milk yield, geographic location, distance to neighboring herds and BCoV status. The logistic regression model had acceptable predictive ability but did not remove the spatial clusters, indicating the existence of spatially dependent, unmeasured risk factors.
Relevance
The determination of “hot spot” areas and risk factors affecting the spatial distribution of BRSV antibodies is important knowledge when designing effective control strategies.

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Rapid spatial risk assessment of wildlife exposure to livestock pathogens using a case study of the critically endangered migratory saiga antelope in Central Asia

Wendy Beauvais[1], Richard Kock[2], Javier Guitian[1], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]Royal Veterinary College, Hatfield, United Kingdom. Contact: wbeauvais@rvc.ac.uk

Purpose

Transmission of diseases between livestock and wildlife is a concern for conservationists and livestock health stakeholders, worldwide. Migratory species such as the critically endangered saiga present a challenge: how can we prioritize research and conservation resources when the species migrates over vast sparsely populated areas and little is known about which pathogens are present and what risks they present to wildlife? Economic assessments of disease for livestock trade or public health often ignore biodiversity and environmental impacts.

Our objective was to develop semi-quantitative and spatially explicit methods to estimate the likelihood of exposure of saiga to 41 systematically-selected livestock pathogens and to describe the uncertainty.

Methods

A framework for risk assessment of saiga exposure to livestock pathogens was developed based on the OIE Risk Analysis framework. A novel time-proximity matrix was developed to capture the range of spatio-temporal interactions that can occur between livestock and wildlife. Risk estimates were gathered via literature review, expert opinion and observational data on locations of livestock and saiga.

Results

Saiga in the Betpak Dala region of Kazakhstan were found to be at low-moderate risk of exposure to Peste Des Petits Ruminants virus in spring, and moderate risk in summer to winter, with moderate uncertainty. A moderate-high risk of exposure to *Brucella* all year was estimated, with moderate uncertainty. Maps show the locations of high, moderate and low risk of all 41 pathogens. The greatest uncertainty arose due to lack of knowledge on pathogen survival in different environments and the presence of pathogens in livestock in this region of Kazakhstan.

Conclusion

The pathogens identified as high priority should be considered as differential diagnoses in the investigation of disease in saiga, and research into the susceptibility of saiga to livestock pathogens should be focused on these pathogens.

Relevance

The described approach can be used to systematically combine data from ecologists, pathogen-specific experts and epidemiologists to rapidly prioritize research and conservation for migratory wildlife species.

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Evaluation of the wild and domestic pig interactions and their association with African swine fever outbreaks using structured questionnaires and spatio-temporal modeling.

Esther A. Kukielka[1], Ferrán Jori Massanas[2], Beatriz Martínez López[1], David Chavernac[3], Charles Masembe[4], Tony Aliro[5], Karl Ståhl[6], [1]University of California, Davis, Davis, CA, [2]CIRAD, Gaborone, Botswana; [3]CIRAD, Montpellier, France; [4]Makerere University, Kampala, Uganda; [5]Ministry of Agriculture, Gulu, Uganda; [6]Swedish University of Agricultural Science, Uppsala, Sweden. Contact: ekukielka@ucdavis.edu

Purpose: Bushpig (*Potamochoerus larvatus*) and warthog (*Phacochoerus africanus*) are African swine fever (ASF) asymptomatic carriers widely distributed in Eastern Africa. Unlike warthogs (WH), which seem to only transmit the virus through tick vectors, experimental evidence suggests that bushpigs (BP) can transmit ASF virus by direct contact to susceptible domestic pigs (DP). However, being an elusive nocturnal species, the level of interaction and potential risk factors for ASF transmission from BP to DP still remains to be elucidated. This study explores the spatio-temporal dynamics of direct and indirect interactions between wild and domestic pigs and their association with reported ASF occurrence in DP.
Methods: The study area comprises the northern boundary of Murchison Fall National Park, Uganda, and the adjoined rural communities -characterized by a growing free ranging DP population and unremitting ASF outbreaks. A census of households-rearing DP during 2014 was created by consulting local village leaders and a random sample of 233 households was selected and surveyed using structured interviews on PDAs. Questions aimed at understanding and assessing the nature, frequency, duration and distribution of interactions between wild and domestic pigs at their interface with special emphasis on BP. Questions regarding human behavior related with DP rearing activities that pose a risk of transmission at the interface (i.e., carcass dressing) were also included. Based on responses, BP's home ranges were estimated by using kernel density estimates and hotspots for BP-DP interactions were identified.
Results:
Preliminary results suggest that 27.2% households reported presence of BP in their area, of which only 17.5% reported more than 20 per year, suggesting that the sylvatic and the non-sylvatic cycle of ASF may not be interlinked in northern Uganda.
Conclusions:
BP-DP dynamics and association with ASF occurrence will be discussed.
Relevance: ASF is an important disease that hinders pig production from becoming a tool for poverty alleviation in the area, one of the poorest of Uganda. Tackling possible reservoirs such as wild pigs must be attained.

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Ecological Niche Modeling for surveillance of Avian Influenza in the United States

Jaber A. Belkhiria[1], Mohammad Alkhamis[2], Beatriz Martínez-López[1], [1]UC Davis, Davis, CA, [2]2Environmental & Life Sciences Research Center, Safat, Kuwait. Contact: jabelkhiria@ucdavis.edu

Avian Influenza (AI) has public health, economical, and environmental implications in both avian and non-avian populations. Recent cases of highly pathogenic AI in the US highlights the urgent need to develop and implement solutions to protect US poultry industry against this devastating disease. The unique peculiarities of the different types of poultry operations coexisting in US (i.e., organic vs commercial, backyard flocks, live bird markets, etc.) pose a challenge on the early detection and control of AI. Mapping the risk of AI may help to increase producers' awareness and guide risk-based interventions. The objective of the study was to develop a risk map for AI outbreaks in the US by exploring the ecological niche of virus on regional level. The study integrates spatial information regarding AI surveillance with relevant demographical and environmental factors, which include avian host attributes, climate, agricultural, socio-cultural and economical aspects. We used presence-only Maximum Entropy ecologic niche approach to model the spatial risk of AI in avian populations. Overall, results suggested that five environmental variables could adequately predict the geographical distribution of AI in birds, as indicated by the values of the area-under-the curve (AUC) of the predictions (AUC for test data = 0.95 and calibrated AUC = 0.74). Highest risk areas (probability > 0.8) covered most Northeastern and Midwestern US and few parts from the west coast of the US. Altitude was the most important predictor (47.8% relative contribution) followed by mean temperature of the warmest quarter, mean diurnal temperature range, land cover, and close proximity to backyard poultry. The presented study provided further insights in into the spatial epidemiology of AI in the US, and subsequently might be useful to guide targeted risk-based surveillance efforts in the US.

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Spatial epidemiology of Porcine Epidemic Diarrhea in the U.S.

Andres M. Perez, **Julio Alvarez**, Gabe Al-Ghalith, Dane Goede, Bob Morrison, University of Minnesota, St Paul, MN, Contact: jalvarez@umn.edu

Purpose: The objective of the study here was to assess the epidemiology of Porcine Epidemic Diarrhea (PED) during the first year of epidemic in the U.S.
Methods: Data on location (latitude, longiture), type (sow farm, nurseries, finishing), PED status (negative and, if postive, date of intection), and suspected source of infection (vertical, horizontal) were collected from two case-studies (Southeast, Midwest US) between May 2013 and February 2014. The Cuzick-and-Edwards' test, and the Knox test, and the Bernoulli and permutation models of the time-space scan statistic were used to identify time-space clusters of disease. The proportion of outbreaks that may be explained by spatial distance between farms was estimated using an optimization model with a radial decay factor adjustment, a spatially-dependent transmission rate, and non-spatial transmission and recovery rate offsets.
Results: In the Southeast study, 614 (29.7%) of the assessed farms broke became PED-infected, of whch 335 (54.6%) were considered lateral cases. In the Midwest, PED was detected in 154 (36.8%) of the farms, with 114 (74.0% of the all positive farms) assumed to be lateral cases. Spatial clustering was detected ($P<0.01$) up to the 4^{th} and beyond the 20^{th} level of neighborhood in the Midwest and Southeast, respectively (Cuzick-Edwards' test). The observed-to-expected number of cases ratio was maximum ($P<0.01$) at short distances (<1 km) and close in time (<1 week) (Knox test). One cluster of infected sow farms was associated with the rapid increase of cases in the Midwest that led to the exponential phase of the epidemic.
Conclusions: The strong spatial pattern observed here is likely the consequence of a highly infectious virus, such as PED, rapidly spreading in a highly connected, densely populated region, in which immunity was absent.
Relevance: The study provides background information on the distribution of PED in the U.S. during the first months of the epidemic, which may be compared with patterns observed in subsequent years when immunity is expected to rise in the population.

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Bovine rabies in Mato Grosso do Sul state, Brazil, from 2003 to 2013: an spatial approach for control and prevention

Juliana Arena Galhardo[1], Vitória Machado Neres[1], Fábio Shiroma de Araújo[2], Ademar Etiro Mori[2], Alice Fernandes Alfieri[3], Amauri Alcindo Alfieri[3], [1]Universidade Federal de Mato Grosso do Sul, Campo Grande-MS, Brazil; [2]Agência Estadual de Defesa Sanitária Animal e Vegetal de Mato Grosso do Sul, Campo Grande-MS, Brazil; [3]Universidade Estadual de Londrina, Londrina - PR, Brazil. Contact: juliana.galhardo@ufms.br

Purpose: In Mato Grosso do Sul state, Brazil, bovine rabies control and prevention policies are held by the State Health Animal and Plant Defense Agency (IAGRO). In order to extend the methodologies used for data analysis and assist in decision making for control and prevention of rabies, the spatial profile of the incidence of bovine rabies was analyzed using spatial analysis.
Methods: IAGRO provided the bovine rabies database, from 2003 to 2013, and a geographic information system has been developed in QGIS 2.8.1 software with a state digital map as cartographic basis, using SIRGAS2000 reference ellipsoid and the UTM coordinate system. Thematic maps were elaborated using Kernel estimator for vampire bat colonies (VBC) density and spatial correlation analysis for incidence, outbreaks and VBC. Serra de Maracaju (SMU), a geographical feature which divides the state in Planalto and Pantanal regions, was also analyzed.
Results: From 2003 to 2013 were reported 276 outbreaks and 1,914 cases in cattle, and a decreasing incidence trend ($p < 0.05$) was observed due to the decrease of cases and effective herd. At the right side of SMU, Planalto region, vaccination is not obligatory and higher densities of outbreaks, cases and VBC were observed. At the left side of SMU, the Pantanal region, vaccination is mandatory in most municipalities and positive correlation was observed between the low incidence of rabies and the low density of VBC.
Conclusions: The decrease of the incidence of rabies is due to the decrease of effective herd. SMU may be considered a relevant geographical barrier for bovine rabies. Vaccination may not be the main factor associated with low incidence, but the lack of fixed shelters for vampire bats in the Pantanal region. Vaccination policies should be reviewed in the Planalto region for better cost-effective control of bovine rabies.
Relevance: IAGRO typically uses descriptive analysis of absolute data, without resorting to epidemiological features such as incidence rates or spatial analysis. Using epidemiological tools may improve decision making on control and prevention of diseases.

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Development of infectious disease modelling for rabies transmission dynamics using demographic and geographic information in current Japan

Hazumu Kadowaki[1], Kohei Makita[1], Katie Hampson[2], Akio Yamada[3], [1]Rakuno Gakuen University, Ebetsu-city, Japan; [2]University of Glasgow, Glasgow, United Kingdom; [3]University of Tokyo, Tokyo, Japan. Contact: kadowaki0826@gmail.com

Purpose:In Japan, rabies has been eradicated in 1957 after introducing current Rabies Prevention Act, and has not occurred ever since. However, vaccination coverage and dog registration stipulated in the act fell dramatically due to the weakened public interest in rabies caused by the long lasted free status from rabies, and it is worth reviewing the risk of rabies transmission under such circumstance. The objective of this study is to predict rabies transmission dynamics in present situation using mathematical modelling.

Methods:An individual-based and spatial mathematical model was developed, expressing onset of rabies, movement of infected dog and generation of secondary cases by rabid dog, taking account vaccination coverage and population density. Hokkaido and Ibaraki Prefectures were selected as study sites for simulation because they had different background related with rabies transmission. For the estimation of parameters: reproduction number, population density-dependency and adjustment of previously reported dispersal kernel in Tanzania, were estimated using the data of past rabies epidemic in Osaka Prefecture between 1919 and 1933, using maximum likelihood estimation. The simulations were repeated 500 times in R. To reveal efficacy of vaccination, simulations were performed with reduced vaccination coverage.

Results:Estimated reproduction number was 2.8. The parameters for population density-dependency and adjusting the kernel were 2.28 and 2.24, respectively. In Hokkaido Prefecture, when vaccination coverages were 55%, 45% and 35%, median of final sizes were 2, 4 and 354, respectively. Durations until outbreak dies out were 53.5days, 92.5days and 339.5days, respectively. When vaccination coverages were 55.6%, 45.6% and 35.6% in Ibaraki Prefecture, median of final sizes were 2, 3 and 389, respectively. Durations until outbreak dies out were 35days, 89.5days and 397.5days, respectively.

Conclusions:These results showed risk of transmission reflecting current situation. The model will be updated further to reflect changed rearing style and to show efficacy of several intervention options.

Relevance:This is informative for risk communication.

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Molecular epidemiology of Mycobacterium avium subsp. paratuberculosis isolated across host species in Chile

Cristobal C. Verdugo[1], C. Encina[2], C. Avilez[2], M. Salgado[2], [1]Universidad Austral de Chile, Valdivia, Chile; [2]Universidad Austral de Chile, Valdivia, Chile. Contact: cristobal.verdugo@uach.cl

Purpose: Paratuberculosis is a chronic infection caused by Mycobacterium avium subsp. paratuberculosis (MAP), mainly affects domestic and wild ruminants. Most infected animals never develop clinical signs. For this reason, it has been suggested pathogenic differences between MAP strains. However, little is known about MAP strain diversity. The recent development of powerful typing techniques has allowed the study of MAP population. The objective was to describe MAP molecular diversity in isolates obtained from different hosts present in Chile.
Methods: 139 independent isolates were sourced from livestock species (cattle, sheep, goat, red deer, & alpaca) and wildlife species (huemul, guanaco, & hares), from different agro-ecological zones of Chile. Isolates were classified as Type I or Type II using a PCR method. Subsequently, isolates were subtyped using a combination of 7 variable number of tandem repeats (VNTR) and 2 short sequence repeat (SSR) markers. Subtypes were classified as a composite assignment, combining the results from the VNTR and SSR markers. Rarefaction analysis, analysis of molecular variance (AMOVA), Fst comparisons and proportional similarity index (PSI), were used to describe subtype richness, genetic structure and potential associations between subtypes and epidemiological factors.
Results: 70% of isolates were MAP Type II and the combination of VNTR and SSR markers generated 14 subtypes (4 subtypes represented 80% of isolates). Dairy cattle was the livestock sector that presented the greatest subtype richness (significantly different). AMOVA and Fst indicated the presence of species specific subtypes (5 subtypes were only retrieved from dairy cattle). The PSI showed an important subtype similarity between wildlife isolates and dairy cattle isolates.
Conclusions:
An important diversity of subtypes was recorded. Data suggest that dairy cattle could be the source of infection in wildlife. A possible adaption of subtypes to specific species was observed.
Relevance: This is the first study describing MAP diversity in Chile and the subtypes identified will the basis for further longitudinal studies, addressing the role of MAP strains on clinical disease.

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The population structure of Mycobacterium avium subsp. paratuberculosis in Canadian dairy cattle determined through whole genome sequencing

Christina Ahlstrom[1], Herman W. Barkema[1], Karen Stevenson[2], Ruth N. Zadoks[3], Roman Biek[3], Rowland Kao[3], Hannah Trewby[3], **Jeroen De Buck**[1], [1]University of Calgary, Calgary, AB, Canada; [2]Moredun Research Institute, Pnicuik, United Kingdom; [3]University of Glasgow, Glasgow, United Kingdom. Contact: jdebuck@ucalgary.ca

Purpose:
Mycobacterium avium subsp. paratuberculosis (MAP) is the causative bacterium of Johne's disease in cattle and is widespread in the Canadian dairy industry. Efforts to control the transmission of MAP have primarily focused on improving management strategies to reduce the risk of cow-to-calf transmission. However, genetic differences between MAP strain types also influence disease progression and transmission. The aim of this study was to determine the genetic diversity of MAP in Canadian dairy herds using whole genome sequencing and assess the distribution and proportion of major strain types.
Methods:
MAP isolates were cultured from individual cow and environmental fecal samples obtained from Johne's disease control initiatives in all Canadian provinces. Whole genome sequencing of 182 isolates was performed and variant sites were identified after reference mapping. Canadian isolates were also compared to an international set of MAP isolates. Phylogenetic analyses were performed using maximum likelihood and Bayesian approaches to measure genetic distance and spatial clustering.
Results:
Nine major phylogenetic clades were identified in the Canadian isolates, including a dominant type that contained more than 80% of the isolates. These isolates represented a fraction of the global population diversity, supporting the hypothesis that MAP was introduced a limited number of times into Canada.
Conclusions:
Phylogeographic structure was present at a national scale, as province of origin was significantly associated with the phylogeny.
Relevance:
An understanding of the true diversity of MAP in Canada is important for epidemiological analyses and rational prevention strategies. The presence of multiple divergent subtypes as well as a dominant type will influence control strategies at both a national and provincial scale.

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Discrete Phylogeography for Molecular Surveillance of Foot and Mouth Disease Serotype O VP1 Genes in the Middle East

Mohammad A. Alkhamis[1], Brian R. Moore[2], [1]Kuwait Institute for Scientific Research, Shuwikh, Kuwait; [2]University of California, Davis, Davis, CA, Contact: mohammad.alkhamis@gmail.com

The foot-and-mouth disease virus (FMDV) remains one of the most contagious diseases of domestic livestock worldwide and causes severe economic losses within affected countries. Presently, FMDV maintains an endemic state in the Middle East (ME), with frequent outbreaks across the region. Here, we describe our analyses of FMDV sequence data sampled from the serotype O VP1 gene region to explore the spatiotemporal patterns of viral dispersal both among regions surrounding the ME (Africa, Asia, and Europe), and within countries of the ME. We performed analyses within a statistical Bayesian framework using phylodynamic models on two datasets comprising of publically available FMDV-O VP1 sequence data: the first is a regional-level dataset of selected sequences collected in Africa, Asia, Europe and ME, and the second is a country-level dataset of all sequences from 18 countries within the ME collected between 1969 and 2014. Our regional-level analyses indicate that FMDV in the ME originated in Asia [Kullback-Leibler (KL) = 2.5], and reveals significant viral dispersal between the ME and both Asia and Africa [Bayes factor (BF) > 6]. We identified a peak in regional dispersal events in 2001, which coincides with global waves of newly emerging FMDV lineages. Our country-level analyses identify Turkey as the point of entry of the FMDV-O into the ME (KL = 3.85), with the most significant viral dispersal route between Turkey and Israel (BF > 6). Our analyses suggest that most strongly supported dispersal routes involve Israel on one side and Asian ME countries on the other. Our study of the spatiotemporal dynamics of FMDV-O within and among regions of the ME illustrates the ability of phylodynamic models to improve molecular surveillance of transboundary FMDVs, with clear implications for the control and prevention at regional levels.

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Distribution and Genetic Variation of Swine H1N1 Influenza Virus in Chiang Mai-Lamphun area, Thailand

Terdsak Yano[1], Nanthicha Jeedang[1], Nisanee Kaewmaneewan[1], Ratchaya Vachirachewin[1], Prapas Patchanee[1], Panuwat Yamsakul[1], Phongsakorn Chuammitri[2], [1]Faculty of Veterinary Medicine, Chiang Mai University, Chiang Mai, Thailand; [2]Faculty of Veterinary Medicine, Chiang Mai University, Chiang Mai, Thailand. Contact: vetjek@gmail.com

Purpose: Swine influenza is a highly contagious respiratory disease that causes economic loss in the swine industry. The aim of this study is to investigate the distribution and genetic variability of swine H1N1 influenza virus in Chiang Mai and Lamphun province.
Methods: Total 127 nasal swabs were collected from 49 farms, including 4-week piglets, 8-week piglets, sows, and fattening pigs. All samples were analyzed by real-time PCR.
Results: The result shows that 6 of 127 samples were found to be a swine influenza virus subtype H1N1. The result of farm level indicated a prevalence of swine influenza virus subtype H1N1 was 4 of 49 farms (8.16%). In addition, distribution of swine influenza virus subtype H1N1 in the district and provincial level found prevalence in Lamphun area was 9.5%. Phylogenetic analysis revealed that swine influenza virus subtype H1N1 isolated in this study resembled those H1N1 isolates in Thailand, which were pandemically outbreaks of 2009. Moreover, these isolates were similar to swine influenza virus in other continents; Asian, Europe, and America.
Conclusions: This particular survey of swine influenza virus subtype H1N1 in Chiang Mai-Lamphun shows the evidence that they are actually derived from the swine H1N1 influenza virus which caused an outbreak in Thailand and various worldwide locations.

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Exploring the diversity and evolution of toxinotype V Clostridium difficile strains from an integrated population of humans and swine through whole genome sequencing

Keri N. Norman, Javier Vinasco, Maria A. Martinez, H. Morgan Scott, Texas A&M University, College Station, TX, Contact: knorman@cvm.tamu.edu

Purpose
Clostridium difficile is most commonly responsible for nosocomial infections caused by antibiotic use; however, the finding of similar strains in human infection and food animals has raised concern for C. difficile to be a potential foodborne pathogen and a source of the increasing number of community-acquired C. difficile infections (CA-CDI). Previously, we isolated C. difficile from a closed population of humans and swine to investigate the potential for occupational exposure. We found that there was not a significant difference in the prevalence of C. difficile in wastewater from swine workers and non-swine workers. Interestingly, the majority of strains isolated from both the human wastewater and swine fecal samples were toxinotype V, North American Pulsed-field type 7 (NAP7). Although Pulsed-field gel electrophoresis is the standard typing methods for C. difficile in the United States, this may not be the most suitable typing method. Next generation sequencing may provide a more discriminatory method to differentiate between strains.
Methods
We are conducting whole genome sequencing on 96 swine and 96 human toxinotype V, NAP7 strains. Library preparation was performed using Nextera XT DNA sample preparation kits and each strain was individually indexed. Libraries were sequenced on the Illumina MiSeq platform. MiSeq Reporter and Geneious Pro Software were used to assemble and align sequences, identify potential nucleotide polymorphisms, and facilitate phylogenetic analyses.
Results
Analysis of sequencing data is currently underway and will be completed shortly
Conclusions/Relevance
Whole genome sequencing will provide a more detailed view of the genotypic diversity among toxinotype V strains. The diversity and evolution of toxinotype V strains is especially important because these strains are commonly found in both food animals and human infection and many questions still remain about potential sources for CA-CDI. Understanding the true diversity within C. difficile toxinotypes and North American Pulsed-field types is essential for discussions regarding standardized typing methods.

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Fecal microbiome and non-typhoidal Salmonella enterica: changes through the transition period of dairy cattle.

Lohendy Muñoz-Vargas[1], Rose Digianantonio[1], Gustavo Schuenemann[1], Santiago Bas[1], Michele Williams[2], Gregory Habing[1], [1]The Ohio State University, Columbus, OH, [2]2Ohio Agricultural Research and Development Center, Wooster, OH, Contact: lohendymv@gmail.com

Purpose: Stressors in livestock have been associated with shedding of Non-Typhoidal Salmonella (NTS) in multiple studies. However, there is a lack of understanding of how stress caused by parturition can influence the stability and diversity of the gut microbiome and the patterns of NTS shedding. The objective of the study was to determine the association between changes in the fecal microbial community, metabolic stress, and shedding of NTS through the transition period of dairy cattle.
Methods: This longitudinal trial included 48 cows from four commercial dairy farms in Ohio. In total, 192 fecal and blood samples were collected at four time points relative to the calving day (3 and 1 wk pre-parturition, 1 and 3 wks post-parturition). Culture of fecal samples was used to determine the prevalence of NTS at each time point. Serum concentrations of non-esterified fatty acids and β-hydroxybutyrate were used to measure metabolic stress. Extracted total genomic DNA of the 192 fecal samples was used as a template for conventional PCR, and subsequent sequencing of the V4 region of the 16S rRNA gene using the Illumina platform. Changes overtime were assessed by a principal coordinate analysis and analysis of molecular variance using the R statistical package.
Results: Preliminary results demonstrated that a significant proportion of cows began shedding NTS closer to the calving day ($p< 0.01$). Overall, 38% of fecal cultures were positive for NTS in the 3 wks pre-parturition, compared to 48%, 52%, and 34% during -1, +1 and +3 wks relative to parturition, respectively. Changes in the microbial community diversity through the calving period and the associations with NTS shedding and stress will be presented. Preliminary results showed a highly diverse microbiome constituted by 1,144 bacterial species, with Ruminococcaceae, Bacteroidaceae and Clostridiaceae families being the most abundant.
Conclusion: We suggest that gut microbiome perturbations could have resulted in the observed increases in fecal shedding of NTS around calving.
Relevance: This study helps to understand the microbial ecological mechanisms associated with an increasing prevalence of human microbial hazards on farms.

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Streptococcus uberis mastitis risk predicted from the occurrence of specific strain types in dairy herds

Simon Archer, Peers Davies, Martin Green, University of Nottingham, Sutton Bonington, United Kingdom. Contact: simon.archer@nottingham.ac.uk

Purpose: The aim was to identify risk factors for *Streptococcus. uberis* clinical mastitis transmission, and investigate the relationship between the occurrence of specific *S. uberis* strain types and *S. uberis* clinical mastitis risk.
Methods: Transmission was assumed from the temporal occurrence of the same multilocus strain types of *S. uberis* mastitis in different cows within each herd. Data were available from 52 English and Welsh dairy farms, this included multilocus strain types of 466 isolates of S. uberis associated with clinical mastitis during the study. Observations were structured longitudinally as repeated measures of week through the study period for each cow. Potential exposure variables included cow factors, milk production and somatic cell count data, and the temporal herd history of clinical mastitis associated with particular *S. uberis* strain types. A multilevel logistic regression model using Markov chain Monte Carlo simulations was used for analysis in a Bayesian framework with vague priors.
Results: The final models were shown to have adequate fit to the data. Factors that increased *S. uberis* risk included cow parity, and week of lactation. Importantly, clinical cases of *S. uberis* mastitis were associated with the previous occurrence of specific strain types of *S. uberis* clinical mastitis in herdmates during the previous 3 weeks.
Conclusions: This result highlights the potential usefulness of molecular diagnostics and Bayesian techniques to predict high risk periods for clinical mastitis transmission.
Relevance: Useful diagnostic information can be obtained from knowledge of *S. uberis* strain types associated with clinical mastitis on dairy farms. This can be developed to allow advice on control measures to precede high risk periods.

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Factors influencing export market recovery for poultry meat and poultry products after a highly pathogenic poultry disease outbreak

Amy Hagerman[1], Kamina Johnson[1], Jada Thompson[2], Christine Kopral[1], [1]USDA-APHIS-VS-STAS, Fort Collins, CO, [2]Colorado State University, Fort Collins, CO, Contact: amy.d.hagerman@aphis.usda.gov

Purpose:
During or after poultry disease incidents, sanitary restrictions may apply to live birds, poultry products, hatching eggs and egg products. Affected countries usually halt all exports from affected species until borders can confidently be reopened. For countries that export a large proportion of poultry production, particularly for poultry products that do not have a strong domestic market, such trade bans can be very costly. A multitude of factors may influence the length of export recovery such as disease type, product type and value, world supply, global economic health, disease management timelines, outbreak size and duration, and country credibility.
The objective of this work is to better inform expectations of export market loss in the future by examining factors that influence the length of export quantity recovery time for affected products after an observed disease incident.
Methods:
This study uses 71 HPAI and END outbreaks affecting birds in 25 countries between 1998 and 2013 to determine what factors have had a significant influence on the length of trade recovery as measured by the quantity of poultry associated exports. Export market recovery is defined as the months elapsed from the first announcement of a livestock disease outbreak until a country's quantity of monthly exports met or exceeded the pre-outbreak forecast of the quantity of monthly exports. A gravity model of trade, which is commonly used on export quantity analyses in trade economics, will be developed.
Results, Conclusions, and Relevance:
Previous work has focused on case studies (available at www.lmic.info) and export revenue recovery (forthcoming, IFAMR). Revenue recovery analysis concluded that measurable export revenue losses did not always occur, and were driven by not only outbreak characteristics and perceived disease risk but also world economic health, and relative affordability of poultry products. However, export revenue losses do not accrue evenly across the products. By breaking out offal and poultry products from poultry meat, the results of this quantity recovery analysis are expected to examine more closely how losses are distributed and if trade recovery differs across products.

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Animal insurance and risk attitude in Vietnam - behavior of small scale dairy farms and role of government-

Hiroichi KONO[1], Satoko Kubota[1], Yasushi Sembokuya[1], Takeshi Nishida[1], Kohei Makita[2], Nguyen Minh Hien[3], Manh Hai Tran[3], [1]Obihiro university of agriculture and veterinary medicine, Obihiro, Japan; [2]Rakuno Gakuen university, Ebetu, Japan; [3]Vietnam National University of Agriculture, Hanoi, Viet Nam.
Contact: kono@obihiro.ac.jp

Purpose:
In Vietnam, animal insurance scheme was started as pilot project; first phase in 1985-1987 and second phase in 2011-2013. But due to asymmetric information problem, there are several difficulties to practice the animal insurance sustainably. Therefore, the purposes of this study were to identify the difference of farmers' attitude to join in animal insurance scheme and to evaluate the conditions for sustainable animal insurance system.

Methods:
The field survey was conducted in February 2015 in Bavi, advanced dairy production area near Hanoi. The data were collected from randomly selected 98 dairy farmers with prepared questionnaire, where 43 farmers joined animal insurance and 54 didn't join. The data were analyzed by using item count technique, risk attitude and time discount rate method.

Results:
The report of Ministry of Agriculture and Rural Development indicated two problems, 1) the variance of dairy cattle insurance value was quite high when the animal was entered the insurance, 2) the rate of dead cows over the total cows in the insurance program was fairly high. These indicated institutional and technical imperfection to evaluate cow insurance value and to diagnose weak cow adequately. Furthermore, we can point out two kinds of problems before and after the insurance contract. One is "adverse selection" that farmers had an incentive to select weak cow when joined insurance, before insurance contract, because farmers have more information about the condition of cow than the insurance company. Another is "moral hazard" that farmers had private information about their own actions after insurance contract and someone else have to bear the costs of a lack of care or effort. This situation will make it difficult to maintain animal insurance market in Vietnam.

Conclusions:
Animal insurance has an important role to stabilize small scale dairy farms in Vietnam. There is necessity of screening using observable information to make inferences about farmers' behavior to avoid adverse selection and to maintain animal insurance in Vietnam.

Relevance:

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Pastoralists' perceptions and motivations for implementing herd health programmes

Abubakar Suleiman[1,2], Elizabeth L. Jackson[2], Jonathan Rushton[2], [1]Ahmadu Bello University, Zaria, Nigeria; [2]Royal Veterinary College, Hatfiled, United Kingdom. Contact: asuleiman@rvc.ac.uk

Purpose: This study was conducted to examine the perception of responsibility and motivational factors influencing the implementation of herd health programmes among Nigerian pastoralists.

Methods: A recently validated "pathway to disease control model" was applied to classify pastoralists based on their present level of herd health programme implementation. This abstract reported on descriptive analysis of the dataset obtained from interviews conducted with 191 Fulani herdsmen. Multivariable ordinal logistic regression will eventually be applied to the dataset to identify motivational factors associated with different stages of programme implementation.

Results: The results revealed that the majority of herdsmen placed major responsibility of animal health care on the government but a quarter accepted financial responsibilities for optimal herd health. All of the interviewed herdsmen had recently taken at least one action intended to control disease on herd but only a few implemented any structured herd health programme.

Conclusions: From these preliminary findings, it can be inferred that the Fulani pastoralists are beginning to accept responsibility for animal health care but complications with identifying substandard drugs and services commonly associated with the private veterinary marketplace may undermine the sustainability of their investment in disease control.

Relevance: Following decades of limited funding for the livestock sector, animal health services in Nigeria, and indeed most countries in West Africa, are being substantially delivered by private veterinary service providers. But whether private sector involvement improves animal health depends on change of farmer behaviour towards accepting responsibility and taking more effective decisions concerning herd health management. Findings from this study will provide empirical options for encouraging farm-level resource allocation into projects intended to improve herd health and productivity.

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The economic impact of malignant catarrhal fever on pastoralist livelihoods

Felix J. Lankester[1], Ahmed Lugelo[2], Rudovick Kazwala[2], Julius Keyyu[3], Sarah Cleaveland[4], **Jonathan Yoder**[5], [1]Washington State University, Pullman, WA, [2]Sokoine University of Agriculture, Morogoro, Tanzania, United Republic of; [3]Tanzanian Wildlife Research Institute, Arusha, Tanzania, United Republic of; [4]University of Glasgow, Glasgow, United Kingdom; [5]Washington State University, Pullman, WA, Contact: yoder@wsu.edu

Purpose:
Malignant catarrhal fever (MCF), a fatal viral disease of cattle transmitted from wildebeest calves, has plagued Maasai communities for generations as it forces them, temporarily, to move cattle to less productive grazing to avoid the disease. This study quantifies the potential economic benefits that a vaccine against MCF could accrue to pastoralists living in E.Africa.

Methods:
To assess the resource costs associated with moving cattle away, we used household survey data. To estimate the costs associated with changes in livestock condition, we exploited an ongoing MCF vaccine field trial and used a hedonic price regression.

Results:
90% of households move 82% of cattle 21 km away from home for 88 days to avoid MCF. In doing so, a herd's productive contribution to the household was reduced, with 64% of milk being unavailable for sale or consumption by the family members remaining at the household. This represents an annual income loss of up to 8%. In contrast cattle that remained on the wildebeest calving grounds (and survived MCF) remained fully productive to the family and gained condition compared to cattle that moved away.

Conclusions:
MCF presents an epidemiological and economic dilemma: Herd cattle away from wildebeest calves to avoid disease, and incur costs from lost opportunities to consume/sell milk, and the energy and labor input required to move or remain on the wildebeest pastures which, without an effective vaccine, also incurs costs through a higher risk of disease. Currently the disease costs associated with the alternative strategy will potentially offset any gains made through increased availability of milk, improved condition and reduced energy demands from movements. This suggests the traditional strategy is currently the least costly option. With the development of an effective vaccine, however, the alternative strategy might be optimal.

Relevance:
This study provides the first quantitative assessment of the annual costs that pastoralists incur avoiding MCF. This study is the first to use hedonic price function analysis to assess the impacts of disease avoidance on value.

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Potential Economic Impacts of a Highly Pathogenic Avian Influenza Outbreak on Upper Midwestern United States Table-Egg Laying Operations

Jada Thompson[1], Todd Weaver[2], Kelly Patyk[2], Sasidhar Malladi[3], [1]Colorado State University, Fort Collins, CO, [2]USDA: APHIS, Fort Collins, CO, [3]USDA APHIS, Fort Collins, CO, Contact: thompson.jadam@gmail.com

Purpose

The current outbreak of highly pathogenic avian influenza (HPAI) in the U.S. could lead to substantial economic impacts on producers, processors, and the final consumer. The response to an HPAI outbreak is to establish a control area and stop movement orders. However, there are possible scenarios where, after assessing the risk, it is beneficial to allow movement of low to negligible spread risk poultry products from monitored premises, those not known to be infected with HPAI virus.

Methods

An economic assessment will be made of movement of egg-industry products within and outside of HPAI Control Areas. Additionally, regionalization, where separating the United States into defined economic regions, will be investigated as a means for non-affected regions to compensate for a HPAI infected region's loss in production. The North American Animal Disease Spread Model is used to model the HPAI outbreak in the Midwestern U.S. Using quarterly data, a multi market partial equilibrium model will be used to estimate the supply chain disruption during an HPAI outbreak estimating the ability of surrounding regions to compensate for stop movement orders with and without trade markets. This will provide a baseline for comparison to scenarios when movement is allowed to occur from monitored premises.

Results

The results will provide insights into the economic assessment for allowing monitored premises to move product in and outside of quarantine zones, which will have significant implications for the entire egg supply chain.

Conclusion

Disease outbreaks among domestic livestock and poultry, especially those that are transboundary and/or zoonotic like HPAI, can spread throughout the supply chain in the absence of control measures creating economic losses. Allowing movement from monitored premises may lessen the financial strain of HPAI and provide business continuity solutions for both domestic and international markets.

Relevance

Economic consequence assessment of controlled movement measures will provide decision makers with an ex-ante evaluation of the feasibility of alternative HPAI response plans to be effective in both disease mitigation and in maintaining business continuity.

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Importance of socioeconomic perspectives in addressing Foot-and-mouth disease control on smallholder farms in South-East Asia

Peter A. Windsor[1], Sonevilay Nampanya[1], Syseng Khounsy[2], Ronel Abila[3], Jim Young[1], Russell Bush[1], [1]University of Sydney, Camden, NSW, Australia; [2]Department of Livestock and Fisheries,, Luang Prabang, Lao People's Democratic Republic; [3]OIE, Bangkok, Thailand. Contact: peter.windsor@sydney.edu.au

Purpose: Of 7 global pools of FMD virus, Pool I in South East and East Asia, is the second most advanced region in FMD control, with eradication completed in Indonesia in 1984 and the Philippines in 2011, plus an OIE Roadmap encouraging regional control through the SEACFMD program of several decades. To guide allocation of FMD investments, we studied socioeconomic impacts of FMD on Lao smallholders in 2011-12, including gender, household financial status and farmer husbandry practices.
Methods: Households (n=124) were classified as 'poor, medium or well-off' and losses included those from mortality, morbidity and costs of treatments. National FMD impacts were determined from outbreak reports and estimates based on the total losses at village level and costs of FMD responses and other related expenditure but excluding revenue forgone. A Monte Carlo simulation accounted for scenarios of over- and under-reporting, with above data used to estimate the benefit to cost ratio of current vaccination programs.
Results: Losses were USD436 (±92) in 'poor' and USD949 (±76) in 'well off' house-hold categories ($P < 0.001$), being 128% and 49% of income from livestock sales, respectively. Variation in losses reflected differences in morbidity, husbandry practices and importantly, choice of treatments with adverse impacts where antibiotics were used. Monte Carlo simulation estimated that national financial losses in 2011 may have exceeded USD 102m, almost 12% of the estimated farm gate value of the national herd. Estimated benefit to cost ratio of the current FMD vaccination program in northern Laos was 5.3.
Conclusions: Findings confirm FMD causes substantial impacts on households and the national economy of Laos, with most severe impacts on poorer households using antibiotics, and females having a significant role in large ruminant production.
Relevance: Sustained investments in FMD control including vaccination and biosecurity education are justified and should include women and avoid the use of antibiotics. Socioeconomic studies are important where resources are limited and expenditure on a relatively low mortality disease of global significance can be difficult to justify.

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An economic evaluation of potential surveillance strategies for the control of Bovine Viral Diarrhoea Virus in England

Betty Bisdorff[1], Richard Booth[1], Jonathan Rushton[1], Joe Brownlie[1], Marisa Peyre[2], Dirk Pfeiffer[1], Barbara Häsler[1], [1]The Royal Veterinary College, London, United Kingdom., North Mymms, United Kingdom; [2]CIRAD, Centre de Coopération Internationale en Recherche en Agronomie pour le Développement, Paris, France. Contact: bbisdorff@rvc.ac.uk

Purpose:
Economic analysis of surveillance systems is valuable for decision-making: it shows the consequences of different alternatives and helps ensure that maximum benefit from disease mitigation is obtained from a given amount of resources. Bovine viral diarrhoea virus (BVDV) is a non-notifiable endemic disease of cattle in England with a significant economic impact, yet it lacks a national control and a decision-making process for its elimination. To improve coordination of existing local schemes a surveillance system is needed to establish prevalence levels in order to develop an efficient control strategy.
Methods:
Therefore a study was designed to holistically develop and evaluate BVDV surveillance for England that would enhance resource use efficiency. A proposed surveillance framework included a centralized data coordination and management system, and was compared to the current system (the baseline) with cost-effectiveness analysis that utilises a new surveillance evaluation tool recently developed by the project RISKSUR (www.fp7-risksur.eu). Surveillance costs were being estimated using publications and interviews with decision-makers from the different existing schemes. The effectiveness is expressed as the ability of the system to detect disease in an endemic situation. A cost-effectiveness analysis looking at technical outcome is conducted to look at different surveillance options, also taking into account different ways of coordinating and managing the data in a centralized way.
Results:
Results indicate that a Surveillance Centre for BVDV would cost £60,000 per annum for personnel and overheads. Further results, as well as further sensitivity analysis on their robustness, will be presented.
Conclusion:
The estimated improvement in effectiveness demonstrates that such a Centre would improve sensitivity of surveillance and if well linked to a national control programme lead to economic gains.
Relevance: An evaluation of the cost-effectiveness of an improved BVDV surveillance system presents a strong case for the implementation of the improved strategy, presenting decision-makers with the requisite evidence of a BVDV control programme.

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Multivariable analysis of factors influencing the efficiency of Village Animal Health Workers in Cambodia.

Flavie L. Goutard[1], Clementine Calba[1,2], **Marie-Marie Olive**[1], Sophoan Min[3], Lotfi Allal[2], Marisa Peyre[1], [1]CIRAD, Montpellier, France; [2]FAO, Phnom Penh, Cambodia; [3]AVSF, Phnom Penh, Cambodia. Contact: marie-marie.olive@cirad.fr

Purpose:
In Cambodia, Village Animal Health Workers (VAHW) have been trained by NGOs or by the government to provide animal health services (treatment, husbandry advice, vaccination) to their communities' farmers. This system is characterised by a high variability of skills because of non-harmonised training plans, poor sustainability with a large number of VAHWs dropping their activities after five years and no harmonised tools for their evaluation.
The objective of the study was to assess the work skills of VAHW.
Methods:
We applied a scoring grid composed of five categories (sustainability, treatment, production, vaccination, reporting). Linked to several evaluation criteria, specific questions were defined to assess if the criteria were fulfilled by the VAHW. An additional questionnaire, with 31 explanatory variables, was developed in order to collect data about factors that could influence the VAHW's score. The study was implemented in three provinces bordering Vietnam (Kampong Cham, Prey Veng and Takeo). A total of 367 villages were selected using a proportional random sampling, g method. We applied a multivariable linear regression model to determine factors associated with high scores for the VAHW evaluation.
Results:
In the population studied, 23% of the villages did not have a VAHW. According to our scoring system, 23.6% of the VAHW interviewed were in a situation of inactivity. From our multivariable analysis, six factors were significantly associated with a high score in the evaluation of the VAHW once they were active: selecting a VAHW from a village with at least 100 heads of cattle, using practical activities during training, having a training duration longer than 30 days, organising refresher courses, being a member of association and having regular contact with the district veterinarian.
Conclusions:
These results demonstrate the need of constant networking activities in the surveillance system to ensure that field staffs do not feel isolated.
Relevance:
Some of these findings could be used as a prerequisite for continued participation in refresher training activities done by the Cambodian government.

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Zoonotic disease risk perceptions in the British veterinary profession

Charlotte Robin[1], Robert Christley[1], Fiona McMaster[2], [1]University of Liverpool, Neston, United Kingdom; [2]Anglia Ruskin University, Cambridge, United Kingdom. Contact: charlotte.robin@liverpool.ac.uk

Purpose:
The veterinary profession has a vital role in safeguarding the animal population, and subsequently the human population from zoonoses. Scant data are available on the attitudes of the profession towards the likelihood of acquiring zoonotic infections during their veterinary work. This study aimed to explore disease risk perceptions within the British veterinary profession.

Methods:
1000 veterinary practices were randomly selected from the Royal College of Veterinary Surgeons database, and contacted with a postal questionnaire. The questionnaire contained open and closed questions, covering veterinary experience, risk perceptions, infection control practices and management of zoonotic cases.

Results:
252 (12.6%) questionnaires were returned, 46.0% by veterinary nurses and 54.0% by veterinary surgeons. The median age of respondents was 41 years, and 61.1% were female. Most respondents worked in small animal practice (79.4%). A large proportion (67.0%) of respondents had previously contracted a zoonotic infection, most commonly dermatophytosis (26.2%).
The majority of respondents were not concerned about zoonotic disease transmission (57.5%), however a considerable proportion were (34.9%). Only a small proportion had not thought about it (7.1%).
History of zoonotic infection was associated with current concern about the risk of zoonoses (P=0.001).
Experience was associated with perceived knowledge of zoonoses; median years in practice for those who felt they had a high level of knowledge was 25 years, compared to 12 years for those that felt less confident about their level of knowledge (P=0.03).
Those who had previously contracted a zoonotic infection felt less able to take action to prevent further infections, compared to those who had never contracted a zoonosis (P=0.003).

Conclusions:
Risk perceptions are circumstance-specific and are influenced by a number of factors including previous experience, knowledge and self-efficacy.

Relevance:
Rather than providing more stringent infection control practices, professionals need to be equipped with the skills to improve the quality of their decision-making for different clinical scenarios they may encounter.

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Zoonotic risks in backyard poultry and swine productive systems in the central zone of Chile

Francisca Di Pillo[1], Soledad Ruiz[1], Stephanie Depraz[2], Elizabeth Gomez[1], Patricio Retamal[1], José-Manuel Yáñez[1], Santiago Urcelay[1], Christopher Hamilton-West[1], [1]University of Chile, Santiago, Chile; [2]CIRAD, Guadeloupe, France. Contact: frandipi@gmail.com

Purpose: Backyard productive systems (BPS) are recognized as the most common form of animal production in the world, being considered as an important component of small farmer's livelihoods. However, BPS exhibit severe biosecurity deficiencies, and could play a major role in the maintenance and spread of animal diseases and zoonoses. The aim of this study was to identify the circulation of influenza A virus (IAV) and *Salmonella enterica* in BPS, and to evaluate risk factors for these infections.
Methods: Serum samples and cloacal swabs were randomly collected from birds and swine among 113 BPS in central Chile.
Results: There was a rate of IAV antibodies of 4.09% (18/440) in poultry, and 1.57% (2/127) in swine, whereas it was of 12.72% (14/110) for poultry and 2.2% (2/89) for swine at BPS level. As for *Salmonella*, a total of 30 birds resulted positive to *Salmonella* spp. Regarding to pigs, 6 were found positive to *Salmonella*. The positivity rates of *Salmonella* in poultry and pigs were 5.71% and 3.85%, respectively. The positivity rate of *Salmonella* at BPS level was 22.12% (25/113) Risk factors were evaluated through a logistic regression model. Variables that showed statistical significance ($p<0.05$) for IAV were sampling in counties bordering coast or lakes (OR = 9.66) and the direct contact between poultry and pigs (OR = 8.18). For *Salmonella*, 4 variables showed statistical significance (p value<0.05); sampling in counties bordering coast or lakes (OR = 11.29), the interaction between total number of poultry and sampling during spring/summer (OR = 1.05), the presence of poultry/swine in neighbors (OR = 6.08) and swine with permanent stabling (OR = 0.09).
Conclusions: The results of this study demonstrate that IAV and *Salmonella* spp. have been circulating in poultry and swine populations at BPS in central Chile.
Relevance: The circulation of these diseases in BPS poultry and swine constitute biological risks that threaten both public and animal health and the sustainability of these production systems.

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Evaluation of brucellosis management practices and vaccination campaign in two districts of Buenos Aires, Argentina

María N. Aznar[1], Matías Arregui[2], Inés Irastorza[3], Patricia Rocha[4], Luis E. Samartino[2], Claude Saegerman[5], [1]INTA/University of Liège, Hurlingham, Argentina; [2]INTA, Hurlingham, Argentina; [3]SENASA, Brandsen, Argentina; [4]Sociedad Rural de Navarro, Navarro, Argentina; [5]University of Liège, Liège, Belgium. Contact: aznar.maria@inta.gob.ar

In Argentina, bovine brucellosis is endemic. Vaccination of heifers with *Brucella* strain S19 is mandatory. The SENASA entrusts the vaccination campaign execution to Local Sanitary Entities (LSEs).Purpose: to evaluate farmers' and veterinarians' management practices concerning the disease and to assess the vaccination campaign and vaccine coverage in two districts of Buenos Aires.Methods: 4 different questionnaires were performed to 113 dairy and beef farmers, 11 veterinarians, 13 vaccinators and 2 people responsible for the LSEs. Also, 5 brucellosis experts answered the farmers' questionnaires, giving their opinion on what should be the ideal and "unacceptable" answers.To check the vaccine coverage, serum samples of 20 heifers vaccinated 21-50 days earlier (vaccine approved by SENASA) from 25 of the 113 farms were randomly taken. The buffered plate antigen test (BPA) verified the vaccine exposure. Farms with at least 19 BPA + heifers were considered as "corrected vaccinated".Results: a) Farmers: 65% of farmers tried to diagnose the cause of reproductive disorders (*Neospora caninum* was the most common cause). Dairy farmers diagnosed more ($P<0.05$) than beef ones.42% purchased cattle in the last year, only 38% did so from free certified farms and 27% tested the purchased animals, although all veterinarians suggested this useful practice. In beef farms, more "unacceptable" answers were found. b) Vaccinators: 77% calibrated the syringe, 40% homogenized the vaccine and 75% injected it again if some vaccine dropped. c) Vaccine coverage: 78% of heifers was BPA+, which is significantly lower ($P<0.05$) than the expected coverage of 100%. At all the farms at least one heifer was BPA+, but only 44% of them can be considered "corrected vaccinated".Conclusions: although well advised by their veterinarians, farmers should improve some management practices. The vaccination campaign is globally well implemented but some aspects should be improved. The low coverage is not due to the quality of the vaccine but more related to the lack of goof vaccination practices.
Relevance: Knowledge of brucellosis practices and vaccination is useful to improve and adequate the National Control Program.

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Assessing public health risk from emerging arboviruses in Canada: a multispecies serology study.

Jean-Philippe Rocheleau[1], Julie Arsenault[2], Robbin L. Lindsay[3], Michael Drebot[3], Pascal Michel[4], [1]Université de Montréal, Saint-Hyacinthe, QC, Canada; [2]Université de Montréal, Saint-Hyacinthe, QC, Canada; [3]Public Health Agency of Canada, Winnipeg, MB, Canada; [4]Public Health Agency of Canada, Saint-Hyacinthe, QC, Canada. Contact: jean-philippe.rocheleau@umontreal.ca

Over the past 15 years, detection of arboviral infections among wild or domestic animal populations has led to important insights on the introduction, the spread and the epidemiology of arboviruses in Canadian populations. However, our experience in interpreting animal data arising from targeted studies and short term programs to infer on public health risk has revealed some challenges. These mainly relate to fluctuating herd immunity or inability to efficiently detect clinical signs in animals and could be partly circumvented by implementing structured population level serological surveillance initiatives. In this context, we believe that the veterinary network represents a rich potential for systematic and ongoing data sources pertinent both to animals and humans.
Purpose: This project aimed at studying the emergence of various arboviruses in Eastern Canada while building the conceptual basis for the use and interpretation of easily accessible companion animal serological data for enhanced public health risk assessment of vector borne diseases.
Methods: Sera from 196 unvaccinated horses, 1627 dogs and 485 humans were collected in the same geographical area of southern Quebec, Canada, from 2012 to 2014. Indicators of mosquito exposure were recorded for all sampled subjects. Serological essays for West Nile virus, Eastern equine encephalitis and Jamestown Canyon virus were conducted on all samples. Seroprevalence estimates, spatial clusters and ecological/individual risk factors were compared among species.
Results: Seroprevalence estimates were consistently higher in horses as compared to other species. Adult dogs and humans had similar intermediate levels of seroprevalence. Risk factors were similar in all species and consistent with previously published data from North-Eastern America.
Conclusions: Animal data generally allowed for a risk detection and characterisation in a more sensitive way than with the human data alone. Advantages and limits of using each species for surveillance and risk assessment are discussed.
Relevance: We conclude that companion animals' serology can provide a valuable insight about public health risk under certain conditions.

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The role of food systems in improving human nutrition in challenging African low-income settings

Paula Dominguez-Salas[1], Barbara Haesler[1], Jonathan Rushton[1], Silvia Alonso[2], Elaine Ferguson[3], Laura Cornelsen[3], Eric Fevre[4], Delia Grace[2], Pablo Alarcon[1], [1]Royal Veterinary College, Hatfield, Hertfordshire, United Kingdom; [2]International Livestock Research Institute, Nairobi, Kenya; [3]London School of Hygiene and Tropical Medicine, London, United Kingdom; [4]University of Liverpool, Liverpool, United Kingdom. Contact: paula181920@gmail.com

Purpose

Overcrowded cities in developing countries present challenging environments for health, where zoonoses and food safety are difficult to control. Whilst animal source foods (ASF) have a well-recognized role in nutrition of vulnerable populations, their availability, safety and quality are often compromised, and nutrition outcomes are rarely considered in livestock studies.

We developed and tested a framework to study the association between consumers' access to and use of different ASF and livestock value chains, and poor nutritional status, to inform decisions on interventions and policies.

Methods

This multidisciplinary study combined quantitative and qualitative methodologies to address unexplored linkages between value chain and nutrition. 205 households and 222 retailers in two Nairobi slums were surveyed to 1) measure consumption and undernutrition; 2) examine ASF role in adequate diets using linear programming; and 3) investigate value chain links with nutrition. For each ASF, consumption patterns, acceptability factors of products and retailers, demand variation with price and availability (expansion potential of value chain) were combined to provide a holistic picture and identify target chains.

Results and conclusions

74% of the children and 26% of the women were anaemic, and had low intakes of several micronutrients. Linear programing analysis indicated that food-based interventions could ensure women's dietary adequacy for women, for all of these nutrients except iron, as long as intakes of milk and other ASF could be increased from median intakes. Milk was the most consumed ASF (98.5% of the households, 5.5 times/wk). Demand for beef was least sensitive to changes in its price and its supply chain had limited expansion potential. Demand for chicken was more responsive to price changes while its supply chains could be expanded quickly. Consumption was often based on 'taste' and 'nutrition', indicating a potential role for nutrition education.

Relevance

Nutrition sensitive agriculture being key to fight malnutrition, we will show the importance of the value chain approach to assess feasibility and upscaling of safe ASF food system-based interventions.

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Using mixed methods to assess food security and coping strategies among smallholders in the Andean region

Georgina Limon[1], Guillaume Fournié[1], Elisa G. Lewis[2], Paula Dominguez-Salas[3], Daniela Leyton[4], Eloy A. Gonzales-Gustavson[5], Armando E. Gonzalez[5], Aurelio H. Cabezas[6], Deyanira Barrero[7], Ximena Quesada[7], Julio Pinto[8], Jonathan Rushton[1], Javier Guitian[1], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]Royal Veterinary College and Birkbeck College, Hatfield / London, United Kingdom; [3]Royal Veterinary College and Leverhulme Centre of Integrative Research in Agriculture and Health, Hatfield / London, United Kingdom; [4]PROMETA, Tarija, Bolivia, Plurinational State of; [5]San Marcos Veterinary School, Lima, Peru; [6]UDLA Veterinary School, Quito, Ecuador; [7]Food and Agriculture Organization (FAO) of the United Nations. Regional office for Latin-American and the Caribbean, Santiago, Chile; [8]Food and Agriculture Organization (FAO) of the United Nations, Rome, Italy. Contact: glimon@rvc.ac.uk

International organizations and national governments in resource-scarce settings regularly support programs for the control of animal diseases as a means to improve smallholder food security. However, the impact of such programs on smallholder food security remains unclear. Instruments currently available only assess availability and access. Therefore, there is a need to evaluate the impact of animal diseases on smallholder food security with a methodology capable to capture the 4 dimensions: availability, access, utilization and stability.

Purpose: The study aim was to conduct a systematic and comprehensive investigation of smallholder food security and their main coping strategies when food security is compromised, in the context of a transnational FMD control program in the Andean region.

Methods: A mixed method design based on the join collection, analysis and interpretation of quantitative and qualitative data was used. It was carried out in 3 selected areas of the central Andean region (Peru, Bolivia and Ecuador) and involved interviews to 632 smallholders. Data were analysed at the household level using multivariate analysis which identified 3 clusters in each study area. Themes were identified using thematic analysis.

Results: Food acquisition capacity and coping strategies varied greatly across clusters. Food produced in the household, season, financial capacity, household demographics and food price were the main factors influencing variation in food consumption. Off-farm income was positively correlated to herd size and coping capacity in shock situations. Although only 1.6% households had a Food Consumption Score below the acceptable threshold, food stability was compromised across study areas.

Conclusions: By using a mixed methods approach we succeeded to assess the four dimensions of food security. The qualitative strand was crucial to evaluate food stability, a dimension frequently ignored in food security evaluations.

Relevance: These results suggest that the impact and benefits of animal disease control programmes on smallholder food security would differ across smallholders. Thus, smallholders should not be considered as single homogeneous group.

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Integration of food safety and nutrition research to promote food security: A case study from Tanzania

Barbara Häsler[1], George Msalya[2], Maria Garza[3], Kimberly Fornace[4], Mahmoud Eltholth[5], Anna Sikira[6], Lusato Kurwijila[2], Jonathan Rushton[1], Delia Grace[7], [1]Royal Veterinary College and Leverhulme Centre for Integrative Research on Agriculture and Health, Hatfield, United Kingdom; [2]Sokoine University of Agriculture, Morogoro, Tanzania, United Republic of; [3]Royal Veterinary College, Hatfield, United Kingdom; [4]London School of Hygiene and Tropical Medicine, London, United Kingdom; [5]Kafrelsheikh University, Kafrelsheikh, Egypt; [6]Sokoine University of Agriculture, Morogoro, Tanzania, United Republic of; [7]International Livestock Research Institute, Nairobi, Kenya. Contact: bhaesler@rvc.ac.uk

Purpose
It is widely recognized that animal-source foods (ASFs) have the potential to improve nutrition and promote health, especially in vulnerable households, and to alleviate micronutrient deficiencies. However, scaling up ASF production bears food safety risks that are often overlooked due to a disconnect between nutrition and animal science. With the aim to bridge this gap, an integrated framework for combined nutritional, food safety and value chain analysis was developed to assess the dairy value chain in two regions of Tanzania, namely Morogoro and Tanga.
Methods
Semi-structured interviews with 150 producers and 157 consumers in 10 villages were conducted to investigate animal production practices and outputs, biosecurity and hygiene, food safety, food security, milk purchasing, processing and consumption practices. Participatory rural appraisals (PRAs) were used to explore seasonality, production constraints, interventions, herd dynamics, the role of ASFs in diets, food handling, and knowledge, attitudes and practices surrounding food quality and safety.
Results
Producer results showed regular use of antimicrobials, commonly sourced from veterinarians, extension officers and pharmacies. Biosecurity was poor and almost all producers (>90%) sold raw milk mainly directly to consumers (63%) or milk collectors (29%). Almost 70% stated that they almost always find a buyer for milk, but there was also a strong demand for quality, confirmed by consumers - 78% said that milk quality is more important than price. 96% households regularly consumed milk; preferentially boiled (85%) and/or raw (26%). Food security indicators were higher in cattle keeping households. The PRAs identified strong seasonal patterns, a widespread belief in the “goodness” of milk, multiple production constraints, and common dairy husbandry and milk handling practices.
Conclusions and relevance
The study promotes understanding of the complexity surrounding the local food environment and ASF consumption practices, livestock expertise, dietary beliefs and nutrition outcomes. The results form an important foundation for the design of nutrition-sensitive livestock interventions and policies.

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Knowledge and attitudes towards Q fever disease and vaccination: a national survey of Australia's veterinary workforce.

Emily Sellens[1], **Navneet K. Dhand**[2], Katrina L. Bosward[2], Jacqueline M. Norris[1], Jane Heller[3], Lynne Hayes[3], Nicholas Wood[4], [1]University of Sydney, Sydney, Australia; [2]University of Sydney, Camden, Australia; [3]Charles Sturt University, Wagga Wagga, Australia; [4]University of Sydney, Sydney, Australia. Contact: naneet.dhand@syney.edu.au

Background: Despite availability of a vaccine (Q-Vax® bioCSL Ltd., Vic.) Q fever was the second most common zoonosis reported by Australian veterinarians in 2013 (Dowd et al. 2013) raising questions about Q fever vaccine uptake among at-risk groups, including the veterinary workforce.
Purpose: to determine and compare the Q fever vaccine uptake, knowledge and attitudes of veterinarians and veterinary nurses in Australia.
Methods: A cross-sectional survey was implemented online via Survey Monkey® in 2014. Data were analysed using SAS® (2002-2012 SAS Institute Inc., Cary). Odds ratios for comparison of veterinarians and veterinary nurses were generated though binary, ordinal or multinomial logistic regression, adjusting for age, sex and state. P-values <0.05 were considered significant.
Results: Responses from 890 veterinarians and 852 veterinary nurses revealed a greater proportion of veterinarians were vaccinated (61%) compared to veterinary nurses (23%). Veterinarians were mostly vaccinated during their university course (81%) while nurses were mostly vaccinated as a job requirement (43%). Among both cohorts the most influential reason for non-vaccination was a perception that "I will not be seriously affected by Q fever" and the most influential sources of biosecurity information were clinic protocols and workplace veterinarians. Compared to veterinary nurses, veterinarians reported higher levels of Q fever knowledge, had 2 times odds (95% CI 1.4-3.4; p = 0.003) of being convinced the Q fever vaccine is important, 3 times odds (2.2-5.1; p<0.001) of agreeing the vaccine is effective and 1.5 times odds (1.05-2.13; p = 0.27) of agreeing the vaccine is safe.
Conclusions: Australia's veterinary nurses rely on workplace protocols and veterinarians, who report high levels of confidence in the Q fever vaccine, for biosecurity information. Vaccine uptake among these nurses falls dramatically short of veterinarians, with many believing they won't be seriously affected by Q fever.
Relevance: Results may reflect a failure to convey health and safety information to veterinary nurses or a misunderstanding of the relevance of Q fever across all veterinary clinics, regardless of species.

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Transmission characteristics of Highly Pathogenic Avian Influenza (H5N8) virus during outbreaks in the Netherlands in 2014

Arjan Stegeman[1], Francisca Velkers[1], Ruth Bouwstra[2], Armin Elbers[2], [1]Utrecht University, Utrecht, Netherlands; [2]Central Veterinary Institute, Lelystad, Netherlands. Contact: j.a.stegeman@uu.nl

Purpose

Outbreaks of Highly Pathogenic Avian Influenza (HPAI) occurred in November 2014 on three layer, one broiler-breeder and one duck farm distributed over four different regions in the Netherlands. The HPAI virus was of subtype H5N8, that before it entered Europe had been found in South Korea, China, Japan and Russia and was subsequently detected in North America. Here we quantify virus transmission during the episode of outbreaks.

Methods

Sharply increasing mortality was most striking in the broiler-breeder and layer flocks, which is in line with reports from other countries. Within-flock transmission was quantified using mortality data assuming that the number of infected birds at day t after virus introduction equals I0*exp(rt), with I0 number of infected birds at the start (assumed as 1) and r the exponential growth rate parameter. Using a GLM with poison error distribution and a log-link function with the number of dead birds as dependent variable and farm as independent variable r was calculated. The duck farm was excluded, because mortality was low and did not fulfill the assumption of exponential growth.

Results

The above model showed r = 1.02 (95% CI :0.98-1.06). Next, using a generation interval T of 2.25 days (95% CI: 1.87-2.63), derived from experimental data, the average number of secondary infections caused by one infectious chicken, was estimated by R0 = exp(rT) at 9.9 (95% CI 6.7-14.6). In addition, on all farms infection was only detectable in one poultry house, indicating absence of transmission between poultry houses at the time of detection. Moreover, genome sequences of the isolates point to separate virus introductions in the four different regions and a single event of between farm transmission in one of the regions. The introductions were most likely caused by contact with wild (water)birds.

Conclusions

The transmissibility of HPAI H5N8 virus among chickens in direct contact is high. However, no indirect transmission to chickens in other houses and only one event of between farm transmission was observed indicating both early detection and effective control of spread.

Relevance

Quantified transmission parameters are useful to improve surveillance and control programs.

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Implications for surveillance in wild birds and poultry following incursion of H5N8 HPAI in Europe

Andrew C. Breed[1], Adam Brouwer[1], Mark Arnold[1], Daisy Duncan[1], Marek Slomka[2], Ian Brown[2], [1]Animal and Plant Health Agency, Addlestone, United Kingdom; [2]Animal and Plant Health Agency, Addlestone, United Kingdom. Contact: andrew.breed@apha.gsi.gov.uk

Purpose:
During late 2014 outbreaks of H5N8 HPAI occurred in poultry farms in Europe in multiple countries and poultry species. Infection was also found in apparently healthy wild ducks in Germany and the Netherlands. Although this incursion could superficially resemble that of H5N1 HPAI almost a decade earlier there are diagnostic and epidemiological features that are different with important implications for surveillance.

Methods:
We evaluated the pattern of detection of this virus across Europe with regard to active and scanning surveillance in wild birds and poultry. We also evaluated the haemagglutination inhibition serological test for the detection of antibodies to this lineage of HPAI 2.3.4.4 with regard to other H5 lineages found in Europe.

Results:
An apparent lack of severe clinical disease in ducks in the UK suggests that scanning surveillance may have very low sensitivity in this species. Haemagglutination inhibition testing of sera from ducks on the holding infected in the UK with standard EU-recommended antigens suggested much lower sensitivity than when the homologous antigen was used. In addition to finding this virus in apparently healthy wild birds of various species in Europe and Asia there are also animal experiments indicating that H5N8 HPAI may have a low virulence in some wild bird species.

Conclusions:
The lineage 2.3.4.4 H5 HPAI virus shows different epidemiological patterns to other HPAI viruses, in particular H5N1 Asian lineage virus, and hence surveillance activities may require modification to maintain optimum sensitivity and efficiency.

Relevance:
These findings are of relevance since the legislatively required surveillance in wild birds in the EU is aimed at detection of H5N1 HPAI and only required to be conducted in birds found dead or ill. Also scanning surveillance may be less sensitive in poultry, particularly domestic waterfowl, then for other HPAI viruses placing greater weight on active serological surveillance.

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Incidence and risk factors for avian influenza and Newcastle disease in village poultry in Mali

Sophie Molia[1], Vladimir Grosbois[1], Badian Kamissoko[2], Kadiatou Diarra Sissoko[3], Maimouna Sanogo Sidibé[3], Idrissa Traoré[2], Adama Diakité[2], Dirk Udo Pfeiffer[4], [1]CIRAD, Montpellier cedex 5, France; [2]Laboratoire Central Vétérinaire, Bamako, Mali; [3]Direction Nationale des Services Vétérinaires, Bamako, Mali; [4]Royal Veterinary College, London, United Kingdom. Contact: sophie.molia@cirad.fr

PURPOSE:
Newcastle disease (ND) and highly pathogenic avian influenza (AI) are a major health constraint/threat for village poultry in Western Africa. However, limited information is available on ND and AI in Mali. Our objective was to estimate their incidence and to identify associated risk factors.
METHODS: We conducted a longitudinal study in 2009-2011 in an area covering 98% of the Malian poultry population. Our 2-stage cluster random sampling involved sampling from 32 poultry in each of 32 villages on 6 sequential occasions. A total of 5,963 blood samples were collected and tested with ELISA for antibodies against AI and ND viruses. Generalized linear mixed models were used to test the association between bird-level seroprevalence, seroincidence, seroreversion and risk factors.
RESULTS:
Circulation of AI viruses was very low (seroprevalence 2.9%, seroincidence rate 0.7 birds /100-bird-months-at-risk) and immunity duration was short (seroreversion rate 25.4 birds /100-bird-month-at-risk). Neither the agroecological zone nor the proximity to a pond or the presence of ducks in the flock were risk factors for AIV. Circulation of ND virus was very high in non-vaccinated poultry (seroprevalence 68.9%, seroincidence rate 15.9 birds /100-birdmonths-at-risk) and was associated with the season, agroecological zone, proximity to a pond and presence of Guinea fowl in the flock. The proportion of vaccinated birds (54.9%) and post-vaccinal seroconversion (90.0%) were higher than in other African countries.
CONCLUSION: Based on our results, we recommend 1) for AI: targeting surveillance at villages located in the inner delta of the Niger river; including virus detection in the diagnosis to increase sensitivity. 2) for ND: reactivating networks of community animal health workers to increase vaccination coverage, especially in flocks with Guinea fowl and in the Sudanian agroecological zone.
RELEVANCE:
Our results help increase cost-effectiveness of surveillance/control programs in Mali where poultry production is actively promoted for poverty alleviation and increased food security.

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Complementary interest of epidemiology and sociology for investigating epidemiological risk factors - a case study on avian influenza H5N1 in Thailand

Mathilde Paul[1], Sirichai Wongnarkpet[2], Chaithep Poolkhet[2], Aurelie Binot[3], Francois Roger[3], **Christian Ducrot**[4], [1]Ecole Nationale Veterinaire de Toulouse, Toulouse, France; [2]Faculty of Veterinary Medicine - Kasetsart University, Bangkok, Thailand; [3]CIRAD, Montpellier, France; [4]INRA, Saint Genes Champanelle, France. Contact: ducrot@clermont.inra.fr

To identify risk factors, epidemiology requires variables that are accessible and consistently measured. This may reduce the choice and conduce to use proxy, making results interpretation difficult due to potential hidden confounders. We hypothesize that social sciences would contribute to improve the relevance of epidemiological results.

Following the Highly Pathogenic Avian Influenza (HPAI) H5N1 epidemics in Thailand in 2004-2005, we implemented epidemiological studies to analyze H5N1 maintenance in backyard poultry. A spatial analysis was conducted at the country level and a case-control study in one province. Results pointed out a higher risk of HPAI spread in the surrounding of major cities, as well as trade-related risk factors. These results called for a better understanding of the processes involved in the field.

In order to investigate further these outputs, we implemented a qualitative sociological study in the province of Phitsanulok. Using a value chain analysis, we characterized everyone involved in the local poultry business, from farmers to market retailers, analyzed how these actors were organized and their strategies when facing HPAI.

These results were of great interest for the local veterinary services, as they deciphered the organization of an economic activity involved in HPAI H5N1 spread, but which was not reached by prevention and control measures. Indeed, we found that traditional poultry marketing chains are organized through informal relations. Traders do not have a clearly identifiable workplace, and are unknown from the authorities. Moreover, we found that the trade of sick chickens, a risky practice regarding HPAI, was justified by local actors by its low zoonotic risk and the need to limit financial losses.

This qualitative approach allowed investigating the practices, reasons, and beliefs which were behind the risk factors quantified in epidemiological studies. More generally, we can hypothesize that the complementarity between epidemiology and social sciences could be extended to various situations. In other circumstances, sociology might also be used at a first stage, to better select the variables or proxies of interest.

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Simulating the spread and control of highly pathogenic avian influenza among commercial poultry: Analysis of intervention options for business continuity planning

Sasidhar Malladi[1], Kelly A. Patyk[2], **Timothy Boyer**[3], Todd Weaver[4], Jada Thompson[5], [1]University of Minnesota, St.Paul, MN, [2]United States Department of Agriculture, Animal and Plant Health Inspection Service, Veterinary Services, Fort Collins, CO, [3]University of Minnesota, St.Paul, MN, [4]United States Department of Agriculture, Animal and Plant Health Inspection Service, Veterinary Services, Fort Collins, CO, [5]Colorado State University, Fort Collins, CO, Contact: boye0087@umn.edu

Control measures intended to reduce the spread of highly pathogenic avian influenza (HPAI) have the potential to disrupt continuity of business in the commercial poultry industry. Government-academic-industry leaders in the United States developed an approach to facilitate the managed movement of egg-industry products from monitored flocks located within a HPAI Control Area to minimize such disruptions. The objective of this study was to evaluate the potential impact of proposed disease control and business continuity measures on reducing disease spread during a simulated HPAI outbreak. A spatially explicit, stochastic simulation model was used to simulate HPAI spread between commercial operations in the upper Midwestern United States. Model parameters were established through consultation with subject matter experts and a review of the scientific literature. The baseline scenario represented a stop movement order for poultry products from premises within the Control Area in addition to other outbreak control measures as described in disease response plans. Alternative scenarios reflected incorporation of business continuity measures to facilitate movement of product, with particular emphasis on movement of nest run shell eggs. Simulation results demonstrating the impact of interventions over time such as a shorter time to detection due to active surveillance testing in comparison with baseline enhanced passive surveillance through detection of elevated mortality are presented. The impact of pre-movement active surveillance on the prevalence of infected birds prior to detection resulting in a lower likelihood of moving virus positive nest-run eggs is discussed. Results demonstrate the potential impact of product-specific control measures on regional epidemiological outcomes and provide inputs needed for economic consequence assessment and weighted cost benefit analysis.

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Modelling the transmission tree of the highly pathogenic avian influenza H5N1 epidemic in Israel, 2015

Timothée Vergne[1], Guillaume Fournié[1], Michal Perry Markovitch[2], Ram Katz[2], Avishai Lublin[3], Shimon Perk[2], Dirk U. Pfeiffer[1], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]Israel Veterinary Services, Jerusalem, Israel; [3]Kimron Veterinary Institute, Kimron, Israel. Contact: tvergne@rvc.ac.uk

Purpose: On the 14th January 2015, unexpectedly high mortality was observed in a turkey farm in Israel. Two days later, the presence of highly pathogenic avian influenza H5N1 virus was confirmed. Within the next four weeks, the virus was isolated in seven other farms. The objective of this study was to unravel the transmission tree using transmission tree modelling and to estimate relevant transmission parameters.

Methods: Except for the index case that has been infected by an unknown source, all subsequent cases were assumed to have been infected by farms in Israel in which H5N1 was isolated since January 2015. To reconstruct the transmission tree, it was assumed that the likelihood that farm A infected farm B increased if A was still infectious when B became infected, if A and B were located close to each other, if A and B had the same owner and if there was no other infectious farms that could have infected B. The likelihood of a transmission tree could be calculated for any set of model parameters by multiplying together the likelihood of the most likely transmission events for each infected farms. The effective reproduction number could also be estimated for each farm by summing the probabilities of all transmission events coming from that farm.

Results: Results indicate that farm infectiousness dropped by 55% every day after the start of the culling. In addition, the average infection pressure exerted by an infectious farm to a susceptible farm at 1 km was 2 times, 3.3 times and 5 times higher than that exerted at 10, 20 and 30 km, respectively. Results also showed that farms 2, 4, 5 and 8 had more than 60% chance to have been infected by farms 1, 3, 4 and 7, respectively. However, it was not possible to determine with at least 50% certainty whether farm 6 was infected by farm 4 or 5 and farm 7 by farm 4, 5 or 6. The effective reproduction numbers were highly variable from 0.41 (95% CI: 0.35-0.47) for farm 6 to 1.85 (95% CI: 1.47-2.24) for farm 1.

Conclusion: This study showed that transmission tree modelling can provide important insights regarding transmission events without being overly computing intensive.

Relevance: We believe that the technique should become a component of outbreak investigations.

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Risk-based decision making tools for HPAI H5N1 in domestic poultry in Asia: a comparison of spatial-modelling methods

Kim B. Stevens, Dirk U. Pfeiffer, Royal Veterinary College, London, United Kingdom. Contact: kstevens@rvc.ac.uk

Risk maps are one of several resources for informing surveillance and control systems but commonly used statistical modelling methods (e.g. generalized linear mixed models) typically require availability of both disease presence and absence data. Surveillance data usually only includes disease presence data, and therefore requires makes assumptions about disease absence. Furthermore, variation in risk of potential occurrence cannot be modelled if a country has never experienced the disease before. For such situations there are now modelling methods suitable for disease-presence only data, or knowledge-driven modelling methods if no disease has occurred yet. The objective of the current study was to predict the spatial variation in risk of highly pathogenic avian influenza (H5N1) in domestic poultry in Asia using different modelling methods, each having different data requirements: boosted regression trees (BRT; presence-absence), maximum entropy (Maxent; presence-only) and multicriteria decision analysis (MCDA; knowledge-driven).

All models identified known H5N1 hotspots as high-risk areas and predictive accuracy of the three approaches varied from excellent (AUC BRT: 0.95) through good (AUC Maxent: 0.80) to fair (AUC MCDA: 0.74). Both the Maxent and BRT models showed two variables together accounted for roughly 75% of the variation in HPAI H5N1 distribution - duck density and proximity to rice.

In conclusion, all three methods modelled the continental-level risk of potential HPAIV H5N1 occurrence in domestic poultry in Asia, in particular the location of hotspots, with a reasonable degree of predictive accuracy. In addition, identifying the main factors influencing risk of H5N1 occurrence together with the range of values over which each variable's effect was most important, the Maxent and BRT models, provide information that could be used to design surveillance strategies targeting regions with these characteristics. The methods also allow identification of areas where there may have been underreporting, or which are at high risk for introduction. The uncertainty associated with the predicted risk needs to be communicated and will guide further research.

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Avian influenza risk to Australian poultry industry from free range farm practices

Mini Singh[1], I. Ruhnke[2], C. De Koning[3], K. Drake[4], G. Hinch[3], A. Skerman[5], A. Scott[1], M. Hernández-Jover[6], P. Groves[1], **Jenny-Ann L. M. L. Toribio**[1], [1]University of Sydney, Camden, Australia; [2]Poultry CRC, University of New England, Armidale, Australia; [3]University of New England, Armidale, Australia; [4]University of Adelaide, Roseworthy, Australia; [5]Department of Agriculture, Fisheries and Forestry, Toowoomba, Australia; [6]Charles Stuart University, Wagga Wagga, Australia. Contact: jenny-ann.toribio@sydney.edu.au

Purpose: The 7 highly pathogenic AI outbreaks in Australia since 1976 all involved non-exotic H7 and caused clinical disease on commercial poultry farms. The two most recent outbreaks in 2012-2013 involved a farm with all/ some of the layer flock under free-range management. Industry concern about the AI risk posed by free-range farms arises from some practices on these farms (eg access to range) and evidence from wild bird surveillance of low pathogenic AI virus (including H5 and H7) present in 25 species of Australian birds, mostly native duck and coot species. However there are limited data to inform the actual risk for AI virus introduction posed by free-range management under Australian conditions.

Method & Results: To start investigating management practices on free-range farms, an online survey was conducted in 2014, advertised via flyers, newsletters and on-line platforms. Responses were received from free range layer farms (LF: n=41: average 9500 hens), and broiler farms (BF: n=28: average 20,000 broilers). Among these, birds had more than six hours of range access on 97.5% of LF and 81.5% BF. Area of range used by birds was found to be significantly different between LF and BF ($p<0.0001$) with 4.9, 17.1 and 78% of LF and 11.1, 59.3 and 29.7% of BF respondents reporting <10, 10-50 and >50% usage respectively. Percentage of flock reported to go out on to the range also varied significantly between LF and BF ($p<0.0001$) with 2.4, 14.8, and 82.9% of LF and 7.4, 66.6, and 25.9% of BF respondents reporting <10, 10-50, and > 50% flock on range. For standard biosecurity measures, LF had lower levels of execution with nine of ten actions implemented by <50% of LF while BF reported higher execution with >80% for seven of the ten actions.

Conclusion & relevance: These findings provide evidence that wild bird contact may occur in free range systems. Further information on wild bird presence and farm structure and management practices is needed to quantify the probability of AI virus entry and establishment on free range farms and to evaluate alternate risk mitigation actions. This paper will present the 2014 survey and outline further research planned to inform **biosecurity guidelines for free-range farms in Australia.**

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Modelling the intangible and economic impacts of emergency animal diseases: the example of PRRS in Australia

Sarah-Jane Wilson[1], Michael Ward[2], [1]Livestock Biosecurity Network, Brisbane, Australia; [2]University of Sydney, Camden, Australia. Contact: sj.wilson.vet@gmail.com

Purpose:
Traditional economic assessment methods for emergency animal disease (EAD) impact can estimate costs and losses to an industry. Missing from this approach is intangible impacts, often overlooked due to their subjective nature and the challenges in their identification and measurement.
Methods:
In this study, intangible impacts on the Australian pork industry are identified and a novel method for estimating the overall impact of a designated EAD (Porcine Reproductive and Respiratory Syndrome, PRRS) is implemented.
We modelled two proposed control strategies for PRRS to elicit both the economic and intangible impacts of a theoretical outbreak. These strategies are based on the current policy options indicated for an outbreak of PRRS in Australia (the Australian Veterinary Response Plan, AUSVETPLAN).
Results:
Cost-benefit analyses of the proposed control strategies, indicate that a modified stamping-out process using salvage and slaughter is the most economic strategy with a benefit-cost ratio (BCR) of 0.65 (compared to a full stamping out strategy with a BCR of 0.31). However this carries with it a greater potential risk for the spread of the disease compared to stamping out. When the intangible impacts are also analyzed in an integrated value analysis, the difference between the value benefits of a modified stamping out approach are greatly reduced (averaged stakeholder integrated value ratio (IVR) of 0.33) when compared to the stamping out strategy (averaged stakeholder IVR of 0.21).
Conclusions:
Intangible impacts have the capacity to add or detract value to an economic analysis of EADs, although they are often neglected as a suitable measurement methodology for their inclusion is lacking. This novel methodology supports the inclusion of intangible measurements in value analysis.
Relevance:
Based on these findings, the decision as to which control option is implemented might be influenced and supported by a more encompassing approach. This methodology has evolved to ensure both economic and intangible impacts are discovered and assessed to support decision making.

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Optimisation of emergency vaccination for a foot-and-mouth disease outbreak

Masako Wada[1], Tim Carpenter[1], Naomi Cogger[1], Mark Stevenson[2], [1]Massey University, Palmerston North, New Zealand; [2]The University of Melbourne, Melbourne, Australia. Contact: M.Wada@massey.ac.nz

Purpose:
Over the last decade, there have been positive changes in the international attitudes towards the use of emergency vaccination for the control of a foot-and-mouth disease (FMD) outbreak in formerly FMD-free countries. In a situation where emergency vaccination is presumed necessary, decision makers need to find an optimal way to apply vaccination. The purpose of this study was to compare the accuracy and efficiency of two methods to determine the optimal strategy for application of emergency vaccination for an FMD epidemic.

Methods:
A 2-dimensional optimisation problem was formulated, where decision variables were the radius of vaccination and subsequent processing of vaccinated animals, and the objective function to be minimised was the total cost of an epidemic, which were simulated using a pre-developed stochastic state-transition model for FMD. Response surface methodology (RSM) and a simulation-based method (NOMAD) were compared with the traditional exhaustive simulation approach.

Results:
Both methods (RSM and NOMAD) produced solutions that could save more than 90% of the maximum avoidable cost (USD 4.0 billion), with less than 20% of the computational power (i.e., reduced smoothness and/or reduced number of evaluations) of the exhaustive epidemic simulation approaches.

Conclusions:
Both RSM and NOMAD were useful in producing satisfactory solutions without requiring expensive disease simulation runs.

Relevance:
The two methods assessed here (RMS and NOMAD) can be used for other optimisation problems in the field of veterinary epidemiology. There is potentially a benefit in running both methods in parallel; RSM can be used to inform decision makers about the structure of the true response of the system, while NOMAD can be used to find the exact optimum point, both without time-expensive simulation runs.

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Preventing foot and mouth disease - how are the costs divided between the public authorities and the pig and cattle industries in Denmark?

Tove Christensen[1], Sigrid Denver[1], Lis Alban[2], Anette Boklund[3], Hans Houe[4], Jens L. Hougaard[1], **Sten Mortensen**[5], Susanne D. Rasmussen[5], Erik Rattenborg[2], Trine V. Tamstorf[2], Nils Toft[3], Henrik Zobbe[1], [1]University of Copenhagen, Copenhagen, Denmark; [2]Danish Agriculture & Food Council, Copenhagen, Denmark; [3]Technical University of Denmark, Copenhagen, Denmark; [4]University of Copenhagen, Copenhagen, Denmark; [5]Danish Veterinary and Food Administration, Copenhagen, Denmark. Contact: stm@fvst.dk

Purpose
Remaining free from foot and mouth disease (FMD) is of key importance to the Danish livestock sector. Control and eradication strategies are in place, but what are the costs of prevention? This question has never been answered in detail.
The objective was to describe all activities related to prevention of FMD and to assess the costs of these activities for the cattle and pig sector. Costs of prevention were estimated at activity level for the involved sectors and veterinary authorities.
Results
Mapping of preventive measures or activities and associated costs was mainly based on expert opinions, either as interviews or group discussions due to lack of hard data. It was a particular challenge to determine the FMD share of the individual activities as many activities have a preventive effect on several diseases simultaneously. For the pig sector, joint costs of FMD and classical swine fever were estimated
Conclusion
In Denmark, 0.5 million cattle and 18.5 million pigs were slaughtered and 9 million pigs were exported in 2013. Denmark spent just over €30 million on preventing FMD - shared between veterinary authorities (12 %), the pig sector (61 %) and the cattle sector (27 %). The most expensive activities in decreasing order were: 1) cleaning and disinfection of trucks after transport of live animals - for the pig sector, this activity accounted for 40 % of total costs; 2) establishing and continuously cleaning of farm facilities after delivery of live animals; 3) publicly funded FMD certified laboratory; 4) clinical FMD related surveillance during veterinarians' farm visits. Low costs were found of testing of suspicious clinical symptoms and of border controls of private imports of meat. Some activities had large, fixed costs while others were proportional to farm size.
Relevance
The study demonstrates that it is possible to assess costs of FMD prevention in detail when industry, researchers and public authorities collaborate. Next step will be to identify a more cost-effective combination of risk-mitigating measures. This exercise is relevant for any country, in order to achieve and maintain a cost effective prevention program.

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Will farmers adopt of a new diagnostic blood test for sheep scab: a game theoretic approach

Louise Matthews[1], Rodney Beard[1], Richard Reeve[1], Alistair Nisbet[2], Ruth Zadoks[1], Matt J. Denwood[3], [1]University of Glasgow, Glasgow, United Kingdom; [2]Moredun Research Institute, Edinburgh, United Kingdom; [3]University of Copenhagen, Copenhagen, United Kingdom. Contact: louise.matthews@glasgow.ac.uk

Background

Sheep scab is a highly contagious disease caused by infestation with the mite Psoroptes ovis. It causes severe irritation, resulting in rubbing and scratching, raw skin, wool loss and reduced growth. Since deregulation of dipping treatments in 1992, the annual incidence of sheep scab in the UK has risen from a handful farms to over 7000 annually. It is now a serious financial and welfare issue for UK sheep sector.

Purpose

An ELISA test to diagnose subclinically infection (Burgess et al 2012) will soon be commercially available. Our objective is to examine the likely extent of uptake by farmers and the impact on sheep scab incidence.

Methods

We take an innovative game theory based approach that allows us to examine how farmer decisions depend on cost of the test, the epidemiology of the disease and strategic interactions between farmers. For example, a farmer may be less likely to adopt the test if his neighbour has done so, thereby reducing the risk of spread of infection onto his farm. Such interactions can result in suboptimal uptake at the population level.

Conclusions and Relevance

Our results show that under the proposed pricing levels for the test, farmers are likely to adopt the test if they or their neighbour experienced clinical infection in the previous year; occasional adoption is likely if either they or the neighbour experienced subclinical infection in the previous year, but is very unlikely if neither farmer experienced infection last year. We show also that the farmers' decisions are not always the optimal decision for the whole population but that the discrepancy in reduction of sheep scab incidence is relatively small. We show that under the proposed pricing levels and the resulting predicted uptake by farmers, the new diagnostic test should produce an over 50% reduction in sheep scab incidence. The new test could therefore play an important role in sheep scab control.

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Cost-effectiveness analysis framework for Animal African Trypanosomosis: Cameroon case study

Hannah R. Holt[1], Albane Fauron[1], Farikou Omarou[2], Anne Meyer[1], William Gilbert[1], Javier Guitian[1], [1]The Royal Veterinary College, Hatfield, United Kingdom; [2]Mission Spéciale d'Eradication des Glossines, Ngaoundéré, Cameroon. Contact: hholt@rvc.ac.uk

Purpose:
Faro et Deo District is part of the most important cattle-rearing region of Cameroon, however, more than 90% of the cattle are at risk of Animal African Trypanosomiasis (AAT). Despite a long history of attempts to control AAT, estimated prevalence remains around 40%. There is funding available for control, however there is little information to inform decisions regarding resource allocation. This study aimed to estimate the impact of AAT on livestock productivity and its associated costs in this region.
Methods:
Parameters were defined from field data, literature review and expert opinion of tsetse control officers in the region. It was assumed 40% of the herd acquire AAT once over the course of a year. Three outcomes were then possible: cattle successfully treated with trypanocides recovering within 2 weeks (50%), cattle experiencing treatment failure which deteriorate for 12 weeks; then either recover (35%) or die (15%).
Production losses were estimated from breed-specific values of baseline productivity adjusted according to the expected percentage decrease due to AAT. Direct losses due to mortality and expenditure on trypanocides were added and scaled up to calculate total monetary losses at District-level.
Results:
Overall, losses for the Faro et Deo region were estimated as 118 tonnes of milk, 681 lactations, 37 tonnes of meat and 217 269 hours of draft power. Mortalities were estimated as 2248, 832, 832 and 1526 for cows, bulls, oxen and calves, respectively. Further it was estimated that 59 198 doses of trypanocides are given per year. The financial value of the impact of AAT on the district of Faro et Deo was estimated at $2.1 mil per year.
Conclusions:
Mortalities were by far the biggest contributor to the total cost but losses caused by morbidity were still significant. Draft power lost was responsible for most revenue foregone highlighting the importance of indirect effects of AAT on crop production.
Relevance:
The model is now being developed further to assess likely impact of different control options in the area. It is also being adapted to other settings and is a tool with potential application in tsetse control planning.

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Liver fluke - Fasciola hepatica: comparative losses in key sectors of the British cattle industry.

Sue C. Tongue[1], Carla Correia-Gomes[1], Jude I. Eze[1], Madeleine K. Henry[1], Alistair W. Stott[2], Cath E. Milne[2], [1]SRUC, Inverness, United Kingdom; [2]SRUC, Edinburgh, United Kingdom. Contact: sue.tongue@sruc.ac.uk

Liver fluke is a common, ubiquitous parasite that affects the health and welfare of cattle worldwide. The costs incurred, via production losses and liver condemnations, and their effects on the economics of the British cattle industry are not entirely clear. In order to effect change and reduce reliance on drugs, we must demonstrate that any improved means to control the disease and reduce infection, cost less than the benefits accrued from their application. Our aim was to develop bio-economic models that provide quantitative estimates of the losses incurred in alternative production systems, as a first step in this process.

Herd-level stochastic models for growing animal, beef suckler herd and dairy enterprises were developed. These can each be modified to simulate the major management systems used. Variables were parameterised with estimates derived from: literature, publically available data, industry and expert opinion, and implemented using @Risk. Linked to partial-budget models, they have been run for fluke vs. no fluke.

Spring/summer calving suckler herds have higher losses per infected cow than those calving in autumn/winter. In the growing animal model, loss per infected fattening animal is similar regardless of calf source and growing period. Higher losses are experienced for growing heifers originating from suckler herds than from dairy herds. Dairy herd losses are the highest, with the loss per infected cow increasing with increased average milk yield (£162-224). The main drivers were: (all models) prevalence and additional costs of treating infected animals; reduction in milk yield (dairy model).

We concluded that, at herd-level, liver fluke has a significant financial effect and we need better estimates of the effect that control methods have on the prevalence of infected animals.

Outputs from these models will be aggregated to estimate national/regional net benefits of improved control of fluke of use for policy decision support. In later stages of the work, the suite of models will also provide a means to rank (by cost-benefit) potential control measures based on improved management practices.

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Economic evaluation of animal health surveillance - moving from infancy to adolescence?

Barbara Häsler[1], Keith Howe[2], Marie-Isabelle Peyre[3], Timothee Vergne[2], Clémentine Calba[3], Betty Bisdorff[2], Arianna Comin[4], Ann Lindberg[4], Adam Brouwer[5], Lucy Snow[5], Katja Schulz[6], Christoph Staubach[6], Marta Martínez Avilés[7], Daniel Traon[8], Linda Hoinville[2], Katharina Stärk[9], Dirk Pfeiffer[2], Jonathan Rushton[1], [1]Royal Veterinary College and Leverhulme Centre for Integrative Research on Agriculture and Health, Hatfield, United Kingdom; [2]Royal Veterinary College, Hatfield, United Kingdom; [3]CIRAD, Montpellier, France; [4]Swedish National Veterinary Institute, Uppsala, Sweden; [5]Animal and Plant Health Agency, Addlestone, United Kingdom; [6]Friedrich-Loeffler-Institut, Greifswald – Island Riems, Germany; [7]Universidad Complutense de Madrid, Madrid, Spain; [8]Arcadia International, Brussels, Belgium; [9]SAFOSO AG, Bern-Liebefeld, Switzerland. Contact: bhaesler@rvc.ac.uk

Purpose
Population growth, changes in food systems, urbanisation, and climate change linked in a web of global trade throw up new challenges for disease control. Animal health surveillance is widely recognized as an effective tool for disease management, but investment is often low and poorly targeted. For European decision-makers, economic criteria are important in decision-making for surveillance. Yet, economic evaluations of surveillance (EES) are sparse and available guidelines for the evaluation of surveillance fail to provide guidance on systematic economic appraisal.
Methods
The RISKSUR consortium (www.fp7-risksur.eu) that investigates novel approaches for cost-effective surveillance has developed a web-based surveillance design and evaluation tool directed at users with advanced surveillance knowledge and skills. A key innovative feature is the provision of user-friendly and practical guidance for the design and implementation of EES. Economic theory underpinning EES is explained and challenges that accrue from application of differing paradigms highlighted. In particular, the three-variable relationship between surveillance, intervention and loss avoidance; value of information, and non-monetary benefits are elaborated and linked to economic analysis methods commonly used in animal health.
Results
The application of the tool for EES for classical and African swine fever, bovine viral diarrhoea, avian influenza, and Salmonella Dublin infection in five European countries showed that cost-benefit, cost-effectiveness, and least-cost analyses were the methods of choice. Difficulties encountered include estimation of fixed and variable costs, non-monetary benefits, co-benefits resulting from using synergies, and the selection of meaningful effectiveness measures. Selected results will be presented.
Conclusions and relevance
The tool promotes understanding of critical concepts, suitable methods, data and time requirements and is expected to nurture the use of EES, which is still in its infancy. In the long term, this will increase professional capacity and help to address the problem of resource allocation for surveillance to the benefit of all.

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Economic Assessment of a Progressive Control Strategy for Bovine Brucellosis in Central America

João S. Afonso[1], Alejandro Acosta[2], Gilberto Real[3], Ronald Bernal[4], **Jonathan Rushton**[5], Hernán Rojas[6], [1]Independent, Coimbra, Portugal; [2]FAO, Rome, Italy; [3]FAO, Panama City, Panama; [4]OIRSA, San Salvador, El Salvador; [5]Royal Veterinary College, London, United Kingdom; [6]Ceres BCA, Santiago, Chile. Contact: jrushton@rvc.ac.uk

Purpose:
In Central America the livestock gross domestic product, comprising the areas of meat and milk, represents about 20% of agricultural GDP. Bovine Brucellosis is a bacterial disease that affects cattle in every country in Central America at different prevalence rates. All the countries rely on national programs, funded by public resources, to control for the disease. However none has achieved the eradication from its territory since the time of their implementation
In 2014 FAO and OIRSA carried out a project in the Central America targeting Costa Rica, El Salvador, Guatemala, Honduras, Nicaragua and Panama. The project aimed to propose a new progressive and risk-based control and eradication strategy, and to assess whether a change in the current strategy would be beneficial, from an economic perspective
Methods:
Using a benefit-cost approach, a deterministic econometric model was developed to evaluate the costs of the new strategy, the saving with discontinuation of the current strategy and production gains due to the change, over a period of 10 years, both at national and regional level. To evaluate the impact in production a deterministic population dynamic model was also created, taking into account the current prevalence of the disease and how it would evolve with the different strategies
Results:
The results indicate that the total discounted costs of the new progressive control strategy proposed would be 195 million USD. The net present value (NPV) at the end of 10 years for the region is of 139 million USD, with a cost benefit (RCB) ratio of 1.71 USD. At the end of 10 years the NPV per head of cattle in the region was estimated at 9.37 USD. The study also projected that the animal health programs would have to be adapted and coordinated at regional level so that the control and eradication can be achieved progressively
Conclusions:
The results show that the Central American region would benefit from a change in the current control and eradication strategy. The study recommends more comprehensive epidemiological studies at the country level, and advocates the need for a more complex economic analysis
Relevance:
Progressive eradication of a zoonosis, technically and economically feasible

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Value of Biosecurity on United States Cow-Calf Operations

Kamina K. Johnson[1], **Dustin Pendell**[2], Christine Kopral[1], [1]USDA-APHIS, Fort Collins, CO, [2]Colorado State University, Fort Collins, CO, Contact: dpendell@ksu.edu

Purpose

Estimating the value of biosecurity communicates the potential benefits and incentives for producers to invest in best management practices that promote livestock health and protect animals from disease. The balance between investing in biosecurity to reduce risks of disease and the costs associated with implementing new biosecurity practices on an operation are considered by every livestock producer. The objective of this research is to evaluate the association between biosecurity practices and economic well-being of U.S. cow-calf operations.

Methods

Analyses will use data from the USDA Economic Research Service's Agricultural Resource Management Survey (ARMS) and USDA Animal and Plant Health Inspection Service's National Animal Health Monitoring System (NAHMS). Methodology will begin with principal component analysis and cluster analysis using the NAHMS data to develop cow-calf producer profiles that describe producers groups that make similar biosecurity implementation decisions (Johnson, Engle, Wagner, 2014). Biosecurity practices include vaccination strategies, isolation for new livestock entering the operation, fence-line contact with other species, etc. Using variables in both datasets the producer profiles will be applied to the ARMS data. Next, detailed operation/operator characteristics, financial well-being, and economic performance of each producer cluster will be provided.

Results, Conclusions, and Relevance

Preliminary results from the principal component analysis show three factors describing most of the variation in the data and U.S. cow-calf producers are clustering based on the type and intensity of biosecurity practice decisions. Estimates from two datasets are used in a new way to provide complementary information that describes clusters of producers. A complete description of the typical herd characteristics, management practices, and economic performance will provide producers with the possible incentives related to biosecurity investments. Results will provide governments and producers groups information to educate and influence producer decisions related to biosecurity practices that promote livestock health.

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Estimating Economic Impact of Reducing the Prevalence of Swine Dysentery in the United States Swine Herd

Kamina K. Johnson[1], Eric Bush[1], Charles Haley[1], Philip Paarlberg[2], Amy Hagerman[1], [1]USDA-APHIS, Fort Collins, CO, [2]Purdue University, West Lafayette, IN, Contact: Kamina.K.Johnson@aphis.usda.gov

Purpose

The United States swine industry has several endemic diseases with low mortality rates, but wider spread morbidity related production effects, like swine dysentery (SD). Swine dysentery is a severe, infectious disease characterized by mucohemorrhagic diarrhea and marked inflammation limited to the large intestine. The prevalence of swine dysentery has increased since 2000, causing production and economic losses for U.S. hog producers, along with increased veterinary and treatment costs. Previous literature estimated the loss to the swine industry due to SD in 1991 was $115 million (Duhamel, 1994), which is estimated to be $169-$236 million today (IPPA, 2011). The objectives of this study are to 1) estimate the economic impact of reducing swine dysentery in the U.S. swine population and 2) develop an innovative framework for evaluating the reduction of an endemic disease, thus expanding the field.

Methods

This research utilizes an updated version of the quarterly livestock model developed by Paarlberg, et al (2008). The economic model determines changes in prices, quantities, and economic welfare due to changes in domestic demand, export demand, and supply. To simulate the reduction in morbidity and mortality rates for swine dysentery exogenous shocks introduced into the model will adjust the supply of pork and feed use. The balance between price shifts for pork and feed will be explored through swine grower partial budgets.

Results, Conclusions, and Relevance

Preliminary model results show that a decrease SD in the U.S. swine herd results in increased pork production. The increase in pork production causes a decrease in the price paid for pork products and lowered demand for feed, as morbidity rates decrease, causes feed prices to fall. The anticipated results of the partial budget analysis will evaluate minimal changes for producers free of SD. Producers struggling with SD may be able to demonstrate a substantial benefit related to reducing SD in their herds. Countries struggling with diseases that mainly cause morbidity, with a smaller percentage of animals dying due to disease, will benefit from understanding the economic impacts of reducing an endemic disease in their country.

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Dynamic drivers of disease in the Scottish livestock sector: An application of a multi-sector, spatial partial equilibrium model

Luiza Toma[1], Karl M. Rich[2], Paul Bessell[3], Aaron Reeves[4], Iain McKendrick[5], Mark Bronsvoort[3], Lisa Boden[6], Harriet Auty[1], Alistair W. Stott[4], **George J. Gunn**[7], [1]SRUC, Edinburgh, United Kingdom; [2]Lab 863 Ltd., Edgware, United Kingdom; [3]University of Edinburgh, Edinburgh, United Kingdom; [4]SRUC, Edinburgh, United Kingdom; [5]BIOSS, Edinburgh, United Kingdom; [6]University of Glasgow, Glasgow, United Kingdom; [7]SRUC, Inverness, United Kingdom. Contact: George.Gunn@sruc.ac.uk

Purpose

Farm-level decisions to control animal diseases are influenced by a variety of policy, macroeconomic, and environmental phenomena. Changes in these factors can influence the trajectory of animal disease status over time, with subsequent impacts on the evolution of the livestock and feed sectors of the economy.

A qualitative assessment of different drivers of change and horizon scanning identified emerging disease threats in the Scottish cattle and sheep sectors. The drivers in this analysis focused on Scottish legislative changes related to technological uptake and changes to Scotland's international trade policies due to the European Union's Common Agricultural Policy reform. This analysis was informed by focus-group discussions with key informants to identify trajectories of change. Validation of these results with simulation analysis is useful to tease out the specific impacts of such changes.

Methods

We use a multi-sector, spatial partial equilibrium model that was adapted for the Scottish livestock sector to forecast the dynamic sector-level impacts of major drivers of change on the disease status of the Scottish livestock industry. These drivers of change are built into modelling scenarios, which were fine-tuned using results of a recent (2013) representative survey of Scottish livestock farmers analysing farmers' uptake behaviour of animal health technologies and intentions to continue/leave/change size of business during the current CAP reform.

Results

Under the scenario of high technology uptake and partial trade liberalisation, results indicate an increase in Scottish livestock production, an increase in exports and reduced dependence on imports, although this depends on maintaining strong disease control measures. Alternatively, where low technology uptake is combined with full trade liberalisation, results indicate lower domestic production, based on increased competition with cheaper imports and introduction of disease from imports from countries with high prevalence of disease.

Conclusions and relevance

Preliminary results illustrate some of the nuances associated with drivers of structural change informed by multi-sector modelling.

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Towards a regional approach for animal health provision: The economics of the CaribVET network

Damian Tago[1], Renaud Lancelot[2], Thierry Lefrançois[2], Nisa Surujbally[3], Cedric Lazarus[4], Paula Morales[5], Maria T. Frias Lepoureau[6], Sandra Vokaty[7], Jennifer Pradel[1], [1]CIRAD, Petit Bourg, Guadeloupe; [2]CIRAD, Montpellier, France; [3]CARICOM Secretariat, Georgetown, Guyana; [4]FAO, Bridgetown, Barbados; [5]USDA, Santo Domingo, Dominican Republic; [6]CENSA, La Habana, Cuba; [7]PAHO, Port of Spain, Trinidad and Tobago. Contact: damian.tago-pacheco@antilles.inra.fr

Context: The Caribbean Animal Health Network (CaribVET) has a bottom-up technical and scientific model recognized by CARICOM Secretariat and official veterinary services (VS) in the region. It garners the efforts of VS, labs, universities, research institutes, and international organizations for co-planning and optimizing the cost effectiveness of coordinated efforts. It interacts with surveillance and research to assist in decision making and to advise on best management practices to mitigate the impact of animal diseases on livestock production and health, human health and welfare and to provide sustainable livelihood to the rural economies.
Purpose: To show how the coordination of efforts associated with a regional animal health network can lead to more efficient equilibria than an individual approach where countries do not collaborate with one other. Moreover, to identify the sources of benefits and the biggest challenges associated with a regional animal health network.
Methods: Based on the CaribVET objectives and a set of its most relevant activities (prioritization, needs assessment, capacity development and evaluation), we propose an economic model in which VS choose the amount of resources to allocate on their control and surveillance strategies.
Results: The provision of animal health services by a country generates positive externalities that benefit other countries in the region. Such externalities are generally not considered when planning resources allocation to disease surveillance and control, leading to equilibrium with less resource allocated to animal health provision than what is optimally required in the region.
Conclusions: Supranational animal health networks facilitate the flow of relevant information by connecting national VS and other organizations together and propose mechanisms to deal with the under-provision problem taking into account the high disparity among countries in a region.
Relevance: The economic benefit assessment is expected to increase advocacy of the network at the highest government and industry levels in the Caribbean countries. The economic model is generic and methodology can be applied to other contexts and regions.

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Economic perspectives of Precision Dairy Farming: conceptual framework to investigate the value of information and tailored advice on dairy farming

Cristina Rojo Gimeno[1], Karen De Ridder[2], Veerle Fievez[3], Erwin Wauters[1], [1]Institute for Agricultural and Fisheries Research, Merelbeke, Belgium; [2]Ghent University, Melle, Belgium; [3]Laboratory for Animal Nutrition and Animal Product Quality, Melle, Belgium. Contact: cristina.rojogimeno@ilvo.vlaanderen.be

In the last decade there has been a sheer increase in the availability of Precision Dairy Farming (PDF) technologies. However, few economic analyses have estimated the value of the information obtained. We present a conceptual framework to estimate ex-ante the potential value of PDF technologies. The framework examines the relationship between the different factors that play a role on the farmers' decision-making: 1) farmers' prior knowledge about the disease's prevalence, 2) the disease's treatment cost, 3) the disease's economic impact, 4) the farm-level prevalence, 5) the test characteristics of the PDF monitoring tools (sensitivity and specificity), 6) herd size, 7) farmer's decisions rules: action taken by the farmers based on the information provided by the new PDF tool. The conceptual framework allows to distinguish between PDF technologies permitting better decision among existing alternatives, and between PDF technologies allowing a new kind of the decision to be made (i.e. to go from a herd-level to a cow-level decision). Depending on the nature of the technology and on the assumption about human reaction to the PDF technology's output, the framework uses Bayesian information theory or decision tree analysis.

To validate our proposed framework we examined ex-ante the value of information provided by Fat/Protein ratio (FP) and the Milk Fatty Acids profile (MFA) which are used to detect sub-acute ruminal acidosis in dairy cattle (SARA). Data on the costs of SARA and its treatment were gathered from literature and consulted experts.

Our results showed that the cow-level information supplied by the FP and MFA has a positive value in a narrow range, defined by the values of disease cost, treatment cost and prevalence. The value increases with herd size. The specific conceptual framework developed can be used to estimate the value of information provided by other PDF tools. It may also be used to set research priorities by identifying which improvements (e.g., lower treatment costs, better test specificity and sensitivity) have the highest impact on the value of PDF technologies.

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Trade costs and livestock diseases

Umesh Bastola, **Thomas L. Marsh**, Washington State University, Pullman, WA, Contact: tl_marsh@wsu.edu

Purpose:
Trade costs of pests and pathogens have not been demonstrated in a comprehensive analysis. For livestock disease outbreaks, the trade impact stems primarily from trade embargoes imposed by the importing countries on imports based on voluntary OIE guidelines. Utilizing Foot-and-Mouth Disease (FMD) outbreak data from the OIE across a panel of 145 countries, we econometrically estimate the costs of FMD outbreak on the countries' export revenue from livestock products.

Methods:
We estimate i) usual panel data models for both meat and live animal export demand; and ii) spatial panel model, where the regional trade agreements comprise the spatial element. The explanatory variables include export prices, GDP, production to consumption ratio, and different levels of FMD outbreak information. In the estimation, we deal with issues such as endogeneity of the disease outbreak as well as missing price data.

Results:
In general, trade agreements, zoning, GDP, and production/consumption ratio were found to have positive impact on exports while prices to have negative effects. The FMD outbreak was found to have significantly negative impact on the meat and live animal exports. Our estimation results showed that as compared to an FMD-free country, countries that realized FMD outbreak suffered about 65-85 million dollars loss in meat export revenue and about 40 million dollars loss in live animal export revenue.

Conclusions:
The aggregate loss on export revenue for an FMD infected country was about 115 million dollars a year, which is quite substantial. This, while demonstrating the associated economic costs of FMD, also highlights the potential economic benefits of the eradication of the disease.

Relevance:
Introduction of livestock diseases are more likely in the modern trade intensified world, which can lead to large economic and environmental consequences. While literature exists on overall economic impacts of pests and pathogens on trade, those specific to livestock trade are quite scarce. To our knowledge, this is the first study that utilizes the disease outbreak data to quantify trade costs associated with FMD across a wide range of countries.

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Financial cost/benefit when treating subclinical Staphylococcus aureus intramammary infections considering micro-cytological scenarios: a stochastic approach.

Inge-Marié Petzer[1], **Eric M. C. ETTER**[2,3], Edward F. Donkin[4], Joanne Karzis[1], [1]University of Pretoria, Onderstepoort, South Africa; [2]CIRAD, Montpellier, France; [3]University of Pretoria, Onderstepoort, South Africa; [4]University of Pretoria, Pretoria, South Africa. Contact: eric.etter@cirad.fr

Purpose: An innovative method was investigated to aid in the elimination of *Stapylococcus aureus* (*S. aureus*) intramammary infections (IMI) from dairy herds in South Africa. Stochastic models were used to explore cost/benefit of 3 or 8-d treatment of subclinical *S. aureus* IMI in all infected cows and in only those with a somatic cell count (SCC) above 200 000 cells/ml compared to no treatment.
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Methods: The model included direct cost such as additional laboratory fees for performing microbiology and indirect effects of treatment on cure and new infection rate. Herds with low and high transmission rates were incorporated into the simulation. A first model used *S. aureus* prevalence provided by retrospective analysis of micro-cytological results (2008-2012) i.e. 3.93% $[3.88; 3.99]_{90\%}$. A second model explored existing severe situations with a higher prevalence of *S. aureus* in a herd varying from 5 to 25% according to the SCC. To compare the different strategies we used a cost-index resulting for one strategy of the sum of the products of the probability of each possible event by its cost, balanced with the reduction of the IMI. These probabilities and costs were calculated for one animal in a herd over a lactation period of 260 days.
"

Results: In the case of 3.93% prevalence, the best scenario, with a cost index of -644 ZAR $[-875; -382]_{90\%}$, is to treat 8d only animals with higher SCC. In case of no teat dip the 3d treatment scenario is even cheaper than no treatment at all. In the high prevalence model the best scenario, with a cost index of -730 ZAR $[-938; -474]_{90\%}$, is to treat 8d only animals with higher SCC if teat dip is used and with a cost index of -765 ZAR $[-975; -515]_{90\%}$ if teat dip is not used. In this model all treatment scenarios proved cheaper than no treatment.
"

Conclusions: Such models have many practical applications that can help with decision making both producers and veterinarians.
"

Relevance: The level of *S. aureus* IMI that was likely to be missed when using a SCC threshold was based on the retrospective study which indicated that 20.57% and 33.23% of *S. aureus* IMI went undetected at 200 000 cells/ml in quarter and composite cow milk samples respectively.

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The pigs are dead - what happens to the farmer? Socio-economic impacts of African swine fever outbreaks in northern Uganda.

Erika Chenais[1], Sofia Boqvist[2], Susanna Sterberg-Lewerin[3], Ulf Emanuelson[4], Tonny Aliro[5], Charles Masembe[6], Emily Ouma[7], Emily Ouma[7], Karl Ståhl[1], [1]National Veterinary Institute, Uppsala, Sweden; [2]Swedish University of Agricultural sciences, Uppsala, Sweden; [3]Swedish University of Agricultural sciences, Uppsala, Sweden; [4]Swedish University of Agricultural sciences, Uppsala, Sweden; [5]Directorate of Production and Marketing,, Gulu, Uganda; [6]Makerere University, Kampala, Uganda; [7]International Livestock Research Institute, Kampala, Uganda. Contact: erika.chenais@sva.se

Purpose

Uganda is a low-income country with 25% of the population living below the national poverty line, and with poverty more prevalent and pronounced in the rural areas. The country has the largest pig population in east Africa. Most pigs are kept on smallholder family farms. The pig production is hampered by poor husbandry skills, poverty and animal diseases. African swine fever (ASF) is endemic in the domestic pig population.

The objective of this study was to investigate the socio-economic impacts of ASF outbreaks in northern Uganda. In addition the study evaluated the the attitudes towards selected biosecurity interventions.

Methods

In a longitudinal household survey, two hundred, randomly selected, pig-keeping households were interviewed three times with six months interval using structured questionnaires. Econometric models were used to investigate the relationships between ASF outbreaks and socio-economic indicators. The attitude of participants towards certain biosecurity interventions was explored using Likert scale questions evaluated with non-parametric tests.

Results

According to the preliminary results pig-keeping was not primarily an income generating activity. Pigs were generally kept as financial safety nets in a low-input-low-output management system. Despite this, the majority of participants were willing to invest in biosecurity, if given relevant advice. Approximately 15% of the households experienced an ASF outbreaks during the study period. The frequent outbreaks continued to hamper the commercial and poverty reducing potential of pig-keeping in the study area.

Conclusions

In conclusion outbreaks of ASF occur regularly in northern Uganda and affects smallholder farmers socio-economic status negatively. Poverty, human attitudes and behavior affects the spread of ASF in this setting.

Relevance

Animal diseases have negative impacts on markets, poverty and public health. In resource poor settings these impacts often become more severe as the dependence on livestock is higher. To successfully argue for the importance of animal health in poverty reduction, and to prove the benefits of disease control, disease impact quantifications are needed.

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The effect of environmental factors on the geographic distribution of Johne's disease in deer farmed in New Zealand, 2007 - 2014

K. A. Goodwin[1], M. A. Stevenson[2], Solis Norton[1], [1]Johne's Management Limited, Dunedin, New Zealand; [2]The University of Melbourne, Parkville Victoria, Australia. Contact: kgoodwin-ray@johnes.org.nz

Purpose:
Johne's disease (JD) is an enteric wasting disease of ruminants caused by Mycobacterium avium ssp. paratuberculosis. Environmental factors such as solar radiation, temperature and rainfall play an important part in the persistence of the bacteria in the environment and therefore the risk of infection transmission within individual herds or flocks.
The aim of this study was to describe the spatial distribution of JD-lesion positive deer herds in New Zealand for the period 2007 to 2014 and to quantify, using a Poisson point process model, the association between climatic features of the landscape and the spatial distribution of JD-lesion positive herds.
Methods:
The spatial location of New Zealand deer herds were sourced from the national slaughterhouse surveillance database via Johne's Management Limited. Herds were classified as either JD-positive or JD-negative based on identification of JD-suspect lesions during routine carcass inspection. A Poisson point process model was developed wherein the intensity of JD-positive deer herds throughout New Zealand was expressed as a log-linear function of fixed effects (including estimates of mean annual solar radiation, maximum air temperature and rainfall) and a spatial interaction term.
Results:
A total of 1141 of 3001 deer herds that submitted animals for slaughter for human consumption were JD-positive, representing an incidence risk of 38 (95% CI 36 to 40) JD-positive herds per 100 herds at risk for the 7 year study period. The spatial intensity of JD-positive deer herds increased with decreases in mean annual solar radiation and increases in mean annual rainfall.
Conclusions:
Climatic factors influence the spatial distribution of JD-positive deer herds in New Zealand.
Relevance:
Our findings help inform the national control programme for Johne's disease in deer to monitor and assist deer farms in areas we have identified as higher risk. To reduce JD risk in deer herds preference should be given to farm locations that receive relatively high mean annual solar radiation. While rainfall is important for year-round production of pasture consideration should be given to the negative impact of high levels of rainfall on JD risk.

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Spatial clusters and temporal behavior of animal rabies in Chile, period 2003-2013.

Raúl A. Alegría-Morán[1], Daniela Miranda[1], Alonso Parra[2], Lisette Lapierre[1], [1]University of Chile, Santiago, Chile; [2]Ministry of Health, Santiago, Chile. Contact: ralegria@veterinaria.uchile.cl

Purpose:
Rabies is a zoonotic disease of great impact in public health. Chile has the status of country free of human rabies transmitted by dogs, according to the World Health Organization. Less is known about the spatial distribution of the disease at a national level. The aim of this study was to detect spatial clusters and to describe the temporal behavior of animal rabies in Chile, for the period 2003-2013.
Methods:
927 positive cases were recorded during 2003-2013 from the National Program for Prevention and Control of Rabies of the Ministry of Health. A spatial autocorrelation analysis was performed using Moran's I indicator for the detection of spatial clusters, using the Local Indicators of Spatial Association (LISA) statistics, at national and regional level of aggrupation (north, central and south zone), for aggregated data. A descriptive analysis was performed for the temporal behavior, using a temporal series.
Results:
Positivity was reported mainly in the central zone (88.1%). Moran's I value for the national level indicates a low positive spatial autocorrelation, but not significant. The north and south zone give Moran's I values of 0.0517 and -0.0117 respectively, but shows p-values not significant (0.21 and 0.34 respectively). For the central zone the LISA test gives a Moran's I indicator of 0.1537 (p-value = 0.02). The descriptive analysis of the temporal series shows that rabies tend to decrease in fall and winter season with 2.9 cases per month during these seasons, compared to the 13 cases per month during summer.
Conclusions:
There is a significant spatial autocorrelation of animal rabies cases in the central zone of Chile, indicating that towns with similar number of cases tend to be close to each other (high-high, low-low relation). Number of reported cases tend to increase during summer, which is related to the reservoir activities during that season.
Relevance:
The knowledge about animal rabies clusters and seasonality becomes relevant to the design of preventive and control measures and surveillance programs, considering the high impact in Public Health of this disease.

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Evaluating the role of aquaculture support vessels in disease transmission in marine aquaculture in Norway

Saraya Tavornpanich[1], Trude Marie Lyngstad[1], Tadaishi Yatabe-Rodriguez[2], Beatriz Martinez-Lopez[2], [1]Norwegian Veterinary Institute, Oslo, Norway; [2]University of California, Davis, Davis, CA, Contact: saraya.tavornpanich@vetinst.no

Norwegian salmonid farming sites spread over 3000 km from the farthest north to south of the country. In this context, reared salmonids are moved extensively over short or long distances throughout their life cycle from hatchery to slaughtering. However, the complexity of the fish transportation network and its implications on disease spread are not well understood and have not yet been studied in Norwegian salmonid farming industry. In this study, we aim to characterize the movement patterns of aquaculture support vessels (wellboat, service boat, etc) and evaluate their role for disease transmission using network analysis and statistical modeling. First, we reconstructed the exact routes of vessel movement using automatic tracking system for identifying and locating vessels. Second, we used network analysis to characterize movement dynamics and identify sites and support vessels that may play an important role for disease transmission (e.g. potential “superspreaders”). Finally, we used a multilevel logistic model to evaluate the association between dynamics and characteristics of the network and occurrence of pancreas disease on salmonid site. Results shown that directand indirect contacts among the farming sites in Norway are complex and abundant with flows of more than 30,000 vessel movements per month. The topology of the system follows a scale-free graph, with clearly defined communities and a majority of sites having few connections per month (<5) while few sites have large numbers of connections (>300). Several network properties were significant predictors of disease occurrence. We found a high occurrence of loops (origin=destination), a very unique characteristic of this type of network, explained by vessel category, site type and area. Outcomes may be used to design risk-mitigation strategies to better prevent and control diseases in Norwegian aquaculture.

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Modelling the spatial distribution of Culicoides biting midges at the local scale

Georgette Kluiters[1], David Sugden[1], Helene Guis[2], K. Marie McIntyre[1], Karien Labuschagne[3], Matthew Baylis[1], [1]University of Liverpool, Neston, United Kingdom; [2]CIRAD, Montpellier, France; [3]ARC - Onderstepoort Veterinary Institute, Onderstepoort, South Africa. Contact: g.kluiters@liverpool.ac.uk

Purpose: The *Culicoides* midge vectors of bluetongue (BT) are ubiquitous on farms in the UK, but little research has explored their spatial abundance, an important determinant of disease risk. Models to explain and predict variation in their abundance are needed for effective targeting of BT control methods. Although epidemiological models are commonplace at the national scale, no investigations have taken place at a finer spatial scale. Our aim is to identify determinants of midge abundance at a local 1 km scale.
Methods: Midge abundances were estimated using light traps on 35 farms in north Wales. *Culicoides* catches were combined with remotely-sensed ecological correlates, and on-farm host and environmental data, within a general linear model. Drivers of local scale variation were determined at the 1 km resolution.
Results: Local-scale variation in Obsoletus Group abundance exhibited an almost 500-fold difference (74 to 33,720) between farms, but the Obsoletus Group model explained 81% of this variance. The variance explained was consistently high for the Pulicaris Group, *C. pulicaris* and *C. punctatus* (80%, 73%, and 74%), the other possible BTV vector species in the UK. The abundance of all vector species increased with the number of sheep on farms, but this relationship was missing from any of the non-vector models. Performance of the non-vector models was also high (65-87% variance explained), but species differed in their associations with satellite variables.
Conclusions: At a large spatial scale, there is significant variation in *Culicoides* Obsoletus Group abundance, undermining attempts to record their nationwide distribution in larger scale models, which have historically explained the abundance of these vectors poorly. Satellite data can be used to explain a high proportion of this variation and may produce effective predictive models of disease vector abundance.
Relevance: This work highlights how novel local-scale modelling of disease vectors can explain a large degree of spatial variation that national-scale models fail to explain. This should be of note to policy makers when deciding upon guidelines for entomological surveys before, during and after disease outbreaks.

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Health monitoring of dairy cattle health using monthly Dairy Herd Improvement Association data

Jason E. Lombard[1], Robert H. Fourdraine[2], R. C. Kristensen[1], Kevin Kuzdas[2], Charles P. Fossler[1], [1]USDA:APHIS:VS:Center for Epidemiology and Animal Health, Fort Collins, CO, [2]AgSource Cooperative Services, Verona, WI, Contact: jason.e.lombard@aphis.usda.gov

Purpose:
The Dairy Herd Improvement Association (DHIA) has collected production and management information for the US dairy industry since 1905. Currently, there are approximately 18,000 herds and 4.3 million cows enrolled in the program. The primary use of the data has been to provide dairy producers production-related information about their herds. Additionally, the data have been used extensively to focus genetic improvements for the industry. The purpose of this study was to use DHIA data to monitor changes in health-related parameters over time, as aggregated DHIA data had not been used for this purpose to date.

Methods:
The National Animal Health Monitoring System (NAHMS) has evaluated monthly DHIA data since 2012. During the months of Dec 2012 - March of 2013 in Wisconsin, USA, an increase in heifer stillbirths was observed. The percent of stillborn heifers increased 50% from 7% to a high of 11%. A similar increase was also observed in Dec 2013 - March 2014. To evaluate potential factors associated with the observed health related changes, NAHMS accessed monthly mean temperature data from weather stations to model the effect of temperature on reported stillbirths. Proc GLM was used to model stillbirth percentage by month using temperature, month, year, herd size and county location in Wisconsin as predictor variables. P-values<0.05 were considered significant.

Results:
Temperature, month, year and herd size were all significantly associated with stillbirths in the final multivariable model. This information was used to inform producers of the impact of cold weather on newborn calves. Additional health related parameters such as somatic cell counts and death loss will be evaluated.

Conclusions:
DHIA data represents a relatively untapped data source to monitor the health of the US dairy herd. In addition to monthly monitoring of the data, NAHMS leverages DHIA data by combining them with other data to determine if observed changes are due to health problems, weather conditions, changes in market conditions, or other factors.

Relevance:
Dairy health monitoring can be improved by combining currently collected data with data from multiple sources.

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Exploring Herd-Level Management Factors and Culling Rates in Québec Dairy Herds

Denis Haine[1], Hector Delgado[2], Roger Cue[2], Asheber Sewalem[3], Kevin Wade[2], René Lacroix[4], Daniel Lefebvre[4], Julie Arsenault[1], Émile Bouchard[1], Jocelyn Dubuc[1], [1]Université de Montréal, St-Hyacinthe, QC, Canada; [2]McGill University, Ste-Anne-de-Bellevue, QC, Canada; [3]Agriculture and Agri-Food Canada, Guelph, ON, Canada; [4]Valacta, Ste-Anne-de-Bellevue, QC, Canada. Contact: denis.haine@gmail.com

Purpose:
Relationship between longevity and health or reproductive performance at the cow level is well demonstrated in the dairy literature but this association might not hold true at the herd level. Many herd-, farm-, and cow-level components are part of the culling decision. The objectives of this study were to: 1) quantify culling rates of Québec dairy herds; and 2) investigate if Québec dairy farms could be differentiated based on herd-level factors such as management, reproduction, production and health indices, and explore their relationship with herd culling rate.
Methods:
A retrospective study was conducted on data from dairy herds in Québec, Canada, by extracting their health and production data. Data were extracted for all lactations taking place between 2001 and 2011. A total of 432,733 lactations records (from 156,409 cows; 763 herds) were analyzed. Thirty herd-level variables were aggregated for each herd/year of follow-up and their relationship investigated by Multiple Factor Analysis (MFA).
Results:
The overall culling rate was 31.6% with a 95% confidence interval of [31.2, 32.1]. The explained variance for each axis from the MFA was very low (first and second axis: 13.7 and 12.6%, respectively) suggesting that there was no relationship among the groups of variables. Associations were found between culling rates and herd-level variables such as seasonality, proportion of primiparous cows, calving intervals, 21-day pregnancy rates, days to first service, and average age at first calving.
Conclusions:
Pregnancy is a known cow-level protective factor against culling and herd reproductive performances were found in this study to be associated with culling rates. However, these were the only herd-level factors associated with culling while there are many cow-level risk factors.
Relevance:
This stresses the importance of acknowledging the discrepancy between herd- and cow-level associations. Inferences at the group level should not be based on individual-level data.

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Influence of personality on milking hygiene behavior of dairy farmer in Japan

Satoko Kubota, Yasushi Sembokuya, Hiroichi Kono, Toshihisa Kanayama, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan. Contact: skubota@obihiro.ac.jp

Purpose:
Big five theory is one of the personality theories, and the utility of the theory is paid attention by the appearance of the techniques of the factor analysis and structural equation modelling. It can be classified the individual behavior of each economic agent (e.g. food firm, farmer, and consumer) for food safety and investigate the characteristic of its behavior by analyzing the producers and suppliers in food system with the personality psychology theory. The objective of the study was to clarify the relationship between the individual personality, milking hygiene management behavior and productivity.
Methods:
The five-factor model of personality was used to describe human personality. The five factors are openness, conscientiousness, extraversion, agreeableness, and neuroticism. A total of 77 samples were collected from the student of agricultural college (42 samples) and the dairy farmers (35 samples) through an internet survey.
Results:
The results of the correlation analysis revealed that students who scored high on the traits of neuroticism and agreeableness have greater awareness of milk hygiene management. Also, these personalities influenced the estimation of SCC (Somatic Cell Count) of raw milk. On the other hand, the dairy farmer who scored high on the traits of openness has a positive impact on milk hygiene management. Moreover, they have achieved improvements in milk quality.
Conclusions:
It was suggested that the position of the respondent in the farm management was related to judgment of milking hygiene management. From the data of agricultural college, the rate of milking is done by own judgement was low. In other words, students were required to follow the guidance of the manager, and they tend to score high on the neuroticism because of the stress from the manager. The respondents by the internet survey was included a lot of managers, and the rate of milking was done by own judgement was high. Results therefore suggest that they received the information by own intellectual curiosity, and they have risen hygienic consideration.

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Predicting the Future Average Production of a Dairy Cow

Kaare Græsbøll[1], Carsten Kirkeby[1], Søren S. Nielsen[2], Tariq Halasa[1], Nils Toft[1], Lasse E. Christiansen[3], [1]Technical University of Denmark, Frederiksberg C, Denmark; [2]University of Copenhagen, Frederiksberg, Denmark; [3]Technical University of Denmark, Kgs. Lyngby, Denmark. Contact: kagr@dtu.dk

Background:
To sustain optimal milk production and consequently a profitable economy dairy farmers are taking the decision of which cows to cull on a daily basis. Thus it is essential to continuously evaluate the cows within the herd to best predict the future production of a cow.
Purpose:
The aim of this project was to develop a novel method for estimating the average future production of a dairy cow.
Methods:
Using data from 610 Danish farms with Holstein cattle over a period of 23 years, we fitted milk yield in energy corrected milk (ECM) and the total somatic cell count (SCC) farm-wise, correlation of these between lactations and survival curves dependent on reproductive status. This information was combined to a single value that gives the predicted future average production per day per cow.
Results + Conclusions:
We demonstrated that our method was 50% better to predict the future production of dairy cows compared to methods only using current value or short term information. We also demonstrated how lactation and SCC curves differ markedly both in level and shape from farm to farm, which gives farm based curves better predictive power than a single standard curve used on all farms.
Relevance:
A cow that is worth 1,000 Euros and only takes a place in the stable for one year is more valuable than a cow that are worth the same value but over a two-year period. Therefore the estimate of the future value of a cow should use the predicted expected lifetime as denominator.

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Factors impacting dairy cow conception risk in Irish herds

Caroline Fenlon[1], Luke O'Grady[2], Michael Doherty[2], Stephen Butler[3], Laurence Shalloo[3], John Dunnion[1], [1]University College Dublin, Dublin 4, Ireland; [2]University College Dublin, Dublin 4, Ireland; [3]Teagasc, Moorepark, Co. Cork, Ireland. Contact: caroline.fenlon@ucdconnect.ie

Purpose:
Previous research into dairy cow reproduction has studied the impact of various factors on the proportion of animals conceiving to first service or within fixed time periods of breeding (e.g. 21 or 42 days). The objective of this study was to analyse individual breeding attempts, in an effort to model the likelihood of success given temporal, animal and herd-related variables.

Methods:
The analysis was performed on 4,919 service events involving 1,018 cows from the research herds belonging to Teagasc, the Irish agri-food research and development authority, at its Animal and Grassland Research and Innovation Centre, Moorepark, County Cork. All animals were of parity 1 or greater and members of spring-calving pasture-based systems. The outcome of each service was confirmed with calving dates and pregnancy diagnosis scans. Binary logistic regression was carried out to find the impact of a range of variables on the probability of successful insemination. As service events from multiple herds and years were included in the analysis, herd and service year were incorporated as random effects in the model.

Results:
The results of this analysis show that factors concerning age, energy balance, milk production, stage of breeding season, previous fertility and genetics all significantly influence the reproductive performance of Irish dairy cattle.

Conclusions:
The variables considered will be used to inform the construction of a multivariate model of conception risk, for use in the fertility component of an animal-level whole-farm simulation model.

Relevance:
Irish dairy farming is currently undergoing a period of extensive change, with the abolition of European Union milk quotas from March 2015 and the Food Harvest 2020 initiative leading a drive for increased milk production. Reproductive performance is a crucial component of dairy herd management. A comprehensive model of dairy cow fertility would allow thorough simulation for the purpose of analysis and decision support.

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Factors affecting lifetime production of calves by beef suckler cows in Norway

Ingrid H. Holmøy, Sindre T. Nelson, Adam D. Martin, Ane Nødtvedt, Norwegian University of Life Sciences, Oslo, Norway. Contact: ingrid.hunter.holmoy@nmbu.no

Purpose: There is currently a deficit in the national beef production in Norway, and an increased output from beef suckler herds is desirable. The aim of this study was therefore to evaluate factors influencing lifetime production (total number of calves born) by beef suckler cows. Methods: A retrospective cohort study was performed utilizing the Norwegian Beef Cattle Recording System (NBCRS) database, which holds records for more than 82% of the suckler cows (NBCRS Annual Report 2013). Cows slaughtered in 2010, 2011 and 2012 were included in the study population, and their lifetime production data accessed. Cows recorded to be between 1.5 and 3.5 years old at first calving were included. Two multilevel Poisson regression models were built (both with herd and cow as random effects); one for all cows and a second model for multiparous cows only where mean calving-interval of cows was included. Results: The study population consisted of 20,068 cows and their 58,707 offspring. Of these, 18,126 cows fulfilled the inclusion criteria, giving birth to 55,805 calves, incl. 1230 twin and 5 triplet sets. The median lifetime production per cow was 2 (min 1, max 18) calves. The multilevel regression models showed that that lifetime production per cow was higher in the lowlands of Eastern Norway compared to all other regions and that Charolais and Limousin cows produced less calves than Hereford cows: IRR (95% CI) 0.90 (0.86-0.93) and 0.83 (0.79-0.87), respectively. Compared to cows experiencing a normal first calving, moderate or severe dystocia at first calving resulted in lower lifetime production: IRR 0.87 (0.84-0.90) and 0.70 (0.66-0.75), respectively. Twinning and a short mean calving interval both resulted in higher lifetime production; whereas first calving before reached 2.5 years did not when herd and cow random effects were accounted for. Conclusion: The total number of calves born to beef suckler cows registered in the NBCRS was influenced by region, breed, mean calving-interval, twinning and whether calving difficulties were present at first calving. Relevance: There might be potential for improving the output from beef suckler herds through choice of breed and optimization of calving intervals.

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Factors affecting birth weights of beef suckler calves in Norway

Sindre T. Nelson, Adam D. Martin, **Ane Nødtvedt**, Norwegain University of Life Sciences, Oslo, Norway. Contact: ane.nodtvedt@nmbu.no

Purpose: Specialized beef production is an emerging enterprise in Norway, where both milk and meat has traditionally been produced by the dual-purpose Norwegian Red breed. Currently there is a deficit in the national beef production, and an increased output from beef suckler herds is desirable. The aim of the current study was to evaluate factors influencing birthweights in beef suckler calves in Norway. Methods: A retrospective cohort study was performed utilizing the database from the Norwegian Beef Cattle Recording System (NBCRS). Recent estimates show that more than 82% of suckler cows in Norway are enrolled in this voluntary database (NBCRS Annual Report 2013). Cows slaughtered between January 2010 and January 2013 were included in the study population, and their lifetime production data accessed. The analysis was performed on the subset of singleton calvings from which birth-weights were recorded. Two multilevel linear regression models were built; one for all animals (with herd and cow as random effects) which included parity as an explanatory variable, and a second model for heifers only where age of calving was included (and a herd random effect). Results: The study population consisted of 20,068 cows and their 58,707 offspring. Of these, birth-weights were available for 32,165 calves born from 19,157 cows. The average birth-weight was 43.5 kg. The multilevel regression models showed that female calves were 2.3 kg lighter than males ($p<0.001$), that calves born in the western part of Norway were smaller than from all other regions and that calvings in the fall yielded lighter offspring. Furthermore, calves born from heifers were surprisingly heavier than calves from older animals. Breed explained part of the variation in birth-weights, and both the herd and cow random effects were highly significant. Conclusion: Birth-weights of beef calves in the NBCRS were influenced by sex of the calf, breed of the mother, region, season, parity and age at first calving. Relevance: There might be potential for improving the output from beef suckler herds through management factors, such as choice of breed, calving season and age of first calving.

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Associations of farm management practices, including feeding high protein fodder trees, with annual milk sales on smallholder dairy farms in Kenya

Shauna Richards[1], John Vanleeuwen[1], Getrude Shepelo[2], George Karuoya Gitau[2], Collins Kamunde[3], Fabienne Uehlinger[4], Jeff Wichtel[1], [1]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada; [2]Faculty of Veterinary Medicine, University of Nairobi, Nairobi, Kenya; [3]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada; [4]Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, Canada. Contact: srichards@upei.ca

Purpose: Cows on smallholder dairy farms (SDF) in developing countries such as Kenya typically produce volumes of milk that are well below their genetic potential. An epidemiological study was conducted to determine reasons for this low milk production, including limited use of best management practices, such as suboptimal nutritional management.
Methods: An observational cross-sectional study of 111 SDF with a post-partum cow was performed in Nyeri County, Kenya in June of 2013 determining the effect of cow factors, farmer demographics and farm management practices on the kg of milk sold/cow in the last 12 months. In particular, the effect of feeding high protein fodder trees and other nutritional management practices were examined.
Results: Approximately 38% of farmers fed fodder trees, but such feeding was not associated with volume of milk sold per cow, likely due to the low number of fodder trees per farm. In the final multivariable linear regression model, square root transformed kg of milk sold/cow was positively associated with feeding dairy meal during the month prior to calving, feeding purchased hay during the past year, deworming cows every 4 or more months (as opposed to more regularly), and having dairy farming as the main source of family income. Milk sold/cow was negatively associated with a household size of >5 people and feeding Napier grass at >2 meters in height during the dry season. An interaction between gender of the principal farmer and feed shortages was noted; kg of milk sold/cow was lower when female farmers experienced feed shortages whereas milk sold/cow was unaffected when male farmers experienced feed shortages.
Conclusions: Feeding variables (dairy meal to close-up cows, purchased hay and short Napier grass) accounted for a majority of the variation in milk sold/cow, particularly the negative association of feed shortages in female farmers. A dairy focus, small family size and strategic deworming were also model factors.
Relevance: These demographic and management risk factors should be considered by SDF and their advisors when developing strategies to improve income from milk sales and animal-source food availability for the farming families.<br

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An innovative way to evaluate farmers' perception of foot and mouth vaccination in Vietnam

Bao D. Truong[1,2], A. Binot[1], M. Peyre[1], H. N. Nguyen[2], S. Bertagnoli[3,4], F. Goutard[1], [1]CIRAD, AGIRs Unit, Montpellier, France; [2]Nong Lam University, Faculty of Animal Science and Veterinary Medicine, Ho Chi Minh, Viet Nam; [3]Université de Toulouse, INP, ENVT, UMR1225, IHAP, F-31076, Toulouse, France; [4]INRA, UMR1225, IHAP, F-31076, Toulouse, France. Contact: dinh-bao.truong@cirad.fr

Purpose

Since 2006, Vietnam has implemented mass vaccination against foot and mouth disease (FMD) for all cattle and buffaloes within specific targeted areas. However this strategy is still facing many logistical and economic constraints. This study aimed to explore South-Vietnamese farmers' subjectivities regarding FMD vaccination using a reflexive research method called Q methodology. This method allowed us to identify groups of farmers who shared similar viewpoints.

Methods

A structured sample of 46 farmers in Tay Ninh province was chosen. These 46 respondents were distinguished in socio - economic variables such as gender, experience level, education level and production's type. Statements relevant to farmers' attitude and perception toward FMD vaccination have been developed from previous groups and individual interviews, to produce a Q-set of 46 items. They covered 4 themes regarding vaccination: confidence, logistic, cost and impacts. Q method results were analyzed performing principal component analysis (PCA) using R version 3.1.2.

Results

Three factors, representing common perceptions between farmers and accounting together for 57,3 % of the variance were selected. Several consensus points were found across the factors: they feeling more secure after vaccination campaign; they strongly thinking that a good vaccination practice will make their animal have a good protection; they taking vaccination decision themselves without influenced from other actors; vaccination is cheaper than treatment cost; vaccines given by governmental authorities are of good quality. However there were several points of disagreement between factors: for some farmers (factor 3) if the housing and feeding conditions are good, they don't need to vaccinate their animals every year; the preferred type of vaccine (individually or multi dose) will depend between factors.

Conclusions

These outputs provided critical elements on the acceptability of FMD vaccination programs by farmers in Vietnam and allowed some recommendations on how to improve their involvement. Further researches are still required to understand and combine viewpoints of other actors involved in the vaccination campaign.

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Predicted improved control of FMD transmission between farms by using preclinical detection

Noel Nelson[1], David J. Paton[1], Sophia Hogdson[1], **Jose L. Gonzales**[2,3], [1]The Pirbright Institute, Pirbright, Woking, United Kingdom; [2]Central Veterinary Institute, WUR, Lelystad, Netherlands; [3]The Pirbright Institute, Pirbirght, Woking, United Kingdom. Contact: jose.gonzalesrojas@wur.nl

Purpose:
Foot and mouth disease is a viral disease of cloven hoofed animals. Outbreaks of this disease in livestock can lead to large epidemics, therefore control measures, such as detection and removal of infected herds, need to be implemented. It has been suggested that detection of infected cattle before the onset of clinical signs may reduce transmission between animals, however whether this would reduce or block transmission between herds remains to be evaluated. Here we evaluate the potential of preclinical detection during reactive surveillance to reduce the risk of between farm transmission.
Methods:
We used data from transmission experiments in cattle where both individual samples such as blood, probang, saliva or nasal swabs and herd level samples such as air samples were taken daily during the course of infection. The sensitivity Se of each of these sample types for detection (PCR testing) of infected cattle during the incubation period was quantified. Then a mathematical model that used both surveillance (type of sample, sample size and sampling frequency) and transmission parameters was used to evaluate the efficacy of surveillance for early detection of an infected herd and reduction of its infectious output. The latter was expressed as the between herd reproduction ratio Rh and an effective surveillance approach would lead to reduce $Rh < 1$.
Results:
We assumed $Rh = 4$ for an infected herd that escapes detection. If surveillance would be applied weekly, clinical inspection won't be able to block transmission. In contrast random sampling of at least 10 animals/farm would lead to reduce $Rh < 1$. Similar efficacies were quantified for all individual sample types. In case of air sampling a higher sampling frequency than once a week would be required.
Conclusions:
In conclusion, preclinical detection during outbreaks would reduce transmission and help control epidemics.
Relevance:
The model and findings here presented can be used to design reactive surveillance to control epidemics.

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Dynamics of foot-and-mouth disease virus persistence in endemically affected cattle populations - time to redefine the “carrier” state?

Barend M. Bronsvoort[1], Ian G. Handel[1], Viviana Malirat[2], Ingrid Bergmann[2], Vincent Tanya[3], Kenton Morgan[4], [1]University of Edinburgh, Edinburgh, United Kingdom; [2]Instituto de Ciencia y Tecnología Dr. César Milstein, Buenos Aires, Argentina; [3]Cameroon Academy of Science, Yaounde, Cameroon; [4]University of Liverpool, Liverpool, United Kingdom. Contact: mark.bronsvoort@roslin.ed.ac.uk

Purpose:
Foot-mouth-disease (FMD) caused by the FMD virus is the one of the most important livestock disease globally both due to direct losses from production declines, mortality of neonates and welfare but also because of the severe restrictions on trade that disease free countries impose. One of the justifications for imposing such severe restrictions are concerns over individual animals becoming persistently infected which is also called the “carrier state”. The carrier state in foot-and-mouth disease has been a useful construct for experimental studies although they have generally failed to provide evidence of transmission from cattle, but there are very few studies that have attempted to look at the factors associated with persistence in naturally infected endemic populations with multiple serotype exposures.
Methods:
Using historic data from 1,077 animals from an age stratified, clustered random sample of herds in the Adamawa Region of Cameroon in 2000, using a multi-level logistic regression model, we have estimated the association between the age of an animal, the months since the last reported outbreak of FMD in the herd it came from, the number of different previous serotype exposures and the probability of recovering viable virus from a probang sample.
Results:
The proposed model suggests that there is an exponential decline in the probability of recovery of viable virus with both age and months since last outbreak, however, the probability of recovering virus increased with the number of serotype exposures.
Conclusions:
These results suggest a need to redefine the “carrier” state for the natural ecological setting.
Relevance:
This has direct relevance both to researchers planning FMD field studies and state veterinarians planning surveillance activities wanting to target animals to recover virus for typing.

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A case-control study on risk factors of FMD outbreaks in Iran

Saied Bokaie[1], **Kayhan Ilbeigi**[2], Morteza Gorjidooz[2], Mohamad Rashtibaf[3], Fereshteh Ansari[1], [1]University of Tehran, Tehran, Iran, Islamic Republic of; [2]Islamic Azad University of Garmsar, Garmsar, Iran, Islamic Republic of; [3]Iranian Veterinary Organization, Mashhad, Iran, Islamic Republic of. Contact: Keyhan.ilbeigi@gmail.com

Purpose: Foot and mouth disease is an important viral disease of cloven-hoofed animals with high economic importance. Although this disease has been eradicated in some countries, it is still endemic in Iran. Therefore, more attention has been paid by research groups and institutes in order to control it during the recent years. The aim of the study is to evaluate the risk factors of the foot and mouth disease in Iran.

Methods: This study was performed in Khorasan Razavi, a northeastern Province in Iran, based on the collected data in a three-year period (from 2012 to 2014). Data have been collected by the animal diseases departments and veterinarian of the veterinary council of the province. The information of 127 farms, including 46 cases and 81 controls was collected by questionnaire. Farms which were frequently infected by foot and mouth disease during the last 3 years were defined as cases, and farms with no report of the infection were defined as controls. Logistic regression analysis was conducted to evaluate Odds Ratio of assessed items using SPSS software version 16.

Results: Based on results of multi-variable logistic regression, four factors, including the hygienic status of the farm (OR=11.83 CI; 3.375-41.43), Vaccination (OR=0.06 CI; 0.005-0.684), limited transportation of livestock (OR=0.40 CI; 0.163-0.981) and no broker and shepherd commutes in the farm (OR=0.362 CI; 0.12-1.093) were identified as important factors influencing the occurrence of foot and mouth disease.

Conclusions: it could be claimed that improving the hygienic status of the farm, proper vaccination, limiting the transportation of the livestock and inhibition of broker and shepherd commutes can be suggested as effective control efforts against foot and mouth disease in Iran.
Key words: Foot and mouth disease, Risk factors, Case-control study, Endemic regions.

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Economic consequences of Foot-and-Mouth Disease on traditional livestock-dependent communities on northern Tanzania

Umesh Bastola[1], Tiziana Lembo[2], Sarah Cleaveland[2], Miriam Casey[2], Harriet Auty[2], Tito Kibona[3], Deogratius Mshanga[4,5], **Thomas L. Marsh**[1], [1]Washington State University, Pullman, WA, [2]University of Glasgow, Glasgow, United Kingdom; [3]Sokoine University of Agriculture, Morogoro, Tanzania, United Republic of; [4]Ministry of Livestock and Fisheries Development, Arusha, Tanzania, United Republic of; [5]Washington State University, Pullman, WA, Contact: tl_marsh@wsu.edu

Purpose:
While available literature on Foot-and-Mouth Disease (FMD) economic impacts has looked at costs incurred due to outbreaks at an aggregate level, microeconometric studies investigating impacts of such outbreaks on individual livestock-owning households are severely limited. The primary objective of this study was to quantify economic consequences of FMD on traditional livestock production systems in Tanzania (including agro-pastoral and pastoral households, and rural small holders).
Methods:
A household survey was conducted in 78 households of northern Tanzania, where FMD is endemic. Data were collected on household demographics, socio-economics, crop and livestock production, and losses due to livestock diseases with a focus on FMD. Various specifications of milk production, traction, cash income, and human capital development were estimated to examine the effects of FMD on these aspects.
Results:
FMD resulted in about one-third reduction in milk production. Cattle that were treated against secondary infections resulting from FMD yielded 145% more milk as compared to the non-treated cattle. FMD outbreaks led to reduced traction capacity and a decrease in cash generation from livestock sales. We found that each additional liter of milk sold per day would allow households to spend about $17 (31,000 TZS) more in child education. Similarly, households that realized milk losses due to FMD outbreaks spent $63 less in child education compared to those that treated their cattle that spent about $135 more. FMD significantly reduced expenses on human health, which could be due to increased availability of milk for home consumption because of curbed milk sales during outbreaks.
Conclusion:
This study adds to the scanty literature on household-level impacts of FMD in endemic settings, providing evidence that the FMD burden on traditional Tanzanian communities is considerable.
Relevance:
To inform policy towards sustainable interventions it is imperative to better understand disease implications at the local level. Here we demonstrate that FMD prevention in livestock-dependent communities in Tanzania would reduce the FMD burden and increase livestock productivity.

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Use of a next-generation matrix to estimate transmission of FMDV and to evaluate different vaccination strategies in mixed populations

Carla Bravo de Rueda[1], **Phaedra Eblé**[1], Aldo Dekker[1], Mart de Jong[2], [1]Central Veterinary Institute of Wageningen UR (CVI), Lelystad, Netherlands; [2]Wageningen University, Wageningen, Netherlands. Contact: phaedra.eble@wur.nl

For understanding transmission of FMDV under field conditions where different animal species coexist, quantification of the reproduction ratio R for heterogeneous populations is needed. Also the effect of vaccination for heterogeneous population should be quantified. It is e.g. not clear whether emergency vaccination of all susceptible species is necessary to control an epidemic or if targeted vaccination (e.g. only cattle) could be sufficient. We developed a method that allowed quantification of R and the evaluation of different vaccination strategies for mixed populations.

For a mixed cattle-sheep population, we quantified R cattle-to-cattle, R sheep-to-sheep and partial R sheep-to-cattle for non-vaccinated and Rvac cattle-to-cattle and Rvac sheep-to-sheep for vaccinated animals with results from transmission experiments. A 4 by 4 table was constructed using these estimates. By assuming separable mixing i.e. assuming that the (partial) R's are the product of a relative infectivity fi and a relative susceptibility gi (i is either non-vaccinated cattle, vaccinated cattle, non-vaccinated sheep or vaccinated sheep), we calculated the missing values in the table. Subsequently, a next generation matrix was constructed where the elements of the matrix are functions of the relative infectivity, the relative susceptibility, the proportion of cattle in the population and the proportion of vaccinated cattle and sheep. The dominant eigenvalue of the NGM, the R for a mixed population, was determined for populations with different proportions of cattle and sheep. Finally, the effect of 3 different vaccination strategies (vaccination of both cattle and sheep, vaccination of cattle only, vaccination of sheep only) was evaluated.

The higher the proportion of cattle in a non-vaccinated mixed cattle-sheep population, the higher R for the mixed population is. Vaccination of all animals results in an R of 0.1, independent of population composition. Vaccination of cattle only seems to be sufficient to reduce R to < 1in mixed cattle-sheep populations with at least 14% cattle.

The NGM technique can be a valuable tool to determine the impact of control measures for heterogeneous populations.

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Social network analysis of cattle movements in Northern Patagonia A, Argentina: implications for risk-based surveillance

Facundo J. Linares, Virginia Perez, Gustavo Comesaña, Bernardo Cosentino, Rodolfo Bottini, Servicio Nacional de Sanidad y Calidad Agroalimentaria (SENASA), Buenos Aires, Argentina. Contact: flinares@senasa.gov.ar

Purpose:
In September 2013 the National Service for Agrifood Health and Quality (SENASA) requested the World Organization for Animal Health (OIE) the recognition of Northern Patagonia A (PNA) as a new foot and mouth disease (FMD) free zone without vaccination in Argentina. Previous to this presentation we carried out risk based surveillance activities in the zone based on the study of cattle movements.
The objective of this study was to characterize the patterns of cattle movements in the PNA of Argentina using the methodology of social network analysis and geographic information systems to establish risk based surveillance measures in the zone.
Methods:
The network analyzed movements corresponding to the network of movements of 2012, made up of all movements (links) of the PNA from farms or animal market to farm or animal market (nodes) obtained from SENASA. Three types of movements were analyzed, a) the internal movements in PNA, b) movements from the rest of the zone with vaccination to PNA c) from PNA to the rest of the zone with vaccination. The distance of each movement was estimated through the Euclidean distance between the coordinates of each node. Movements were performed using social network analysis and graph theory using R Language v2.10.1 with igraph library and networks were visualized with Arc View 3.2 software (Crime Analysis tool) and ArcGIS version 9.3 (ESRI) using Kernel density method.
Results:
The cattle contact network was composed by 2,116 nodes and 7,033 links for movement a; 236 nodes and 302 links for movement b; 860 nodes and 1,704 links for movement c.
Conclusions:
This is one of the very first studies characterizing cattle movements in PNA.
Relevance:
The characterization of patterns movement of cattle in Argentina provides valuable information for prevention and upgrading surveillance systems (risk-based surveillance) and control of future outbreaks, not only for FMD but for other cattle diseases. Furthermore, these studies will allow us to identify farms with an increased risk of potential spreading in an outbreak of FMD and we will be able to provide valuable information for its control in a future epidemic.

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Cost benefit analyses of foot and mouth disease control options in Ethiopia

Wudu T. Jemberu[1,2], Monique Mourits[1], Henk Hogeveen[1], [1]Wageningen university, Wageningen, Netherlands; [2]University of Gondar, Gondar, Ethiopia. Contact: temesgenha@yahoo.com

Purpose:Foot and mouth disease (FMD) is endemic in Ethiopia. There is, however, limited information on the economic impact of the disease nor on the potential control options to support decision making in the control of the disease. The objectives of this study were to estimate the annual national cost of the disease and conduct cost benefit analyses of FMD control options within the cattle production systems of Ethiopia.
Methods:A stochastic cost benefit model was built and simulated for 10 years based on data collected from literature, secondary sources, field survey and expert opinion. Three control strategies: 1) ring vaccination (vaccination around outbreak area and movement restrictions during an outbreak) 2) strategic vaccination (annual preventive vaccination in selected strategic areas with ring vaccination and movement restrictions during outbreaks in the rest of the country), and 3) preventive mass vaccination (annual preventive vaccination of the national cattle population) were compared with the base line scenario of no official control which was the status quo.
Results:The annual national costs of FMD in the status quo were estimated to be about 1.35 (95%CI = 1.05-1.67) billion Birr (USD 67.5 million). The major costs were related to production losses which account 92% of the total annual cost; the other costs were derived from trade losses and control expenditures. Preliminary results from the ongoing cost benefit analyses of the alternative control strategies indicated that all strategies resulted in positive economic returns. Strategic vaccination had the highest net present value and ring vaccination has the highest cost benefit ratio. Preventive mass vaccination was most efficient in reducing the national incidence, followed by the strategic vaccination.
Conclusions:FMD incurs large economic losses every year in Ethiopia and the proposed control strategies all show positive economic return. The cost benefit analyses results suggest that strategic vaccination could be the best strategy because of its good performance both economically and epidemiologically.
Relevance:The results of this study can be used to support decision making in control of FMD in Ethiopia.

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Evaluating vaccination strategies to control foot-and-mouth disease: a country comparison study

Thomas Rawdon[1], Graeme Garner[2], Mark Stevenson[3], Sharon Roche[2], **Robert Sanson**[4], Charlotte Cook[5], Colin Birch[5], Thomas Smylie[6], Kelly Patyk[7], Neil Harvey[8], Zhidong Yu[1], Kimberley Forde Folle[7], Ruth Moir[5], [1]Ministry of Primary Industries, Wellington, New Zealand; [2]Department of Agriculture, Canberra, Australia; [3]The University of Melbourne, Melbourne, Australia; [4]AsureQuality Limited, Palmerston North, New Zealand; [5]Animal and Plant Health Agency, Weybridge, United Kingdom; [6]Canadian Food Inspection Agency, Montreal, ON, Canada; [7]Animal and Plant Health Inspection Service, Fort Collins, CO, [8]University of Guelph, Guelph, ON, Canada. Contact: robert.sanson@asurequality.com

Vaccination is recognised as an important potential tool to supplement 'stamping out' for controlling severe foot-and-mouth disease (FMD) outbreaks in non-endemic countries. Simulation models offer valuable insights to assist disease managers, and there is a growing interest in using multi-model simulation to improve the robustness of modelling outputs. Our earlier study, which used a UK outbreak scenario, identified consistent relative effects of specific vaccination strategies among different modelling platforms. To extend this work, we assessed the relative effectiveness of vaccination strategies under country-specific conditions, including the geographic distribution of farms, production and marketing systems, and approaches to resourcing, and implementing disease control. Four different modelling platforms were used to study FMD outbreaks in five countries (Australia, New Zealand, United States, United Kingdom and Canada). Disease spread and control parameter settings relevant to each country were used. With the objective of providing a consistent but not identical severe FMD outbreak scenario, each country selected a study area containing high farm densities, and simulated the introduction of Pan Asia type O FMD virus. Models were initially run for an agreed-upon duration of time to represent the 'silent spread' phase and an iteration representing the 90th percentile was chosen to provide a fixed starting point for comparing baseline (without vaccination) and five standardised vaccination strategies. Strategies were selected to explore key areas of interest from a disease response perspective, including: timing of vaccination, species vaccinated (farms with cattle), area vaccinated (high-risk zones) and resources (constrained versus unlimited). Findings highlight the benefit of early vaccination and the negative effect of constrained resources. The presentation will report the top-ranking strategies for each country, explore whether the findings are country-specific or universal, and discuss any differences. This work supports the development of effective disease control policies for FMD and end-user confidence in modelling outputs.

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Can spatial and temporal patterns of serotype-specific foot-and-mouth disease outbreaks in Tanzania be predicted?

Miriam Casey-Bryars[1], Richard Reeve[1], Harriet Auty[1], Pip Hamblin[2], Daniel Haydon[1], Rudovick Kazwala[3], Tito Kibona[3], Donald King[4], Anna Ludi[4], Ahmed Lugelo[3], Valerie Mioulet[4], Deogratius Mshanga[5], Satya Parida[4], Krupali Parekh[4], David Paton[4], Sarah Cleaveland[1], **Tiziana Lembo**[1], [1]University of Glasgow, Glasgow, United Kingdom; [2]Pirbright Institute, Pirbright, United Kingdom; [3]Sokoine University of Agriculture, Morogoro, Tanzania, United Republic of; [4]The Pirbright Institute, Pirbright, United Kingdom; [5]Tanzania Veterinary Laboratory Agency, Ministry of Livestock and Fisheries Development, Arusha, Tanzania, United Republic of. Contact: lembo.tiziana@gmail.com

Our research on endemic foot-and-mouth disease (FMD) in northern Tanzania has shown that it has substantial consequences in traditional livestock-dependent communities, and that infection is driven by livestock-related factors even in proximity to susceptible wildlife. Prevention of infection in livestock would reduce disease impacts in these communities. Yet FMD control in East Africa is constrained by a diverse antigenic and genetic landscape (with serotypes O, A, SAT1, SAT2 and SAT3 circulating) and the lack of effective polyvalent vaccines. For FMD control in these settings, an understanding of virus dynamics over space and time is necessary.
We investigated spatial and temporal patterns of FMD infection in northern Tanzanian cattle over a three-year period (2010 - 2014) combining (1) information on FMD viruses (n = 64 from 33 herds) responsible for outbreaks during the study period; (2) virus neutralisation testing (VNT) data from a subset of herds (n = 128 from 77 herds); and (3) outputs of Bayesian models developed to ascertain retrospectively the serotype of FMD causing outbreaks from longitudinal serological cattle data (n = 100).

FMD outbreaks were linked to specific virus types, with four serotypes responsible for cattle outbreaks during the study period. The sequence of serotypes causing outbreaks appeared to be related to serotype-specific neutralising antibody levels in cattle populations (the “immunity landscape”) at a snapshot in time prior to the outbreaks occurring. In one district in 2011, the highest proportion of animals were VNT positive for serotype O (93.3% [95% CI: 77.9-99.2%]), followed by SAT1 (37.5% [21.2-56.3%]), A (34.4% [18.6-53.2%]) and SAT2 (0% [0-10.8%]). The sequence of outbreaks recorded between 2012 and 2014 after this snapshot was inversely related to antibody levels (i.e. SAT2 in early 2012, A in late 2012/early 2013 and SAT1 in late 2013). This suggests that there is a predictability to circulation of FMD serotypes in relation to space, time and herd immunity that raises the potential for novel disease control strategies, including serotype-specific vaccination implemented in advance of predicted waves of infection.

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Adaptation of a Danish-Californian simulation model to inform decisions and increase preparedness against foot-and-mouth disease in Sweden

Fernanda C. Dórea[1], Maria Nöremark[1], **Karl Ståhl**[1], Stefan Widgrén[1], Tariq Halasa[2], Anette Boklund[2], Jenny Frössling[1], [1]National Veterinary Institute, Uppsala, Sweden; [2]Technical University of Denmark, Copenhagen, Denmark. Contact: karl.stahl@sva.se

Purpose: To minimize the potential consequences of an introduction of foot-and-mouth (FMD) disease in Europe, EU member states are required to present a preparedness plan. We aimed at using a simulation model to study potential outbreak scenarios in Sweden, and evaluate the best control strategies options.
Methods: We adapted the previously published model DTU-DADS (Boklund et al 2013; Halasa and Boklund 2014) to the Swedish livestock structure using herd information from cattle, swine and small ruminant holdings in the country. The contact structure were based on animal movement data and studies investigating the movements between farms of veterinarians, service trucks and other farm visitors. All scenarios of outbreak control included depopulation of detected herds, 3 km protection and 10 km surveillance zones, movement tracing and 3 day national standstill. The effect of availability of surveillance resources - number of field veterinarians per day, and timeliness of enforcement of interventions - was assessed. We also evaluated the effect of additional intervention measures, such as more days of standstill, ring depopulation and ring vaccination.
Results: With the currently available resources, an FMD outbreak in Sweden is expected to be controlled within 30 days of detection in the basic control scenario. Farm density would have little impact on the time to control the outbreak, but spread in high density areas would require significantly more surveillance resources. Ring depopulation decreased the time to control the outbreak, but the gain may be too small to justify the cost.
Conclusions: The results indicate that the duration and extent of FMD outbreaks could be kept limited in Sweden. However, the surveillance resources needed may be considerable and will depend on the introduction pathway. Model results will be complemented with cost analyses.
Relevance: FMD preparedness is improved in Sweden by determining the most cost-effective control strategies and resource requirements under various scenarios of FMD spread.

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An integrated epidemiological-economic analysis of foot and mouth disease: Application to the dry zone of Sri Lanka

Anoma Gunarathe[1], Hiroichi Kono[1], Satoko Kubota[1], Pradeep Kumarawadu[2], Kamal Karunagoda[3], [1]Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan; [2]Department of Animal Production and Health, Peradeniya, Sri Lanka, Japan; [3]Department of Agriculture, Peradeniya, Sri Lanka, Japan. Contact: thaburu@yahoo.com

Purpose

Food and mouth disease (FMD) is endemic in dry zone of Sri Lanka and considered to be a common disease among cattle and buffaloes in this area. Currently there is no regular, nationwide vaccination programme devised to control FMD. The objectives of this study were to identify and quantify the economic viability of preventive biannual vaccination against FMD employing the integrated epidemiological and economic model.

Methods

The Susceptible–Exposed–Infectious–Recovered (SEIR) model (based on the assumption that susceptible cattle were homogeneously mixed over space) was used to quantify the link between vaccination coverage and change of FMD incidence. The 2014 Sri Lankan epidemic data used to fit the model. The index case of this epidemic in North Central Province was reported on 17 January 2014 (epidemic day 1). Over 102 consecutive days, 8,384 cases (infected animals) were reported. Moreover, the benefit-cost analyses was performed to evaluate the economic viability of FMD vaccination.

Results

The transmission coefficient was estimated to be 0.618 by the SEIR model. The reproduction number, R_0, varied between 4.9 and 8.6, corresponding to recovery rates of 0.125 and 0.071, respectively. Thus, lower and upper bounds of the critical vaccination coverage, P_c, were estimated to be 79.5% and 90.5%. Moreover, the economic model revealed that the every Sri Lankan Rupee 1 spent on biannual vaccination resulted in positive benefits of Sri Lankan Rupee 3.7.

Conclusions

The current vaccination rate of 35% is not sufficient to eradicate FMD and it required to be increased at least by 45%. Nevertheless, FMD disease control is constrained by a low budget allocation and there is a shortfall from the actual allocation and the required allocation of 13.80 million Sri Lankan rupees. If the government can just allocate 0.025 % of additional budget annually for each province it would generate 78.09 million Sri Lankan rupees additional benefits each year from FMD eradication.

Relevance

The preventive biannual vaccination is economically viable option and should therefore be encouraged.

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Economics of zoonoses surveillance in a "One Health" context: An assessment of campylobacter surveillance in Switzerland

Sara Babo Martins[1], Jonathan Rushton[2], Katharina DC Stärk[1], [1]Royal Veterinary College/SAFOSO, Liebefeld, Switzerland; [2]Royal Veterinary College, Hatfield, United Kingdom. Contact: sara.martins@safoso.ch

Cross-sectorial collaboration between the animal and the public health sectors is increasingly highlighted as a means to improve the management of zoonotic threats. However, there is little evidence of the costs and benefits of such collaborative efforts for surveillance activities.
In Switzerland, campylobacter surveillance information generated in the poultry and human populations is shared and integrated in a multi-sectorial stakeholder forum since 2009- the Campylobacter platform. The objective of this work was to estimate the economic costs and benefits of such cross-sectorial efforts in surveillance.
We identified cost items and benefit streams associated with the surveillance and mitigation system using a conceptual framework. Cost items identified included labour and operational costs for surveillance activities, the linking of information and the triggered interventions in the two sectors. To evaluate non-monetary benefits, we estimated the burden of campylobacter associated disease in the country using Disability Adjusted Life Years (DALYs). Intermediate and other intangible benefits associated with knowledge generation were also assessed. Data used to parameterize the cost and the benefit estimation models were collected for two periods - prior and after the existence of the Campylobacter platform.
The marginal cost for the overall campylobacter mitigation activities in 2009-2013 was of 1.23 million CHF, with a low break-even point in terms of DALYs averted. The preliminary results suggest a slight increase in burden of disease over the period of the study, of up to 1751 DALYs in 2013. We investigate the role of an increase in poultry consumption in the country in the same time period in this result. The assessment of the intangible and intermediate benefits associated with surveillance is further incorporated in the results.
By providing information on the economics of cross-sectorial surveillance of zoonoses as well as the tools for this assessment, the results of this work can contribute for improved resource allocation to mitigation of zoonoses.

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A preliminary assessment of Rift Valley fever epidemiology in two wildlife/livestock/human interfaces areas in Zimbabwe

Michel de Garine-Wichatitsky[1], Katherine Knight[1], Alexandre Caron[1], Moses Zimba[2], Eve Miguel[1], Philippe Marianneau[3], Véronique Chevalier[4], [1]CIRAD/RP-PCP, Harare, Zimbabwe; [2]UZ/RP-PCP, Harare, Zimbabwe; [3]ANSES, Lyon, France; [4]CIRAD, Montpellier, France. Contact: degarine@cirad.fr

Purpose:
Rift Valley Fever (RVF) is an emerging disease threatening human and livestock health in Africa and the Middle-East. The role of wildlife in the maintenance and transmission of the virus at human/livestock/wildlife interfaces in Southern Africa remains unclear. In order to elucidate RVF epidemiology in the Great Limpopo (GLTFCA) and the Kavango-Zambezi (KAZATFCA), we combined preliminary data from serology, entomology, telemetry and field experiments in Zimbabwe.
Methods:
At each site, blood samples were taken between 2008 and 2011 from livestock and buffalo. The samples were tested with I-ELISA for RVF antibodies and the data analysed with Generalized Linear Model. Four mosquito trapping sessions were conducted at water holes used by livestock and/or wildlife. Potential contacts between wildlife and cattle were assessed using data of GPS collared cattle and buffalo published elsewhere. Bags of viscera were used as a proxy to estimate residence time of aborted fetus and potential infectious contacts between livestock and wild ruminants.
Results:
KAZATFCA serological results were all negative. In GLTFCA, the seroprevalence was 4.6% in cattle (27/587), 3% in small ruminants (2/66) and 6.8% in buffalo (14/205). The disease was endemic in livestock, with 2009 prevalence lower than 2008 (p=0.04). Buffalo prevalence was significantly higher in 2010 (p=0.05). Six species of mosquitoes were captured, including 3 potential RVF vectors: *Culex quinquefasciatus*, *C. theileri* trapped at both sites; *Anopheles coustani* identified in KAZATFCA only. Home ranges of sympatric cattle and buffalo overlapped, with significant differences in seasonality and frequency of indirect contacts across sites. Estimated residence time of aborted fetus ranged between a few hours and several days.
Conclusions:
These results indicate that RVF circulates in cattle and buffalo populations within the GLTFCA, with inter-annual and spatial variations, and that transmission between wild and domestic compartments may be due to both vectors and direct contacts
Relevance:
This innovative study combining different field data will contribute to improving zoonotic RVF at wild/domestic interfaces in Africa

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Joint analysis of human and bovine serological data: new insight on the risk and mechanisms of transmission of Rift Valley fever in Madagascar

Marie-Marie Olive[1], Jean-Michel Heraud[2], Vladimir Grosbois[3], Soa Fy Andriamandimby[2], Annelise Tran[3], Fanjasoa Rakotomanana[2], Christophe Rogier[2], Veronique Chevalier[4], [1]CIRAD-AGIRs and Institut Pasteur de Madagascar, Antananarivo, Madagascar; [2]Institut Pasteur de Madagascar, Antananarivo, Madagascar; [3]CIRAD-AGIRs, Montpellier, France; [4]CIRAD-AGIRs, Montpellier, France. Contact: marie-marie.olive@cirad.fr

Purpose:
In 2008-09, an outbreak of Rift Valley fever (RVF) virus occurred in Madagascar. Spatial heterogeneity in seroprevalence (SP) and case occurrence frequencies suggested that some areas are more favorable to RVF circulation. The objectives of our study were to identify environmental factors in favor to human and cattle infections; test the relevance of using local cattle infection as human infection predictor and give a new insight on the respective role of direct and vectorial transmission both in human and cattle.
Methods:
We used 2 independent cattle and human serological datasets originating from two national surveys (2009 and 2011-13). Multiple Factor Analysis (MFA) was used to characterize environments of the whole island in terms of climate and landscape. The datasets were analyzed independently using a generalized linear mixed model (GLMM) with the individual serological status- human or cattle- as the binomial response. Explicative variables were age and MFA factors for cattle model (M1) and age, gender, MFA factors and contact with ruminants and their product for human model (M2). Then human and cattle data were analyzed jointly by GLMM with the human individual status as binomial response. In addition to the previous explicative variables cattle SP predicted by M1 was used. Models accuracies were tested using ROC curve method.
Results:
Four MFA factors were selected. Age and factor4 - humid (irrigation, lake, marshland) environment - had a positive effect on SP of cattle and human living in rural areas ($p<0.001$ and $p<0.01$) while factor1- warm, dry and herbaceous environment- had a negative effect ($p<0.05$). Humans consuming raw milk were at risk. Predicted cattle SP were associated with human SP ($p<0.05$).
Conclusions:
Our results support an endemic transmission of RVF in rural area with humid landscape settings in both human and cattle populations suggesting the predominance of vectorial transmission for both populations. Local cattle infection seems to be a good predictor of human infection.
Relevance:
This joint analysis allowed deciphering transmission mechanisms and should help health and veterinary authorities to assess risk of RVF and optimize surveillance network.

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Using Ecological Niche Modelling for mapping the risk of Rift Valley Fever in Kenya.

Purity N. Kiunga[1], Phillip M. Kitala[2], Alex Kiprono[3], Gladys Mosomtai[4], Bernard Bett[5], [1]UoN(University of Nairobi)/, ILRI(International Livestock Research Institute), Nairobi, Kenya; [2]UoN(University of Nairobi), Nairobi, Kenya; [3]KALRO (Kenya Agriculture and Livestock Research Organisation), Nairobi, Kenya; [4]ICIPE (International Centre for Insect Physiology and Ecology), Nairobi, Kenya; [5]ILRI(International Livestock Research Institute), Nairobi, Kenya. Contact: pnkiunga@yahoo.com

Rift valley fever (RVF) is a viral zoonotic disease of economic importance caused by a virus of the Phlebovirus genus, Bunyaviridae family. The disease occurs cyclically between 5 to 15 years which is associated with El Nino weather phenomenon. Various studies have been done to map RVF distribution using a variety of approaches including the use of disease occurrence maps, statistical models which uses presence and absence data such as logistic regression method. However, acquiring correct absence data is not easy and hence maps generated from standard statistical models might not be a true representation of the disease distribution.

In this study Ecological Niche Modeling was used to model the supporting niche of RVF and determine the distribution of RVF in Kenya using Genetic Algorithm for Rule set Production (GARP) which uses presence-only data. Rift Valley Fever occurrence data were obtained by geo-referencing all the known hotspots in the country based on historical data acquired from the Directorate of Veterinary Services (DVS). The environmental variables that were used as the input data included: landuse, soil type, elevation, vegetation index acquired from Moderate Resolution Imaging Spectroradiometer (MODIS) satellite spanning from October 2006 to march 2007, rainfall and temperature for the same period of time as the satellite imagery.Of the sampled data 70% was used to train the model while 30% to test the model.

The result mapped the actual and potential distribution of RVF in Kenya with an Area Under Curve (AUC) of 0.82. A model evaluation was done using Partial Receiver Operating Characteristic (ROC) which had a 1.74 indicating that the model predicted well.

The results will be used to improve the already existing maps and for better planning of mitigation measures. It will also be used together with socio-economic variables to evaluate vulnerability indices in all the divisions across the country.

Key Words: Rift Valley Fever, Ecological Niche Model, GARP algorithm, AUC pROC.

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Maintenance mechanisms of Rift Valley fever virus in a temperate and mountainous ecosystem of Madagascar: dynamic and spatial modelling based on field data

Gaëlle Nicolas[1], Véronique Chevalier[2], Luciano M. Tantely[3], Didier Fontenille[4], Benoit Durand[5], [1]ULB - Université Libre de Bruxelles, Brussels, Belgium; [2]CIRAD, Montpellier, France; [3]Institut Pasteur de Madagascar, Antananarivo, Madagascar; [4]IRD, Montpellier, France; [5]Anses, Paris, France. Contact: gaelle.nicolas6@gmail.com

Purpose:
Rift Valley fever virus (RVFV) is a mosquito-borne zoonosis endemic in Africa. Since 1930, outbreaks have occurred in tropical, hot-irrigated or arid ecosystems. In 2008-2009, an outbreak occurred in a temperate and mountainous area of Madagascar highlands. We conducted a 3-year serological follow-up in cattle in a pilot area of these highlands (894 bovine in 2009, 516 in 2010 and 210 in 2011). Cattle exchange and vector population dynamics were investigated. Despite unfavourable climatic conditions and absence of Aedes mosquitoes (main vectors in Africa), results showed that the virus kept circulating till 2011 in absence of clinical cases.
The objective of this study was to understand the mechanisms allowing the virus to circulate in this unfavourable ecosystem. We propose a model coupling cattle exchange practices and vector-borne transmission to explain the RVFV spread and persistence in this area.
Methods:
The model is parameterized to reproduce the local conditions of Madagascar highlands, using observational data collected in the area: villages/ rice field locations, number of cattle per village, cattle birth/death rates, cattle exchange networks built using SNA methodology, monthly abundance of mosquitoes, monthly variations of the mosquito parity rate. Non-observable parameters such as transmission parameters were estimated using collected serological data.
The model was used to analyse 3 potential mechanisms that could explain the recurrent circulation of RVFV in the area: (i) recurrent introductions from other regions of Madagascar, (ii) RVFV direct transmission between cattle during calving period, (iii) a low level vector-based circulation during winter thanks to a residual vector population. All possible combinations were tested.
Results:
Predictions satisfactorily reproduced field observations. Results appeared robust according to the sensitivity analysis.
Conclusions/ Relevance:
Interweaving between agricultural works in rice fields, seasonality of vector proliferation, cattle exchange and traditional practices (socio-economic practices) could be a key element for understanding RVFV circulation in this area of Madagascar highlands.

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Identifying Dutch pig herds at risk for Toxoplasma gondii : prevalence and test characteristics

Manon Swanenburg[1], Gertjan Boender[1], Henk Wisselink[1], Lourens Heres[2], Joke Van der Giessen[3], **Aline De Koeijer**[1], [1]Central Veterinary Institute (CVI), Lelystad, Netherlands; [2]VION, Boxtel, Netherlands; [3]RIVM (National Institute for Public Health and Environment), Bilthoven, Netherlands. Contact: aline.dekoeijer@wur.nl

Purpose:
Toxoplasma gondii is considered an important zoonotic infection. Therefore, monitoring of T. gondii in the pork supply chain was initiated by Vion, a pork slaughter company in the Netherlands and Germany. The monitoring was aimed at detecting herds at risk and quantifying the prevalence of the infection in pigs.
Methods:
Active serological monitoring on pigs entering their slaughterhouses was initiated, using the PrioCHECK Toxoplasma Ab porcine ELISA. The collected data were evaluated to quantify the prevalence of T. gondii infections in pigs and to identify herds at risk. An analysis of appropriate cut offs of the ELISA test for active field monitoring was performed, since knowledge on this issue was limited.
Results:
We found that for the studied population a very high test sensitivity can be obtained with a cut-off value around 10 percent positivity (PP). A high specificity can be obtained with a cut-off value around 20 PP. Using a cut-off value of 20 PP, we found that 2% of the pigs at slaughter are infected with T. gondii. The seroprevalence on organic farms (with outdoors areas) was twice as high. Furthermore we found a clear seasonality in the data, with a higher T. gondii risk for pigs that go to slaughter in the first quarter of the year, as compared to the third quarter.
Conclusions:
The prevalence of T. gondii in Dutch pigs is limited but existing. A further study into risk factors and the sources of the seasonality may help in reducing the prevalence in pigs or in pork.
Relevance:
T. gondii has repeatedly been named as one of the most important zoonotic infections in Europe, in terms of its impact on human health. When more is known about its prevalence, intervention measures can be developed and implemented.

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Is weather really important for arbovirus infection? The case of dengue in Central Java

Thibaud Porphyre[1], Siwi P. M. Wijayanti[2], Margo E. Chase-Topping[1], Alain Kohl[2], [1]University of Edinburgh, Edinburgh, United Kingdom; [2]MRC–University of Glasgow, Glasgow, United Kingdom. Contact: t.porphyre@ed.ac.uk

Purpose: When planning for interventions of prevention against arboviruses, the common dogma is to identify key environmental factors (e.g. temperature, humidity) that would influence vector populations and drive the risk of infection. However, these factors may vary between countries as weather, geography, and other local features can differ. In particular, it is little known how the role of environmental drivers may change in regions of the world where environmental conditions do not vary significantly across years but remain suitable for sustaining mosquito populations throughout. Here, we explore the risk of dengue as an arbovirus of high public health importance, and focused on infections occurring in the Banyumas regency, Central Java, Indonesia. While environmental conditions in the regency are tropical with two seasons, mosquitoes remain in high numbers throughout the year. Between 2000 and 2013, the number of dengue cases progressively increases, making an ideal area to evaluate factors associated with transmission in this type of environment.
Methods: We used hospital-reported dengue cases to build Bayesian spatial and spatio-temporal models and evaluate the association of several factors including weather, geography, population density, education, status, and access to health care facilities on the number of cases reported in local communities.
Results: We found that, although the temperature was the only ecological factors associated with the risk of dengue infection, its impact was limited. Instead, dengue infections were more influenced by the employment type and economic status within the risk population.
Conclusions: These results suggest that most reported cases are triggered by indoors transmission events in the study area. We therefore argue that, in this tropical setting, preventive measures should target specific environments such as schools and work areas over large scale control measures such as larvicide or insecticide spraying which may have little effect to achieve significant effects in the community.
Relevance: This study can also inform preventive measures in areas with similar patterns of reported dengue cases and environment.

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Estimating bacterial cross-species transmission in Michigan

Liliana C. M. Salvador[1], Daniel J. O'Brien[2], Melinda K. Cosgrove[2], Suelee Robbe-Austerman[3], Tod P. Stubber[3], Rowland R. Kao[1], [1]University of Glasgow, Glasgow, United Kingdom; [2]Michigan Department of Natural Resources, Lansing, MI, [3]USDA/APHIS National Veterinary Services Laboratories, Ames, IA, Contact: liliana.salvador@glasgow.ac.uk

Purpose: Cross-species transmission of bacterial pathogens has major implications for livestock and wildlife management because of the implications for disease management and conservation. In recent years bovine Tuberculosis (bTB) has experienced an ecological shift in the US, with spillover from cattle leading to an endemically infected white tailed deer (WTD) population in Michigan that appears to serve as a reservoir of infection, with spillback to the sympatric elk population and cattle herds. Our objective is to better understand how the disease is maintained in WTD and how it is transmitted across species. Using epidemiological and Next Generation Sequencing data of Mycobacterium bovis isolates, we compare patterns of disease transmission with genetic similarity (based on SNP differences) between elk, deer and cattle.
Methods:BTB-positive deer that are spatially and temporally close to each positive elk are selected for inclusion from among the available archived isolates, as well as positive deer from the margins of the occupied elk range. Positive cattle herds in the same area are also selected. In total we identify isolates from 5 elk, 41 deer and 4 cattle herds. After verification of purity of isolates, DNA is collected and submitted for sequencing using Illumina NexteraXT 2x 250 chemistry and MiSeq instrument technology. Raw sequences are aligned to the reference AF2122 using BWA and SNPs are called using GATK. RAxML is used to build phylogenetic trees from the aligned SNPs.
Results: Preliminary results from analyses of discrete traits mapped into phylogenetic trees suggest that there may be highly variable evolutionary rates in sequences between the different species: there is little variability within outbreaks, but often large between outbreaks.
Conclusions: Further research on the role of each species on the maintenance and transmission of bTB In Michigan will be needed to determine the likely direction of the transmission and its evolutionary rate.
Relevance: With this study we will be better informed about the necessity of establishing new control programs in this area.

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Index Based Livestock Insurance in the Developing World - What is it, how does it work, and why should you care?

Huybert Groenendaal[1], Shadreck Mapfumo[2], [1]EpiX Analytics, Boulder, CO, [2]World Bank Group, Johannesburg, South Africa. Contact: Huybert@epixanalytics.com

Purpose: Weather related risks can have devastating effects on livestock, particularly for poor farmers in developing countries. The objective of this concept talk is to discuss what index insurance is, how it works, and how veterinary epidemiologists and economists could contribute to this novel and growing risk management tool.
Methods: In the developing world, index insurance is a relatively new insurance product that pays out to policy holders if a weather related index (e.g. cumulative rain or temperature during a season) exceeds policy-defined thresholds. Important benefits of index insurance products include that logistically they are low-cost to administer (i.e. no need to visit every farm to evaluate actual losses), they prevent moral hazards and adverse selection, and they can provide quick payouts to producers.
A disadvantage of index insurance is however that an insurance policy may not always pay out (because the index hasn't met the threshold) even if producers have experienced losses. In designing index insurance, it is therefore important to design a product in which this risk, also called basis risk, is small.
Results: Designing high quality index insurance products requires expertise of actuaries. However, veterinary epidemiologists and economists also play an important role in this process, for example by conducting studies investigating the link between weather-related factors and economic losses. Selected examples will highlight the significance of such inputs for the improvement of index insurance.
Conclusions: The presentation will highlight a number of important characteristics of index insurance, and how future contributions of veterinary epidemiologists and economics can help to further improve it.
Relevance: Index insurance has the potential of providing animal producers in low-income regions with an accessible and affordable risk management tool against weather related risks, which will help them improve and secure their livelihoods.

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Use of data mining techniques for health management in wean-to-finish, nursery, and finishing pig operations

Ana Alba-Casals[1], Julio Alvarez[1], Javier Sarradell[2], Andrés Perez[1], Robert Morrison[1], [1]University of Minnesota, Saint Paul, MN, [2]Veterinary Faculty, National University of Rosario, Department of General and Systemic Pathology, Argentina. Contact: aalbacas@umn.edu

Purpose:
Modern wean-to-finish, nursery, and finishing pig operations provide an excellent platform for exploring the use of data-mining techniques to inform decisions on disease prevention and control in near real time. However, implementation of dynamic systems that integrate and analyze large amount of multiple data sources faces numerous technical challenges, including the need for identifying robust indicators related to animal health, the recognition of clusters in heterogeneous subpopulations, and the definition of spatiotemporal aggregates. This study aimed to identify indirect indicators for the early detection of disease and define appropriate units for their measurement in multisite production system.
Methods:
During a complete closeout, environmental, sanitary and production data were compiled exhaustively from 4 rooms with 60 pens and 34 pigs per pen. Animals were tested biweekly for detection of porcine reproductive and respiratory syndrome (PRRS), Influenza A (IA), and other respiratory pathogens. The study is classified as an intervention because data were obtained from a commercial operation, resembling a traditional observational study, but the cohort of pigs was oversampled to collect data for assessing the efficacy of alternative survey strategies.
Using regression modelling, visualization, bivariate time series, and clustering techniques, relations between mortality, morbidity, environmental parameters, growth performance, and detection of respiratory pathogens were studied.
Results:
Highest incidence of IA and PRRS were associated with death peaks, increased coughing and lethargy, and drop in water consumption and environmental temperatures at 12-day lags. Pen-level production performance varied significantly between-, compared to within, rooms.
Conclusions:
This work shows the potential use of tracking indirect parameters for early detection of anomalies in pig operations and suggests that the preferred unit of analysis for implementing surveillance systems in pig operations should be at room level.
Relevance:
This study provides novel tools to monitor swine health and production in highly intensive systems.

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A hoof telehealth system: using mobile phone image capture technology to remotely diagnose lameness lesions in dairy cows

KATE J. CHAPLIN, Tamsin S. Barnes, John Wright, Andreas A. Avila, John Alawneh, University of Queensland, Gatton, Australia. Contact: kate.chaplin@hotmail.com

Purpose
To determine whether digital photographs of lameness lesions captured by a farm worker (FW) can be used by a remote veterinarian (RV) to diagnose lesions of the lame cow.
Methods
Digital images of lameness lesions taken by a FW were sent via multi-media messaging service to a RV for assessment while the FW and a farm veterinarian (FV) independently performed assessment of the lesions on site, each categorising severity, classification, claw zone, body region, tissue and limb/claw. The bhapkar test was used to assess the marginal homogeneity between assessors. Non-homogeneity was declared at an alpha ≤ 0.05 and no further analysis was performed. Inter-rater agreement was determined for categories demonstrating marginal homogeneity using the kappa (κ) statistic. Prevalence and bias adjusted κ (PABAK) was determined to address the κ paradox.
Results
Although FV and RV assessment of lesion severity, body region and classification differed systematically (P-value 0.00, 0.00 & 0.01), they showed good to very good agreement of claw zone (κ 0.73, 95% CI 0.64 – 0.82; PABAK 0.80), tissue (κ 0.75, 95% CI 0.66 – 0.83; PABAK 0.79), and limb/claw (κ 0.99, 95% CI 0.96 – 1.0; PABAK 0.99).
There was a systematic disagreement between FV and FW, and RV and FW pairings in all categories except for limb/claw (FV: FW κ 0.95, CI 0.91 – 0.99; PABAK 0.98; RV: FW κ 0.95, CI 0.91 – 0.1.00; PABAK 0.98).
Conclusions
FV and RV demonstrated high concordance in assessment of claw zone, tissue and limb/claw. Systematic disagreement was present for severity, body region and classification. FV and FW, and RV and FW demonstrated high concordance for limb/claw only. Remote diagnosis of lameness
lesions has potential for application on the dairy farm providing dairy farmers with enhanced opportunities to diagnose lameness cases.
Relevance
This project presents a novel telehealth system specifically designed for improving the hoof health of dairy cows, creating a platform for improved surveillance and treatment of lameness by farm workers. This in turn will enhance dairy cow welfare and productivity.

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“Ok, Google”: Google Tools in Epidemiology - Where are we heading?

Ulrich Muellner[1], Flavie Vial[2], Petra Muellner[1], [1]Epi-interactive, Wellington, New Zealand; [2]Veterinary Public Health Institute, Bern, Switzerland. Contact: uli@epi-interactive.com

PURPOSE

Google Maps is the most widely used App for smartphones worldwide and Google visualisation tools are being increasingly used to display animal and human health data interactively. Functionality is expected to continuously improve, driven by the demand for intuitive and accessible information visualisations. At the same time, epidemiologists now widely recognise the need to communicate their work and decisions to a range of audiences more effectively. However, as information exposure increases, cognitive overload is rapidly reached.

METHODS AND RESULTS

Google Maps and Charts are for most uses freely available, multi-device capable software tools for the web-based visualization of epidemiological data. Google tools can also be used to create an up-to-date and mapped inventory of scientific information on specific topics, as recently illustrated by an e-review on global NDM-1 occurrences. The tools allow a separation of data, business and visualization layers supporting dynamic visual outputs which has several advantages over the time-consuming and error-prone manual creation of graphics, which require frequent extraction of data from the database source, creation of an image-based graph and then upload into a specific website.

In this concept note, we will demonstrate the advantages and challenges of Google tools for veterinary epidemiology, drawing from applied case studies. The discussions will extent to integration with existing epidemiological software and methods, as well as privacy and data protection considerations.

CONCLUSIONS & RELEVANCE

In times of metadata and whole genome sequencing, our ability to see connections and aberrations within datasets is becoming crucial to our capacity to make sound decisions to improve health. In particular visual and interactive approaches to reporting can facilitate evidence-based decision-making by risk managers and contribute to bridging the gap between science and policy. Furthermore there is an increasing demand that the reporting of outputs from health surveillance systems should be done in (near) real-time and in an interactive manner to identify, assess and manage hazards as early and efficiently as possible.

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Vet-client communication and approaches to managing equine laminitis

Claire Scantlebury[1], Elizabeth Perkins[2], Cathy McGowan[1], Gina Pinchbeck[1], Rob Christley[1], Debra Archer[1], [1]University of Liverpool, Neston, Wirral, United Kingdom; [2]University of Liverpool, Institute of Psychology Health and Society, United Kingdom. Contact: claire.scantlebury@liverpool.ac.uk

Purpose:
Effective vet-client communication is
essential to support the management and prevention of equine disease.
Objectives
To use Sociological research methods to explore veterinary surgeons' and horse-owners' experiences of managing laminitis and, to examine the influence of vet-client communication on the adoption of equine disease management strategies.

Methods:
Focus group discussions with first-opinion equine veterinary surgeons from three regions of the UK explored; veterinary perceptions of information sources, reasons for horse-owners' seeking veterinary advice, veterinary perceptions of horse-owner knowledge, attitudes and practices and, the role of other professionals. Horse-owner's, recruited via social media and equine forums and magazines, were purposefully selected for interview from a range of different equestrian backgrounds and experiences of laminitis. Discussions were recorded and transcribed *verbatim* and a thematic analysis conducted. An online questionnaire was developed to examine emergent hypotheses among a larger population of horse-owners.

Results:
Core themes from the focus groups included;challenges faced by vets, managing client's expectations, client recognition and management of laminitis, feeding and obesity management, issues of compliance, strategies to prevent laminitis, diagnostics and prognoses in laminitic cases, sources of veterinary information and, working with other professionals. Key themes from 13 horse owner interviews included; perceptions of the role of the veterinary surgeon in providing advice on the management and prevention of laminitis, the relative position of veterinary advice in relation to other information sources and, end-of-life decision making.

Conclusions:
Collaborative veterinary-client communication is important due to the uncertainty and variable course of this complex disease. Of note was the veterinarian's role in assisting owners in recognising and managing laminitis and obesity.

Relevance:
This information may aid the development of methods to communicate advice to owners within the veterinary consultation and more widely in equine disease prevention programmes.

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Using high-performance computing to investigate historical outbreaks of bluetongue and African horse sickness due to the long distance wind dispersal of Culicoides midges

Peter A. Durr[1], Kerryne Graham[1], Rieks van Klinken[2], [1]AAHL-CSIRO, Geelong, Australia; [2]Biosecurity Flagship - CSIRO, Brisbane, Australia. Contact: peter.durr@csiro.au

Purpose:
The possibility that wind-borne, long distance wind dispersed (LDWD) *Culicoides* midges - the insect vectors of bluetongue and African horse sickness (AHS) - was proposed by R.F. Sellers in a series of papers published almost 40 years ago. These investigations used simple synoptic "trajectories" as the basis for their conclusions.
Methods:
We used high-performance computing (HPC) to investigate the validity of the original research. This combined an established particle dispersal model ("HYSPLIT") and a custom-built web-interface ("TAPPAS"). Using internationally accessible climate data-sets of atmospheric conditions, we investigated the scenarios described in Sellers' papers, but allowing for the dispersal of individual midges - modelled as particles - from the purported sources.
Results:
We successfully re-ran all the important historical scenarios of the introduction of bluetongue or AHS ascribed by Sellers to be due to wind-borne virus infected *Culicoides* midges. These included bluetongue in Portugal in 1956, Cyprus in 1977 and AHS to Spain in 1966.
Conclusions:
Most of Sellers hypothesised LDWD of *Culicoides* events which then resulted in outbreaks of exotic viral disease were supported by our re-analysis. An important exception was the 1956 incursion of bluetongue into Portugal, which Sellers believed originated from Morocco.
Relevance:
LDWD modelling is most effective in "ruling-out" this as a possible source of an incursion of an insect-vectored viral disease. When it is shown to be a plausible source of introduction of the virus, further investigations are needed for "ruling-in" wind-dispersal of virus carrying vectors. Molecular methods, and particularly the comparison of full genome sequences of the virus at the purported source and the incursion site, have an increasingly important role in providing supporting evidence for such inference.

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Focus groups or interviews; our experience of the perks and pitfalls.

Wendela Wapenaar, Imogen Richens, Marnie Brennan, University of Nottingham, Sutton Bonington, United Kingdom. Contact: wendela.wapenaar@nottingham.ac.uk

Purpose
This presentation aims to inform researchers about the strengths and weaknesses of focus groups and interviews, based on experiences during a research study carried out to investigate attitudes, motivators and barriers of farmers towards biosecurity and vaccination.
Methods
Two researchers were involved in organising focus groups and interviews with farmers across England, Scotland and Wales, focussing on vaccination and biosecurity practices. Inductive thematic analysis was used to identify key themes and topics highlighted by interviewees.
Results
The comparison of the two different data collection methods was much dependent on literature research. In the presentation we will discuss several issues which hampered carrying out focus groups and led us to switch our data collection methodology to interviews. The published research highlights the advantage of focus groups over individual interviews for the richness of information that can be collected from a group of people interacting in a discussion. On the other hand, this interaction can be hampered by the combination of people in the group.
Conclusions
Although in theory a focus group can be more appropriate to collect a wide range of topics and thoughts within a group of people, it is important to consider the feasibility of such a study, if one wants to gather important information to inform further studies.
Relevance
A short presentation about the strengths and pitfalls and perks of interviews and focus groups can help other epidemiological researchers to decide on the best study design, which is most likely to lead to meaningful research outcomes.

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Using video and YouTube to engage future veterinary leaders and decision-makers in epidemiology, biostatistics, spatial and social network analyses

Simon M. Firestone[1], Caitlin N. Pfeiffer[2], Mark A. Stevenson[1], [1]The University of Melbourne, Parkville, Australia; [2]The University of Melbourne, Werribee, Australia. Contact: simon.firestone@unimelb.edu.au

Purpose:
Recent advances in spatial epidemiology and social network analysis have provided a range of new tools and techniques for informing disease control intervention and response, yet it can be challenging to engage students in technical skill development. We evaluated an educational intervention involving a series of instructional videos for key epidemiological skills.
Methods:
A series of 27 videos were developed on biostatistics, epidemiological study design and analysis, spatial and social network analyses. These were posted on YouTube and incorporated into web content in a distance online epidemiology subject. Metrics of student engagement and performance compared using multivariable Poisson regression on data from student cohorts, for 93 student-weeks before and 130 student-weeks after the videos were available. Two outcome variables were assessed: number of postings in discussion threads linked to weekly assignment tasks and number of times students accessed subject content web-pages, per student-week, adjusting for confounding by student gender and age.
Results:
Each video was watched a mean of 1.7 times per student (SD=0.7, range=0.7 to 2.8 times per student). Students in cohorts taught with instructional videos accessed course content web-pages 4.64 times more often (95% CI of the incidence rate ratio [IRR]: 4.19, 5.15) than students in cohorts without the videos. Numbers of posts per student-week were similar in the two cohorts. Younger students posted 10% more often than older students (IRR 95% CI: 1.01, 1.21). Differences in student performance are still being formally assessed on tasks specifically related to the video content.
Conclusions:
The educational intervention was highly successful in increasing student engagement on complex tasks.
Relevance:
Familiarity with the capabilities of new epidemiological tools and understanding of their application is vital for future leaders of our profession, especially those that will take up key decision-making roles in future animal disease emergencies. The students' improved understanding of these advanced epidemiological techniques will be of direct benefit in future animal disease responses.

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A Monte-Carlo simulation model to evaluate surveillance options for future analysis and detection of genetically modified (GM) feed related effects.

Louise Vince[1], Marta Terre[2], Manon Swanenburg[3], Barbara Desantis[4], Timothee Vergne[1], Dirk Pfeiffer[1], Javier Guitian[1], [1]The Royal Veterinary College,, London, United Kingdom; [2]Institute of Food and Agricultural Research, Barcelona, Spain; [3]Wageningen UR, Wageningen,, Netherlands; [4]National Institute of Health, Rome, Italy. Contact: lvince@rvc.ac.uk

Purpose: To inform policy decisions on the longer term strategy for monitoring of possible animal health effects from GM feed in production animals. Consideration was given to both plausible outcomes and novel conditions.
Methods:A comprehensive review of current animal health monitoring was undertaken and surveillance components were established for evaluation; these include passive, abattoir, post mortem, production records and active components. At risk populations were determined by production type for analysis and include diary, pigs, poultry and aquaculture. Models describing each surveillance component were generated for each production group. Expert elicitation was performed to parameterise the models. A Monte-carlo simulation in @risk version 6.3 was used to establish 'normal' detection probabilities for each disease syndrome assuming baseline GM exposure. Simulation sensitivity analysis was performed by varying the relative risk associated with trans-genic feed to access for a detectable change in disease syndromes with respect to the risk.
Results: The sensitivity of each surveillance component was evaluated for the syndromes and population groups of interest. The most sensitive component for unknown severe diseases was consistently the post-mortem system. The most sensitive method for analysis of less severe conditions with a lower relative risk is the use of industry available production data across population groups.
Conclusions: Strengthening of currently established surveillance systems and improving capacity for detection of emerging conditions could be extended to include monitoring of GM feed adverse effects. Identification of unforeseen adverse effects and plausible risk effects should be approached through different methods of animal health surveillance.
Relevance:GM feed consumption has increased dramatically in livestock and humans and is predicted to continue both in feed concentration and number of strains. Future surveillance methods for detection of both known and unknown, risk syndromes can now be tailored more specifically to the most sensitive components of the existing surveillance network.

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Herd-level associated factors for multidrug-resistant bacteria from Brazilian dairy herds

Waldemir Santiago Neto[1], Gustavo Machado[1], Suzi Camey[2], Thais de Campos[1], Adil K. Vaz[3], Carla C. Lange[4], Geraldo M. Costa[5], Guilherme N. de Souza[4], Lisiane A. Martins[6], Marcos V. dos Santos[7], Letícia C. Mendonça[4], Marisa R. I. Cardoso[1], Maria Aparecida V. P. Brito[4], Luís Gustavo Corbellini[1], [1]Rio Grande do Sul University, Porto Alegre, Brazil; [2]Rio Grande do Sul University, Porto Alegre, Brazil; [3]UDESC, Lages, Brazil; [4]Embrapa, Juiz de Fora, Brazil; [5]UFLA, Lavras, Brazil; [6]UNIPAR, Umuarama, Brazil; [7]USP, Pirassununga, Brazil. Contact: wal_sanet@hotmail.com

Several bacteria can colonize the bovine´s mammary gland and between them Staphylococci have been reported as the most prevalent mastitis agents. Such bacterial species can carry multidrug-resistant elements coming inclusive from other bacteria species, and so has been rising as a great public health concern. The present study evaluated the occurrence of multidrug-resistance among more than 3500 isolates from a repeated cross-sectional study performed from 2010 to 2011 in cows from 105 dairy farms at the main Brazilian dairy production area. The bacteria were classified according to phenotypic methods and the antimicrobial resistance patterns were determined by disk diffusion test. Factors associated with the response variable, the proportion of bacteria resistant to three or more antimicrobial classes (or multidrug resistance), were assessed by a multivariable mixed model. The random effects were the farm regions from which the herds were selected. The variables used as fixed effects were obtained by means of an epidemiological questionnaire and tested for univariable association. The model was controlled by the effect of farm's production system, highly correlated with average daily milk production. Penicillin-group antimicrobials, followed by tetracycline and sulfonamide, were the less effective antimicrobials to staphylococci (n = 3009). Streptococci (n = 480) showed moderate to high resistance to tetracycline, gentamycin and clindamycin, and high frequency of multidrug resistance. The mixed model identified that the immediate treatment of clinical mastitis and the interaction variable "antimicrobials used not under the care of the veterinarian practitioner along with the intensive, modern production system" increased the likelihood of multidrug resistance at the herd level. A low intraclass correlation coefficient showed that resistance variations were most explained at herd level and its characteristics rather than at region level. These dairy management practices potentially select multidrug resistant bacteria in Brazilian dairy herds.

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Development of a Bayesian Belief Network by machine-learning, as a tool for evidence-based management of disease emergence on swine farms in Canada.

Ruth Cox, Javier Sanchez, Crawford Revie, University of Prince Edward Island, Charlottetown, PE, Canada. Contact: rucox@upei.ca

Purpose
Bayesian Belief Networks (BBNs) are mathematical modelling tools that can be used to explore epidemiological scenarios and aid decision-making. Here we develop a BBN that can be used to identify biosecurity practices that may be associated with disease emergence in the Canadian swine industry.
Method
Data about biosecurity practices, health status and disease outbreaks were collected from commercial swine farms across Canada. The diseases covered were Porcine Reproductive and Respiratory Syndrome (a highly prevalent endemic aerosol pathogen), Swine influenza (a potential zoonosis), *Mycoplasma pneumonia* (an endemic respiratory disease spread by close contact) and Swine dysentery (an enteric disease which is re-emerging in Canada). First a BBN was built using a naïve Bayes structure. We then used machine learning algorithms (e.g. filter and wrapper methods) to refine the model. This included selecting the biosecurity practices thought to have the most influence on disease emergence and designing the most parsimonious model with high sensitivity and specificity.
Results
The biosecurity risks that were incorporated included proximity to other livestock holdings and procedures for admitting vehicles and staff. The best non-naïve BBN model included 10 risk factors and had a true positive rate of 81%, compared to 74% for the naïve structure. Sensitivity testing indicated that there were a number of manageable biosecurity practices that influenced disease outbreak. For example, there was an increased probability of PRRS and *Mycoplasma pneumonia* when spilt feed is not disposed of immediately. Increased probability of PRRS was also associated with waste being brought onto the farm, while this practice did not appear to influence outbreaks of the other diseases.
Conclusion and Relevance
Development of a BBN in this epidemiological scenario allows the potential impacts of management to be explored and management trade-offs to be identified. Machine learning can be used to aid model development and analysis.

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Improving efficiency of identification of dairy herds with poor welfare

Marion de Vries[1], Eddie Bokkers[1], **Gerdien van Schaik**[2], Bas Engel[1], Thomas Dijkstra[2], Imke de Boer[1], [1]Wageningen University, Wageningen, Netherlands; [2]GD Animal Health, Deventer, Netherlands. Contact: g.v.schaik@gddiergezondheid.nl

Purpose:
Aim was to evaluate the potential of herd, housing, and management data for estimating the level of welfare in dairy herds, and to estimate the associated reduction in the number of farm visits required for identifying dairy herds with poor welfare in a population.
Methods:
Seven trained observers collected data regarding the housing and management of cattle in a selected sample of 181 loose housed Dutch dairy herds (herd size: 10 to 211). Severely lame cows, cows with lesions or swellings, cows with a dirty hindquarter, and very lean cows were counted and avoidance distance at the feeding rack was assessed for a sample of cows, and occurrence of displacements (social behavior) was recorded during 120 min of observation. Herd data relating to demography, management, milk production and composition, and fertility were extracted from several national databases. Variables of herd, housing, and management data were used as potential predictors for prevalence of severely lame cows, cows with lesions or swellings, cows with a dirty hindquarter, and very lean cows, an index score for avoidance distance, and frequency of displacements in logistic regression at the herd level.
Results:
Prediction was less accurate for the index score for avoidance distance, and moderately accurate for the other five welfare indicators. Compared to visiting all farms, the number of farm visits required for identifying nearly all herds with poor welfare (i.e. sensitivity of at least 97.5%) reduced by 2% (avoidance distance index) to 35% (prevalence of severely lame cows) when levels of welfare were first estimated based on herd, housing, and management data. For identifying 70% of the herds with poor welfare (i.e. sensitivity of 70%), the number of farm visits reduced by 19% to 53%.
Conclusions:
Efficiency of identifying dairy herds with poor welfare can be improved when levels of welfare in herds are first estimated based on herd, housing and management data.
Relevance:
Animal welfare assessment is time-consuming and expensive. Predicting levels of welfare in herds based on data that are more easily obtained is a promising strategy to improve efficiency of identifying dairy herds with poor welfare.

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Use of epidemiology and innovation tools for enhancing disease surveillance in the context of developing countries

Julio Pinto, Fairouz Larfaoui, FAO, Rome, Italy. Contact: julio.pinto@fao.org

Animal diseases impact livestock production and farming systems, people and livelihoods. The livestock sector plays an important role in the economies of most of developing countries accounting for 40% of GDP and employing around 1.3 billion people. Animal diseases cause mortality and loss of production; market disruption as a result of consumer fears, or supply shortage causing market shocks, or as a consequence of restrictions on international trade in livestock and livestock products. FAO provides policy advice and technical support to animal health systems to prevent, control or eradicate animal diseases. FAO supports member countries in the use and development of approaches for enhancing disease surveillance tools and promoting innovative approaches to improve surveillance and disease management such as SMS Gateways for Avian Influenza in Bangladesh, Digital Pen Technology in Africa and EMA-i app in Uganda. Participatory approaches has been a very useful tool to improve detection and response to avian influenza cases in Indonesia using Participatory Disease Surveillance and Response (PDSR) and in Egypt through the development of the Community Animal Health Outreach program. FAO is continuously supporting the development of national core capacities and competencies on veterinary epidemiology and disease surveillance through the implementation of field veterinary epidemiology training in Asia and Africa. Strengthening existing national or regional networks facilitates rapid detection, information sharing, and harmonization of methodologies and development of strategies for disease control and builds trust among countries. Continuing education, training on veterinary epidemiology is essential to better understand animal diseases and risk factors influencing the emergence or spread of diseases. These competencies include basic disease recognition, risk factors/drivers, use of participatory epidemiology and qualitative methods for risk assessment, conducting field outbreak investigation, design, implementation and assessment of the effectiveness of disease surveillance.

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Power to the people: creating people-powered information systems

Jonathan Happold[1], Catriona Mackenzie[2], **Albertus T. Muljono**[1], Sigit Nurtanto[3], Chornelly K. Yohana[3], Siti Yulianti[3], Muhammad Syibli[3], Pudjiatmoko Pudjiatmoko[3], [1]Australia Indonesia Partnership for Emerging Infectious Diseases, Jakarta, Indonesia; [2]AusVet Animal Health Services, Lyon, France; [3]Directorate General of Livestock and Animal Health Services, Jakarta, Indonesia. Contact: albertus.muljono@aipeid.org

Animal health information systems are an essential element of national veterinary services and central to disease control programs, policy development, advocacy and the delivery of field services. Substantial funds may be invested in their development and immeasurable opportunity costs are associated with decisions based on poor information.

National animal health information systems are often designed to meet 'top level' needs and development may focus on the technological elements of the system. Consequently, there may be a lack of attention to the important roles that people play at all levels of the veterinary service as contributors and users of information.

The principle that people are central to information systems has important implications for the creation of information systems. System design must be based on a solid understanding of the people who are expected to engage with the system. This includes technical and practical matters (the work people do and how they do it); social and psychological factors; and the cultural, political and economic context in which the system is intended to operate. These factors, more so than technology, are likely to determine whether an information systems is useful and sustainable.

With this principle in mind, a multi-disciplinary team has developed an integrated national animal health system in Indonesia, known as iSIKHNAS. Modern technology (mobile phones, cloud servers, etc.) replace slow and fragmented paper-based systems. However, the innovation and power of iSIKHNAS comes from its ability to provide 'positive transactions' to all (or almost all) users; for example by making communication easier, removing menial reporting tasks and providing immediate and positive feedback. With a focus on people, the 'personality' of an IT system can be crafted as one that is responsive, useful and courteous.

Currently in 48 (approximately 10%) districts across Indonesia, the system is receiving in excess of 7,000 general disease reports by SMS per month and almost 20,000 other reports on treatment, case outcome, animal movements and slaughterhouse statistics. This level of usage suggests that real benefit is perceived at the field level.

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Preventative services offered by veterinarians on sheep farms in England and Wales: opinions and drivers for proactive flock health planning

Camille Bellet[1], Jo Woodnutt[1], Laura Green[2], Jasmeet Kaler[1], [1]University of Nottingham, Sutton Bonington, United Kingdom; [2]University of Warwick, Coventry, United Kingdom. Contact: camille.bellet@nottingham.ac.uk

Purpose:
Recent independent government reports and studies in the UK have highlighted the importance but lack of flock health preventive services provided by veterinarians (vets) on sheep farms. Although farmers report that they consider their vets the most useful source of new information, they also consider their veterinarians to have lack consistency and expertise (beyond disease). No study to date exists on the views of veterinarians on their role. The aim of the current study was to use psychological constructs to understand veterinarians' opinions of and drivers for the services they provide to sheep clients.

Methods:
Previous work and 12 interviews were used to form 30 belief statements. These statements and demographic information were sent in a questionnaire to vets (n=515) registered with the RCVS in 2012. An exploratory factor analysis was conducted on the respondents' belief statements to identify factors of vets beliefs. A beta regression model was built to identify influential factors associated with the time vets spent in an advisory role.

Results:
Response rate was 31%. Median time spent by vets in advisory role was 20% (IQR=5-50). A total of 65% of vets believed that they provided a good service to their clients but only 53% considered that they understood their clients' needs and 80% of vets acknowledged that they did not see their clients sufficiently often. The 30 belief statements were reduced to 3 factors: vets motivation (Cronbach α=0.8), their perceived confidence (0.7) and their perception of external factors (0.6). Factors contained 10, 4 and 4 items respectively.Vets with higher self-reported confidence in their sheep expertise, higher motivation of their current services and stronger normative beliefs reported spending significantly more time in providing advisory services

Conclusions:
The study results suggest 3 key factors 'motivation 'capability and 'opportunity' underlying veterinarians' beliefs about the preventive services they provide. There was some discrepancy in the associated beliefs.

Relevance:
The results provide a framework to understand factors underlying the current behaviour of sheep vets in the UK in order to promote/facilitate change.

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The future of UK farm animal veterinary practice in a changing business landscape

Katherine E. Adam[1], Sarah Baillie[2], Jonathan Rushton[3], [1]Scotland's Rural College, Inverness, United Kingdom; [2]University of Bristol, Bristol, United Kingdom; [3]Royal Veterinary College, Hatfield, United Kingdom. Contact: katherine.adam@sruc.ac.uk

Purpose: Major changes are occurring in the UK farm animal veterinary sector in response to an evolving business landscape. In particular, concerns have been raised about insufficient numbers of veterinary graduates entering farm animal practice, leading to a shortfall in service provision for farmers and government and potentially compromising animal health, welfare and food safety. The study aimed to provide an evidence base for strategy development to ensure that the UK veterinary profession is able to provide sustainable production animal health services.
Methods: A sequential, mixed methods research approach was used, consisting of three phases: a spatial assessment of veterinary coverage of cattle; a cross-sectional study to identify factors associated with vets remaining in farm practice and a series of business case studies of rural veterinary practices.
Results: The quantitative results indicate that there is no overall shortage of veterinary practices or of graduates willing to work with farm animals. Instead, innovative business management is required in private practices to retain experienced farm animal practitioners and adapt to a declining livestock population and changing farming systems. Examples from the case studies include a robust system of support for new graduates, consolidation through practice mergers, increasing species specialisation and the formation of group and corporate practices to share knowledge and provide business support.
Conclusions: The relationship between vets, farmers and government is being redefined with the increasing provision of public animal health services by private businesses and new models for service delivery must meet the needs of all stakeholder groups.
Relevance: Similar concerns about the future of veterinary service delivery to agriculture have been raised in other countries and the study provides a framework for addressing these issues.

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Strategic alliances in animal health: The Technical Cooperation Agreement between the Official Veterinary Service and the University in the Rio Grande do Sul state / Brazil

Diego V. Santos[1], **Luis G. Corbellini**[1], André M. R. Correa[2], Antônio A. R. Medeiros[1], Gustavo Machado[1], Gustavo S. Silva[1], Eduardo F. Costa[1], Waldemir Santiago Neto[1], Fernando H. S. Groff[2], Bernardo Todeschini[3], [1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil; [2]Secretaria da Agricultura e Pecuária do Rio Grande do Sul, Porto Alegre, Brazil; [3]Ministério da Agricultura, Pecuária e Abastecimento, Porto Alegre, Brazil. Contact: luis.corbellini@ufrgs.br

Purpose: The OIE has been stressing on veterinary education as a pillar for solidness of animal health programs. This study details strategic alliances built to promote sustainable, long-term capacity building of the Veterinary Services of state of Rio Grande do Sul (RS), Brazil.
Methods: a Technical Cooperation Agreement (TCA) was signed in 2011 by the Official Veterinary Services of RS, the Veterinary Epidemiology Laboratory of the Federal University of RS and Private Regional Animal Health Fund. The TCA comprised three sections: (1) technical consultancies in veterinary epidemiology area, (2) development of epidemiological researches and (3) continuing education of official and private veterinarians on data analysis and use of epidemiological tools.
Results: So far, 14 consultancies were concluded, including the construction of the Ovine Health Official Program, the risk assessment on the validity period of Equine Infectious Anemia test, and , prevalence and risk factors analysis for IBR, BVD and Neosporosis. In addition, two risk analysis and a multi-criteria analysis are ongoing. On continuing education TCA is offering 360-h post graduation course, stratified in basic, intermediate and advanced levels aiming to reach the majority of veterinarians linked to animal health programs, which has trained 150 professionals to date.
Conclusions: The TCA has created a stable relationship between the stakeholders of major influence on the improvement of Animal Health Services of RS. Furthermore, it generated synergy by bringing together knowledge from different sectors to create solutions for actual to animal health issues of RS. This ambience has been the driving force which allowed the TCA to exceed strictly formal aspects to become a real partnership which allowed broader discussions on a common agenda. Finally, its development has allowed that qualitative progress of both of Veterinary Services actors and academics scholars occurs within a coordination environment joining scientific production and actual on-field demands.
Relevance: Development of TCA reuniting relevant animal health related bodies to create synergy on research and continuing veterinary education.

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Creating owner demand for animal health service provision

Laura Skippen[1], **Polly Compston**[2], Klara Saville[1], Aurelie Thomas[1], [1]The Brooke, London, United Kingdom; [2]The Brooke, London, United Kingdom. Contact: polly.compston@the brooke.org

Purpose: The Brooke works internationally to improve the welfare of working equids through strengthening animal health service provision among other activities. Millions of working equids in low-income countries, despite being essential to many rural and urban livelihoods, often lack appropriate healthcare. The Brooke's interventions have trained many animal health service providers (SPs) to a good standard. However, within some Brooke initiatives well-qualified SPs have been unable to maintain a business due to lack of demand for their services. Community engagement work with owners has focused on training owners to recognise poor health but it does not inevitably follow that owners choose the best available SPs.

Methods: A workshop during a meeting of senior vets from 7 Brooke country programmes discussed owner demand for SPs. Each country programme described successes and challenges in forging links between owners and SPs to improve service provision uptake.

Results: Successes were reported when 1) owners had the opportunity to choose a preferred SP, facilitated through SP participation in equid-owner community meetings; 2) Brooke policy is to refer owners to SPs rather than providing free services; 3) owners use word of mouth recommendations; 4) key opinion leaders in communities led change; 5) SPs and owners are trained with the same messages through established institutions.

Conclusions:

Challenges remain in converting knowledge obtained in training into practice. Location is important: lack of community in urban areas can make owner initiatives difficult. Owners currently perform some procedures themselves: defining activities that require an external SP from those requiring owner capacity building is required. The low status of working equids, especially donkeys, among owners exacerbates these challenges.

Relevance: Economic arguments for improving equid welfare, thus increasing productivity, are frequently used. However these discussions did not identify this as a useful argument. An important future component of designing healthcare interventions for working equids must be to develop strategies to identify and resolve reasons for a lack of demand for services.

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Caribbean Veterinary Information System (C-VIS), a pilot GIS platform for regional Avian Influenza surveillance

Eva M. De Clercq[1], Bryan Sanford[2], Els Ducheyne[3], Cedric Lazarus[4], Pastor Alfonso[5], Mark Trotman[2], Nonito Pages[1], Desmond Ali[6], Victor Gongora[7], Davic Chavernac[8], Renaud Lancelot[8], Jennifer Pradel[1], [1]CIRAD, Petit Bourg, Guadeloupe; [2]Veterinary Services, St Michael, Barbados; [3]AviaGIS, Zoersel, Belgium; [4]Food and Agriculture Organization of the United Nations, St Michael, Barbados; [5]Centro Nacional de Sanidad Agropecuaria, Mayabeque, Cuba; [6]Caribbean Poultry Association, St Augustine, Trinidad and Tobago; [7]Belize Poultry Association, San Ignacio, Belize; [8]CIRAD, Montpellier, France. Contact: eva.de_clercq@cirad.fr

Purpose: The Caribbean is a complex region particularly vulnerable for animal and zoonotic disease emergence and spread. Situated along migratory birds' flyways, the region is at high risk of Highly Pathogenic Avian Influenza (HPAI) strains introduction from North America, where HPAI emerged early 2015. This threat is important in the Caribbean, as poultry production is the most rapidly growing subsector, and some countries have the capacity to be self-sustaining in poultry meat production. Though animal health surveillance is implemented in the countries, the collection of georeferenced data, their management and their analysis is poorly developed, and not fit for epidemiological studies or risk mapping. We aim to provide the official veterinary services (VS) with tools to alleviate the lack of manpower, competence and databases as well as gaps in geographic detail, as evidenced by preliminary surveillance network assessments conducted in the region in 2008-12. The tools are developed along with the regional HPAI surveillance by the Caribbean Animal Health Network (CaribVET).
Methods: A Caribbean Veterinary Information System (C-VIS) is being developed to optimize collection and systematic organization of georeferenced data using smartphones or tablets, ensuring homogenous data collection and topographic integrity. It will use open source software such as KoboToolbox®, QGIS® and VECMAP ®. Online data storage and sharing will be provided by a GeoNetwork platform. An educational programme has been planned to increase basic knowledge on GIS through a monthly newsletter and the organization of regional workshops.
Results: A protocol has been developed to formalize the regional organization of the data collection, centralization, analysis and reporting at the regional level.
Conclusions: These tools will be integrated in the regional early warning systems for the surveillance of HPAI and other emerging diseases with a similar epidemiology, such as West Nile or Saint Louis encephalitis. It will also provide opportunities to develop the national GIS capacities.
Relevance: The technology and know-how can be transferred to other developing regions with limited resources.

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Changing the paradigm: investing in veterinary leadership

Agus Lelana[1], John P. Weaver[2], Joko Daryono[2], Jonathan Happold[2], Krisnandana Krisnandana[3], Pudjiatmoko Pudjiatmoko[3], Karen Rodrigues[4], **Jenny-Ann Toribio**[4], [1]Institut Pertanian Bogor, Bogor, Indonesia; [2]Australia Indonesia Partnership for Emerging Infectious Diseases, Jakarta, Indonesia; [3]Ministry of Agriculture, Jakarta, Indonesia; [4]University of Sydney, Sydney, Australia. Contact: jenny-ann.toribio@sydney.edu.au

Purpose:
In Indonesia central government provides policy but field veterinary services are delivered by 500 autonomous districts. There is no direct line management of field services and disease prevention and control has become fragmented. Various internal and international reviews identified the need for a more coordinated 'chain of command'. Improved skills in veterinary leadership were recognised as being paramount. This project is developing skills in veterinary leadership to deliver effective national policies and programmes for disease prevention and control.
Methods:
A 'Trainer of Trainers' approach was applied. Six Indonesian veterinary academics took part in a veterinary management course at the University of Sydney. A contextualized veterinary leadership curriculum was then developed jointly by Indonesian academics and University of Sydney staff with three themes - Personal Leadership, Leading Others and Organisational Leadership.
Critically the curriculum is presented not as one dimensional didactic format but uses experiential learning involving directed self study, project work, individual reflection, group discussions and role plays.
Indonesia Veterinary Leadership (IVL) courses have been delivered with support from the Australia Indonesia Partnership for Emerging Infectious Diseases. Feedback from participants and from workplace line managers and senior managers was collected and evaluated in a formal survey process.
Results:
The IVL course has trained 9 trainers and 52 middle managers; it has been a resounding success with participants, mentors and line managers all describing the course as effective, innovative and life changing (>90% on review). Participants feel more confident and competent and ready to take on leadership roles. These young managers have already brought changes to their work places; they will become the future leaders.
Conclusion:
The IVL course has changed the training approach and is contributing to a shift in leadership paradigm of government veterinary services.
Relevance:
It has developed next generation veterinary leaders with vision, communication and motivational skills, and the ability to drive change.

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Framework for the design, improvement and documentation of surveillance systems

Fernanda C. Dórea[1], Arianna Comin[1], Birgit Schauer[2], Lucy Snow[3], Marta M. Avilés[4], Linda Hoinville[5], **Ann Lindberg**[1], [1]National Veterinary Institute, Uppsala, Sweden; [2]Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany; [3]Animal and Plant Health Agency, Surrey, United Kingdom; [4]Universidad Complutense de Madrid, Madrid, Spain; [5]Royal Veterinary College, London, United Kingdom. Contact: ann.lindberg@sva.se

Purpose: Surveillance for animal diseases aims to protect animal and public health. Those tasked with surveillance decisions, however, have to navigate through the diversity of advice and published guidelines, often lacking tools to help them choose the best methods. The objective of this work was to develop a framework for surveillance design to increase the quality and cost-effectiveness of animal health surveillance activities, as well as increase transparency in underlying design decisions.
Methods: A surveillance design framework was developed under the RISKSUR project (http://www.fp7-risksur.eu/) with the aim of structuring the process of designing, documenting and re-designing animal health surveillance. Informed by extensive reviews of the literature, as well as a review of existing surveillance systems in Europe, the framework supports the design of surveillance at two levels, the surveillance system and its surveillance components.
Results: When designing a surveillance component the user is guided through ten steps: target population, defining disease suspicion, surveillance enhancements, testing protocol, study design, sampling strategy, data generation (sample collection), data/sample transfer, data translation (sample analyses), epidemiological analyses, dissemination of results and surveillance review. Through each of these steps, the user is presented with the surveillance decisions he or she needs to make and document. The user is given advice and information gathered from the literature and expert opinion, as well as links to any relevant statistical and epidemiological tools. A WIKI website allows users to contribute and keeps advice dynamic and peer-reviewed.
Conclusions: The output of the process is a surveillance design informed by current epidemiological knowledge and tools as well as full documentation of the design and decisions made. Moreover, the framework is linked to the RISKSUR tool for evaluation of surveillance components (EVA tool).
Relevance: Together, the two frameworks promote a structured and systematic approach for surveillance design and evaluation, promoting comparable, transparent and cost-effective surveillance.

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Development of a tool for prioritising exotic disease threats to Scotland

Paul R. Bessell[1], Lisa A. Boden[2], Ian G. Handel[3], Harriet K. Auty[4], Barend M. D. C. Bronsvoort[1], [1]The Roslin Institute, Edinburgh, United Kingdom; [2]The University of Glasgow, Glasgow, United Kingdom; [3]University of Edinburgh, Edinburgh, United Kingdom; [4]SRUC, Inverness, United Kingdom. Contact: paul.bessell@roslin.ed.ac.uk

Purpose:
Countries such as Scotland that are free from many notifiable livestock diseases remain at risk of introduction of these diseases. This risk changes as the global distribution of diseases change and as pathways for introduction evolve. However, the impact in Scotland will be different for each disease due to properties of the pathogen itself or the ability of the environment to support the pathogen. So in prioritising exotic diseases one must consider both the risk of introduction and the potential impact. Here, we develop a framework to combine these risks in a single tool for prioritising livestock disease threats to Scotland.

Methods:
The model framework combines a semi-quantitative model on the risk of incursion of exotic diseases with a model of the potential impact of the disease following introduction. The model of risk of introduction is based on the global distribution of the disease, trade linkages and pathways of introduction. The model of impact combines potential spread, the size of the at-risk population and indices of impact on animal welfare, society, human health and international trade.

Results:
Of the 20 priority livestock diseases identified, the model identifies that foot and mouth disease is the greatest priority in terms of the combination of risk of introduction and disease impact, the impact is in part a result of the large numbers of susceptible animals of three species (cattle, sheep and pigs). Avian influenza and bluetongue virus are also at high risk of introduction and high impact but the risks of introduction of all diseases changes as their global distribution changes. Disaggregation of the results by industry sector demonstrates that diseases generally have the greatest impact in the pig sector rather than the diseases of the cattle and sheep sector.

Conclusions:
Using a simple metric for comparing threats, a tool has been developed for disease monitoring and prioritisation. Further adaptations will incorporate additional pathways of infection such as illegal imports and human movements.

Relevance:
This model provides a valuable tool for government and livestock industries for prioritising limited resources in the face of multiple disease threats.

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Evaluation of a surveillance system implemented to provide early detection for animal health hazards

Katharina D. C. Stärk[1], Manon Schuppers[1], Martina Brägger[2], Sandra Balmer[3], Annette Nigsch[3], Barbara Häsler[4], Daniela Hadorn[3], [1]SAFOSO Inc., Bern-Liebefeld, Switzerland; [2]Landert Brägger Partners, Zurich, Switzerland; [3]Federal Office for Food Safety and Veterinary Affairs, Bern, Switzerland; [4]Royal Veterinary College, London, United Kingdom. Contact: katharina.staerk@safoso.ch

Evaluation is increasingly used as part of the life cycle of surveillance systems to assure that objectives are met and available resources are used effectively. A substantial portfolio of activities, tools and programmes was introduced in Switzerland for the early detection of signals caused by animal health hazards. The legal basis for this early detection system was passed in 2013. Since, selected elements of this programme as well as its over-all performance were formally evaluated. The evaluation built on recommended good practice both from the veterinary field as well as from general good practice in evaluation from other sectors.

The activities covered by the evaluation were numerous and diverse. The main focus was on syndrome detection, and all reporting was on a voluntary basis. Most livestock species were included. The evaluation was meant to be formative, i.e. to inform and improve the next phase of programme implementation and operation. System attributes were used as recommended in available evaluation guidelines. These attributes included a.o. coverage, representativeness, sensitivity and acceptability. Additionally, economic evaluation was attempted including cost-effectiveness assessment. However, because evaluation attributes had not been defined at the start of programme implementation, the capacity to collect the required data post hoc was limited, and the evaluation remained largely qualitative. Assessment of stakeholder opinion was an integral part of the evaluation. Beneficiaries of each early detection component were identified and included as stakeholders. Data were collected using online questionnaires, individual interviews and group workshops.

Results varied for individual system components reflecting the diverse nature and approaches implemented. The main challenges were identified in aligning what different stakeholders expected from a system, in quantifying the utility of a component and in assuring the sustainability of voluntary engagement in syndrome reporting. The evaluation of the over-all programme demonstrated that system borders were difficult to draw as many activities informed surveillance as well as control.

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Stratification of veterinary antimicrobial sales per species - the Swiss example.

Luís P. Carmo[1], Gertraud Schüpbach-Regula[1], Cedric Müntener[2], Anne Chevance[3], Gérard Moulin[3], Ioannis Magouras[1], [1]University of Bern, Bern, Switzerland; [2]University of Zurich, Zürich, Switzerland; [3]Anses - French Agency for Food, Environmental and Occupational Health & Safety, Paris, France. Contact: luis.gomesdocarmo@vetsuisse.unibe.ch

Purpose:
Despite the ongoing development of European monitoring systems on antimicrobial (AM) sales, a fundamental piece is still missing: to monitor consumption on a species level. This has been recommended by several institutions and was set as a future objective for the ESVAC project (European Surveillance of Veterinary Antimicrobial Consumption). Economic, infrastructural, political and confidentiality issues have been impeding the development of such systems in most countries. The aim of this study is to propose alternative methods to stratify AM sales per species, using Swiss data as an example.

Methods:
In Switzerland, yearly sales data at package level are collected since 2004. Veterinary medicinal products can be divided into two groups: products licensed for one (monospecies/ mSp) and for multiple species (MSp). While for mSp products the attribution of amounts sold for use in each species is straightforward, for MSp medicines modeling methods are needed to estimate species repartition. Three approaches are suggested and compared: (1) in the equal distribution approach (EDa), sales of MSp products are distributed evenly for every species each product is licensed for. (2) The repartition based on total body mass (BMa) stratifies the consumption of the MSp products weighting the representativeness of each species total body mass. (3) Finally, the Monte Carlo simulation model (MCa) assigns AM sales per species based on data generated from a study performed in 2004-2005 which analyzed prescription patterns in Switzerland.

Results:
Average AM sales (2006-2013) were calculated for each species feeding the models (EDa; BMa; MCa) with Swiss data. Cattle/calves (43.2%; 60.6%; 60.0%) and pigs (44.8%; 35.6%; 31.1%) received most of the AMs sold in Switzerland. Poultry have the smallest share (1.0%; 0.4%; 1.0%), even less than pets (4.5%; 1.8%; 2.7%), horses (2.3%; 0.8%; 1.6%) or small ruminants (4.2%; 0.8%; 2.7%).

Conclusions: Generated estimates allow monitoring of AM consumption trends per species.

Relevance:
This helps to improve management strategies and to analyze the evolution of antimicrobial resistance in relation to the use of AMs.

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Evaluating the ability of aberration-detection temporal algorithms to detect simulated disease outbreaks in routinely collected cattle mortality data

Rahel Struchen[1], Jakob Zinsstag[2], Flavie Vial[1], [1]Veterinary Public Health Institute, Bern, Switzerland; [2]Swiss Tropical and Public Health Institute, Basel, Switzerland. Contact: rahel.struchen@vetsuisse.unibe.ch

Purpose:
Mortality data are routinely collected in national livestock identification systems ("Tierverkehrsdatenbank" or TVD in Switzerland). Such data may be used for the real-time detection of mortality clusters potentially indicative of a disease outbreak. We evaluated the performance of temporal outbreak detection algorithms retrospectively applied to Swiss cattle mortality data.
Methods:
We extracted the daily number of on-farm cattle deaths from the TVD between 2009 and 2011. Negative binomial regression models were used on the historical data to simulate baseline time-series, into which we injected simulated disease outbreaks of different size, duration and shape (n=60,000). The performance of Shewhart, cumulative sum (CuSum) and exponentially weighted moving average (EWMA) control charts were assessed based on several measures including sensitivity, false positive rate (FPR) and time to detection (TTD). Control charts were evaluated separately, under different combination rules, and using different detection limits.
Results:
Sensitivity and FPR generally decreased with increasing detection limit, but the strength of this effect was not the same for all three algorithms and depended on the size and shape of the outbreaks. EWMA exhibited overall the highest sensitivity. The Shewhart algorithm was the best performer in terms of FPR, but required a longer TTD compared to EWMA. CuSum was between Shewhart and EWMA for most performance measures. The combination rules (two or three out of three algorithms, respectively) only marginally lowered FPR without improving the system's overall performance.
Conclusions:
None of the algorithms showed a superior performance in detecting outbreak signals. For the prospective use of cattle mortality data in Switzerland, output from both EWMA and Shewhart should be concomitantly used by decision-makers when interpreting statistical alarms.
Relevance:
Surveillance systems have intrinsic statistical trade-offs, as illustrated by the trade-off between sensitivity, FPR and TTD that we observed. Algorithms need to be carefully optimised for a particular data stream before their integration into a national early detection system.

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Evaluation of the nationwide serological surveillance for paratuberculosis using individual based simulation model

Takehisa Yamamoto[1], Sachiko Moriguchi[1], Yoko Hayama[1], Sota Kobayashi[1], Arata Hidano[2], Toshiyuki Tsutsui[1], [1]National Institute of Animal Health, Tsukuba, Japan; [2]Massey University, Palmerston North, New Zealand. Contact: mtbook@affrc.go.jp

Purpose: In Japan, a nationwide serological surveillance targeting all dairy and beef breeding cattle had been conducted for paratuberculosis since 1998. For positive farms, all positive animals were culled and a series of follow up tests were applied as control measures. Since the effectiveness of these measures have not yet been evaluated, we developed a novel stochastic individual based model to elucidate the effect of these measures to the spread of paratuberculosis within farms.
Methods: Dairy and beef farm was modeled separately with the different life length and production manners. Infection stages were defined as susceptible, latent, subclinically infected and clinically affected. Infection routes were defined as vertical (in utero), dam-calf horizontal and other horizontal infection via contaminated environment. Clinical surveillance was assumed to detect only clinically affected cattle while routine surveillance was assumed to also detect asymptomatic animals developing antibody (for ELISA) or antigen (for real time PCR). In case of any infected animal detected, 5 step follow-up tests will be applied; first three were with 4 months intervals, latter two were with 12 months interval. Using the model, disease transmission within a farm after the introduction of one infected parity one cattle was monitored for 40 years with one month intervals with 1,000 runs. Simulations with variety of farm type (dairy and beef breeding), farm size (50, 200 and 500 adult cattle) and different interval for routine and follow up surveillance were examined.
Results: Regardless of farm size, type or surveillance strategy, around 90% of runs lacked secondary infection. Among the runs with secondary infection, large farms had more runs with infected cattle after 40 years from introduction. As a result of comparison between simulation with current surveillance system and with that assuming no serological surveillance, the current surveillance seemed greatly reducing the scale of infection. Although, the complete freedom of disease seemed difficult to be accomplished solely by increasing frequency of surveillance especially in large farms.

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Effectiveness of risk based surveillance for small ruminant brucellosis in endemic countries

Sabina Seric-Haracic[1], Nihad Fejzic[1], Semra Cavaljuga[2], Mo Salman[3], [1]University of Sarajevo Veterinary faculty, Sarajevo, Bosnia and Herzegovina; [2]University of Sarajevo Faculty of Medicine, Sarajevo, Bosnia and Herzegovina; [3]Colorado State University, Fort Collins, CO, Contact: sabina.seric-haracic@vfs.unsa.ba

Purpose: Endemic brucellosis poses significant problem in developing countries such as Bosnia and Herzegovina (BiH) for animal health and production, and even more for public health sector. This study seeks to assess applicability of risk based surveillance for small ruminant brucellosis in comparison to standard population based “test and slaughter” approach. Methods:Stochastic scenario tree models representing active surveillance component (annual surveys) were simulated over the period of 8 years on small ruminant population data from BiH. High prevalent area and transhumance were considered as risk factors effecting flock and within flock prevalence in different exposure groups. Risk based model included targeted sampling of flocks exposed to both or one risk factor. Three different start flock prevalence and 3 annual among flock spread rates were considered. Simulations and sensitivity analysis were done using @Risk with 1000 iterations per each year. Model outputs were probability distributions of identified and unidentified diseased flocks and also identified, unidentified and falsely identified non-diseased flocks, at the end of each year. Direct implementation costs of population and risk based surveillance strategies were assessed using average estimates of model outputs. Results:According to our results population based “test and slaughter” strategy despite relatively high annual proportion of sampled flocks, provides identification only about half of diseased flocks on annual level. Risk based “test and slaughter” was far superior in reducing flock prevalence, however its efficacy depends on availability and quality of data on flocks exposure to different risk factors. Conclusions:Science based modeling estimates can promote purposefulness and quality of specific surveillance programs during design and planning, as well as later through estimating efficiency of their implementation. Relevance:Stochastic approach allows founded estimates, especially if good and complete data are not available and expected outputs of disease surveillance is influenced by many uncertainties, which is often the case in developing countries.

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Evaluation of Caprine Arthritis-Encephalitis Surveillance and Control in Switzerland.

Beat Thomann, Laura C. Falzon, Hans-Rudolf Vogt, Giuseppe Bertoni, Gertraud Schuepbach, Ioannis Magouras, University of Bern, Bern, Switzerland. Contact: beat.thomann@vetsuisse.unibe.ch

Purpose: Caprine arthritis-encephalitis virus (CAEV), a group of small ruminant lentiviruses (SRLVs), may cause important economic losses in goat production. In Switzerland, an eradication program initiated in the 1980s has succeeded in reducing the seroprevalence to ~1%. However, current surveillance and control is still associated with high costs, whereas CAE as a clinical manifestation is no longer an issue. Considering these developments, the specific aims of this project were to: (i) estimate the current CAEV prevalence; (ii) determine risk factors (RF) associated with CAEV infection; and (iii) predict disease dynamics of CAEV for proposal of alternative intervention strategies.
Methods: Initially, a census on Swiss goat farms was carried out in 2012. In contrast to previous prevalence studies, blood samples were tested using a newly developed diagnostic test that distinguishes CAEV genotypes from other SRLVs. Then, a mail questionnaire was developed and sent to all 41 CAEV positive farms and 300 control farms. A logistic regression model was built to determine RF associated with CAEV positive farm status. Finally, a deterministic infectious disease model, assuming transmission of CAEV through colostrum and within-herd transmission rates from 0% to 20%, was developed to predict the spread of the infection.
Results: The estimated herd- and animal-level prevalences for CAEV were 0.38% and 0.06%, respectively. CAEV seropositive goats had a median age of 4 years and 1/5 (20.6%) of them were dwarf goat breeds. No statistically significant RF ($p \leq 0.05$) could be detected, but “purchase of female goats” was marginally associated ($p=0.09$) with CAEV positive farm status. The infectious disease model predicted future animal-level prevalences ranging from 0.04% to 2.18% within the next 20 years.
Conclusions: These results show that CAEV prevalence remains low and is not expected to increase considerably, even without the implementation of control strategies.
Relevance: These estimates have been communicated to the policy-makers and stakeholders involved, allowing for science-based and optimized decision-taking on future implementation of CAE control strategies in Switzerland.

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Investing in the right research: Adapting research prioritisation methods from medicine to veterinary medicine

Rachel S. Dean[1], Katherine Cowan[2], Marnie Brennan[1], Sharon Mickan[3], [1]University of Nottingham, Loughbourough, United Kingdom; [2]Katherine Cowan consulting Limited, St Leonards-on-Sea, East Sussex, United Kingdom; [3]Centre for Evidence-Based Medicine, Oxford, United Kingdom. Contact: Rachel.Dean@nottingham.ac.uk

Patient and public involvement (PPI) in medical healthcare has become an important part of the prioritising, planning and delivery of research which is cost effective, impactful and relevant to the end user. The James Lind Alliance (JLA) involves patients and healthcare professionals to identify research priorities for medicine. It is important that the limited amount of money available for veterinary research is directed to answer the most relevant questions, if significant cost effective improvements in patient health and welfare are to be made. The aim of this study was to adapt the priority setting partnership (PSP) framework used by the James Lind Alliance and apply it to the veterinary setting. The JLA protocol was adapted to identify research priorities in the treatment of cats with Chronic Kidney Disease (CKD). A list of questions about treatment of CKD was obtained from cat owners and veterinary surgeons via and online survey and the evidence-base was searched to identify which questions were 'treatment uncertainties'. The treatment uncertainties were then prioritised in a workshop of veterinary surgeons and cat owners. Three hundred veterinary surgeons and cat owners provided 651 questions; 382 were about treatment. After duplicates were combined, 28 treatment uncertainties were identified and considered in the PSP workshop. The workshop participants agreed on a shared list of 28 prioritised questions regarding the treatment of CKD. The number one prioritised question concerned the single most cost effective treatment modality for this disease. The JLA framework was successfully adapted to a veterinary setting and highlighted important research questions for which there is currently no evidence., To ensure money is spent in a targeted fashion in veterinary research further participation from stakeholders is needed.

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Improving methods for downscaling livestock census data

Gaëlle Nicolas[1], Tim P. Robinson[2], William G. R. Wint[3], Giulia Conchedda[4], Giuseppina Cinardi[4], Marius Gilbert[1], [1]ULB - Université Libre de Bruxelles, Brussels, Belgium; [2]International Livestock Research Institute (ILRI), Nairobi, Kenya; [3]University of Oxford, Oxford, United Kingdom; [4]Food and Agriculture Organization of the United Nations (FAO), Rome, Italy. Contact: gaelle.nicolas6@gmail.com

Purpose:
Global change is likely to have a major impact on emerging infectious disease, altering the spatiotemporal patterns of transmission, with wide-ranging implications for populations and ecosystem health. Predicting the spatial pattern of a transboundary disease is becoming of huge interest worldwide but is thwarted by incomplete knowledge of livestock distribution. In 2007, the Gridded Livestock of the World (GLW 1) database provided the first modelled livestock densities of the world. It was adjusted to match official FAOSTAT national estimates for the reference year 2005, at a spatial resolution of 3 minutes of arc. Recently, GLW 2 was published, which included higher resolution (a 30 arc-second), more recent livestock census statistics and bootstrapped estimates which allowed inferences to be made regarding uncertainties in the predicted values. Both version was based on stratified linear multiple regressions. We aimed to improve the GLW by evaluating alternative modelling options.
Methods:
We compared the use of different dependent variables (livestock: density vs numbers per person) and of different modelling methods (stratified regression (SR) vs. Random Forest machine-learning technique (RF), and we complemented this by evaluating the benefit of modelling at high spatial resolution with models of cattle in Africa and chickens in Asia. We evaluated the model through the accuracy of the predictions in its downscaling and gap-filling capacities.
Results/ Conclusions:
Time processing was divided by 10. RF models provided consistently better predictions than the SR method for both modelled species and continents. Modelling animals per capita instead of absolute densities avoided the prediction of non-zero densities in unpopulated locations, but tended to overestimate livestock numbers in peri-urban areas. The relative merits of modelling at the different spatial resolutions varied according to the scale.
Relevance:
Distribution maps for all species on the world are under progress. Dissemination will be done through the Livestock Geo-Wiki at global (10km resolution) and continental scale (1km resolution).

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Use of multiple imputation for dealing with missing values in observational studies: a case study and simulation

Ian Dohoo[1], Ulf Emanuelson[2], [1]University of PEI, Charlottetown, PE, Canada; [2]Swedish University of Agricultural Sciences, Uppsala, Sweden. Contact: dohoo@upei.ca

Purpose

The purpose of this study was to investigate the use of multiple imputation as an alternative to complete-case analysis for dealing with missing values. A study of factors affecting a dairy farmer's perception of the importance of various mastitis control procedures provided the data. Perception of the importance of keeping cows standing after milking was the outcome of interest and a variety of factors (eg age, participation in a mastitis control program, etc) were predictors of interest. Attitudes toward other mastitis control procedures were used (as auxiliary variables) in the imputation process.

Methods

In the original data (n=269) missing values were primarily in the outcome variable (n=74). Results from a complete case analysis were compared to those from a multiple imputation process. In order to determine which set of results was most likely to be “correct”, a simulation was carried out in which a complete data set was created (replacing missing values with imputed values). Missing outcome values were then generated (1000 times) under a variety of missing data mechanism assumptions. Starting with the same complete data set, the simulation procedure was then extended to evaluate the impact of various levels and types of missing data among predictors. Comparisons of the complete case and multiple imputation analyses included: % bias, mean SE of estimates, SD of individual estimates and proportion of estimates within 20% of the “truth”.

Results and Conclusion

Imputation was of little use in dealing with the problem of missing outcome values, but in all cases where missing values were in predictor variables, analyses based on multiple imputation produced superior results to those derived from a complete case analysis.

Relevance

Missing data are a common problem in epidemiologic studies and methods that are commonly superior to complete case analysis are now widely available. However, limitations to the use of multiple imputation do exist and will be presented.

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Filling gaps in notification data: a model-based approach applied to campylobacteriosis cases in New Zealand

Ermias Amene[1], Beverley Horn[2], Ruth Pirie[2], Rob Lake[2], Dörte Döpfer[1], [1]University of Wisconsin-Madison, Madison, WI, [2]Institute of Environmental Science and Research Ltd, Christchurch, New Zealand. Contact: amene@wisc.edu

Purpose

Disease notification regarding demographic and movement of the cases can inform about the epidemiology and risk factors for the disease. This study explores the use of Fully Bayesian Specification (FBS) and Multiple Imputation(MI) models to fill risk factor data gaps. As a test case, the status of overseas travel as a risk factor for campylobacteriosis notification in New Zealand has been studied.

Methods

A data on short term international travel, campylobacteriosis notification and potential predictors of overseas travel have been obtained from national databases. Two methods, namely FBS and MI, were compared regarding predictive performance for various levels of artificially induced missingness of overseas travel in the dataset. Predictive performance of the models was assessed through *Brier Score, Area Under the Curve* and *Percent Bias* of regression coefficients

Results

There was no difference in the predictive performance of the FBS and MI models whenever the missing rate was less than 10%, but the FBS performed better than MI at a higher rate of missingness. The added advantage of using a Bayesian approach is that the model's prediction can be improved whenever new information arrives.

Conclusions

Through plausible assumptions regarding the nature of missing data mechanism, the FBS offers a flexible approach for data augmentation particularly when the missing rate is very high. Due to a strong Missing At Random assumption, the FBS may not be the optimal approach for prediction for a dataset including missing values.

Relevance

There has been a need for quantitative tools to leverage from and describe the full extent of available information while acknowledging data gaps. Using a dataset of notified campylobacteriosis cases in New Zealand, this report explores the application of a Bayesian approach to fill data gaps for risk factor information. The methods described can be applied to other related global health challenges concerning missing data. Moreover, identifying and quantifying travel-associated campylobacteriosis and other infectious diseases will help prioritize intervention strategies for the control and prevention of the diseases.

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New for the epi-toolbox: confidence interval for the population attributable risk

Sarah Pirikahu[1], Geoff Jones[1], **Cord Heuer**[2], [1]Massey University, Palmerston North, New Zealand; [2]Massey University, Palmerston North, New Zealand. Contact: c.heuer@massey.ac.nz

Purpose: The population attributable risk (PAR) measures the public health impact of the removal of a risk factor. A gap in the epi-toolbox was discovered when analysing a cohort study of the population impact of sero-conversion on illness due to leptospirosis in a population of abattoir workers. No standard is available for the calculation of a variance of the estimated PAR. Hence no valid method exists for the confidence interval of PAR. To fill this knowledge gap, we developed four methods and validated them by simulation: Delta method (linearization), Bootstrap, Jacknife, and Bayesian.
Methods:With a given PAR, total sample size N (380), probability of disease for exposed (p) and unexposed (q) groups and the prevalence of exposure (e) in the population, a population was simulated (x 10,000) using multinomial distributions for each of the 4 cells of a 2x2 table. This provided the reference of true (nominal) confidence intervals. The proportions of confidence intervals generated by the four methods that included the true PAR (coverage), was the criterion for evaluating each method's performance under various scenarios of sample size and p, q, and e. Scenarios included large ranges of p, q and e, small counts, expected cell size<5, and performance under appropriate sample size.
Results: All methods except Bayesian had some parameters combinations (p, q, e) where the actual coverage was less than the nominal. The Bayesian method was superior as the coverage was always above the nominal interval for all values of e and for low cell values. Confidence intervals of all methods were above coverage when sample size was adequate. The Bayesian solution is available at https://spirikahu.shinyapps.io/PARCIs/
Conclusions: The Bayesian approach produced superior intervals in terms of percent coverage, but the delta method can be used as a fast alternative estimate in certain situations.
Relevance: The confidence interval calculator for PAR is new and of particular relevance for public health research.

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Estimating historic disease trends from cross-sectional data using combined diagnostic tests

Gustaf Rydevik[1], Glenn Marion[2], Giles Innocent[2], Ross Davidson[3,2], Piran C. L. White[4], Michael R. Hutchings[3], [1]Edinburgh University, Edinburgh, United Kingdom; [2]Biomathematics and Statistics Scotland, Edinburgh, United Kingdom; [3]SRUC, Edinburgh, United Kingdom; [4]University of York, York, United Kingdom. Contact: gustaf.rydevik@roslin.ed.ac.uk

Purpose: We show how to estimate the historic trend of incidence in a population from cross-sectional diagnostic test data collected at a single point in time. We combine two or more quantitative diagnostic tests operating at different time scales, and their test kinetics to estimate the time since infection for the individual, and the historic incidence trend in the population as a whole.
Methods: We used simulated data based on either the UK 2007 bluetongue epidemic, or a situation similar to endemic bovine TB as in the UK. Data were analysed in a Bayesian MCMC framework and inference compared to the simulation parameters.
Results: For bluetongue we found that using a cross-sectional sample of 20 positive animals taken 14 days after the start of the epidemic, tested for viral load and antibody levels, we were able to reconstruct the trajectory of the outbreak up until that point (R^2 of 0.85 compared to the true trend). Further, for bovine TB, a sample of 100 positive animals tested for bacterial load and antibody response would be enough to determine whether the incidence trend up until sampling had been steady, increaseing, or decreasing, with estimated slopes to within 10% of the true values.
Conclusion: We have developed a Bayesian approach that can estimate the historic trend of incidence from cross-sectional samples, without relying on ongoing surveillance. This could be used in endemic settings to evaluate changing disease trends; or in epidemic settings to inform outbreak response.
Relevance: The described approach is generic, applicable to a wide range of human, livestock and wildlife diseases. It can estimate trends in settings for which this is not possible using current methods, including for diseases or regions lacking in surveillance, to recover the pattern of spread during the initial “silent” phase once an outbreak is detected, and for emerging infections. Being able to estimate the past trend of disease from single cross-sectional studies has far-reaching consequences for the design and practice of disease surveillance in all contexts.

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True prevalence estimation under heterogeneity and clustering with an imperfect test

Simon Firestone[1], Nadeeka Wawegama[1], Philip Markham[1], Anna Kanci[1], Megan Schibrowski[2], Sally Oswin[3], Tamsin Barnes[2,4], Timothy Mahony[2], Glenn Browning[1], Mark Stevenson[1], [1]The University of Melbourne, Parkville, Australia; [2]The University of Queensland, St Lucia, Australia; [3]Zoetis Ltd., West Ryde, Australia; [4]The University of Queensland, School of Veterinary Science, Gatton, Australia. Contact: simon.firestone@unimelb.edu.au

Purpose:
Bayesian latent class modelling is well established for estimating diagnostic test sensitivity and specificity using data from animals of unknown disease status. Methods are also available for estimating prevalence under clustering and heterogeneity (clustering involving animals derived from different source populations). In this analysis we combined these methods to estimate the true prevalence of Mycoplasma bovis (a possible cause of bovine respiratory disease) in cattle entering Australian feedlots.
Methods:
Blood was collected at two time-points from 7448 animals entering Australian feedlots in a case-control study of bovine respiratory disease. Serum was tested with a new enzyme-linked immunosorbent assay for Mycoplasma bovis-specific IgG. These cattle were sourced from 867 different locations 13 days prior to entry then kept in 161 pens in 14 feedlots for approximately 42 days (follow-up). True prevalence on entry and at follow-up was inferred using Bayesian latent class modelling. Estimates were re-weighted with sampling fractions of cases and controls for the fully enumerated target population and mixture analyses undertaken to estimate appropriate variance inflation factors (VIF).
Results:
True prevalence of M. bovis was estimated to be 15.0% (95% probability interval [PI]: 11.5, 18.8%) in the target population on feedlot entry and at follow-up had risen to 80.5% (95% PI: 75.7, 85.3%). There was considerable clustering owing to heterogeneity by immediate source on entry (VIF=7.2). At follow-up, clustering by pen (VIF=11.1) was stronger than due to heterogeneity by source (VIF=7.6).
Conclusions:
Heterogeneity of prevalence on entry suggests that the source groups themselves fall into subpopulations. A high rate of infection and clustering by pen was observed after entry into the feedlots.
Relevance:
This is the first study to integrate estimation of true prevalence in the absence of a ‘gold standard’ with characterisation of the nature of clustering and adjustment for its effects. The methods developed will be important when applying new diagnostic tests in studies of animals derived from multiple source populations.

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Bayesian prevalence estimation under misclassification with individual or pooled samples

Matthias Flor[1], Matthias Eckardt[1], Michael Weiss[1], Andrea Ernert[2], Matthias Greiner[1], [1]Federal Institute for Risk Assessment, Berlin, Germany; [2]Charité, Berlin, Germany. Contact: matthias.flor@bfr.bund.de

A reliable estimation of the true prevalence of a pathogen is often pivotal in a number of fields, e.g. animal disease surveillance or the scientific evaluation of health risks. Nonetheless, such estimation processes are subject to certain limitations due to uncertainty or misclassification caused by imperfect diagnostic tests (i.e. when sensitivity or specificity are less than one). In addition, due to economic as well as feasibility constraints, the estimation of an individual prevalence is often based on pooled rather than individual samples, thereby potentially decreasing sensitivity and specificity even further. Recently, Bayesian statistical approaches have been proposed to overcome these problems by integrating *a-priori* information as well as expert knowledge into the estimation process. In the course of this, information about prevalence and test sensitivity and specificity provided e.g. by expert opinion or predecessor studies are converted to probability distributions. These distributions are then updated by new data thus yielding *a-posteriori* estimates of the distributions. Here, we apply a Bayesian modelling framework to prevalence estimation under misclassification based on Markov Chain Monte Carlo (MCMC) algorithms. Furthermore, we present an easy-to-use open source web application based on the statistical programming language R and the cross-platform Gibbs sampler JAGS. Our approach offers a highly flexible tool for statistical analysis due to the simultaneous updating of different statistics with regard to interactively entered parameters and data. Convergence plots provide assistance in evaluating the quality of the *a-posteriori* estimates which reflect the true prevalence. In addition, we propose a method for detecting specific forms of conflict between *a-priori* assumptions and data.

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Estimation of transmission parameters with heterogeneity.

Mart C. M. de Jong, Wageningen University, Wageningen, Netherlands. Contact: mart.dejong@wur.nl

Purpose:
To develop a method to estimate difference in infectivity.
Methods:
To separate the different multiplicative components of a rate parameter, like the transmission rate parameter, in statistics the complementary log log (cloglog) link function is used with generalised linear models(GLMs).
Results:
To see what happens when applying cloglog link in a GLM consider the contact rate (c), and two types of susceptibles with susceptibility on one type being g (and that of the other being 1) and two types of infectives with infectivity of one type being f (and that of the other being 1). The rate parameter is the product of the three parameter components (c, 1 or g, and 1 or f). The equation for the explanatory variables distinguishing two types of individuals with respect to infectivity and susceptibility after applying cloglog link becomes linear i.e. C0+C1.VarS+C2.VarI. In this equation VarS and VarI are the explanatory variables and C0,C1 and C2 are estimated by the GLM. The VarS is the 0/1 variable indicating whether or not the recipient is the one type of susceptible individual for which the parameter is estimated. Then, C0 is an estimate of log(c), C1 an estimate of log(g).
Conclusions:
However, for the heterogeneity in infectivity this is different and to choose VarI so that C2 estimates log(f) is in principle not possible. Why this is and how we can use the GLM to estimate log(f) anyway will be discussed.
Relevance:
Managing infections in animal populations is a key issue in veterinary epidemiology. To do that we estimate transmission parameters taking into account different heterogeneities, i.e. in contact rates, susceptibility, and infectivity. Estimates based on the effect of these heterogeneities are used to reduce transmission by changing the conditions to lower the contact rate, the overall susceptibility, or overall infectivity. As the different aspects of transmission interact in a non-linear manner estimation is only possible when methods are used that can deal with that nonlinearity.

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Analysis of risk factors using life history - a partial membership approach to estimating the risk of liver fluke infestation.

Giles T. Innocent[1], Lucy Gilbert[2], Ed Jones[3], Manuel Sanchez[4], Glenn Marion[1], Iain McKendrick[1], [1]Biomathematics and Statistics Scotland (BioSS), EDINBURGH,, United Kingdom; [2]James Hutton Institute, Aberdeen, United Kingdom; [3]University of Aberdeen, Aberdeen, United Kingdom; [4]SRUC, Inverness, United Kingdom. Contact: giles.innocent@bioss.ac.uk

Purpose:
Liver fluke is a serious disease of cattle and sheep throughout the world. The fluke species most common in Scotland (Fasciola hepatica) requires damp and warm conditions in order to infect new hosts. Around 25% of cattle livers are condemned in Scottish slaughterhouses; this imposes welfare costs on the animal and economic costs on the farmer.

Methods:
Within the UK cattle have all their movements between farms registered. It is therefore possible to reconstruct the life history (in terms of farm residency periods) for any individual animal.
The time spent on each farm was used as a weighting in a partial membership model in which the binary response described whether or not the animal's liver was condemned at slaughter. Indices of wetness and temperature, position in both Northerly and Westerly directions, animal age and sex were all considered as explanatory variables. As part of the model,a stochastic partial differential equation model was fitted to account for spatial autocorrelation between farms close to each other.

Results:
We looked at the life histories for 7858 animals. In total 2068 unique addresses were identified as involved in the raising of these animals. The total number of at risk days that each animal spent on each farm was calculated.
The fitted model associates fluke liver condemnation with animals spending time on farms that have high average temperatures and/or rainfall, and are positioned more Westerly. There was no association with age, sex or Northerly position.

Conclusions:
This method allowed us to estimate risks for several animal- and farm-associated covariates. In addition, a map of spatially correlated risk can be extracted from the model, representing the varying regional risk compared to that expected due to overall position, rainfall and temperature. A spatially-agnostic random effect was also fitted for individual farms highlighting farms with higher or lower than expected risk.

Relevance:
This approach represents a useful tool that allows us to make inference not just from the status of the animal at slaughter, but also to integrate these with readily available administrative data to provide a much more informative result than would otherwise be possible.

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Using quantile regression to explore *Salmonella* serosurveillance data in Ethiopian village chickens

Judy M. Bettridge, Elisabeth Waldmann, Paul Wigley, Robert M. Christley, University of Liverpool, Neston, United Kingdom. Contact: judybett@liv.ac.uk

Purpose:
Serological surveillance is widely used in epidemiology, and most ELISAs are used to classify individuals as positive or negative for exposure to the disease of interest. However, this approach may lose valuable information, as antibody titres may vary widely between individuals. *Salmonella* is one such pathogen where different serovars may induce very different antibody profiles.
Methods:
We sampled 1225 village chickens in eight villages in Ethiopia and tested for antibodies to *Salmonella* O9 serotypes using a non-commercial ELISA. A multilevel multivariable regression model of sample:positive ratios identified certain villages as risk factors for higher titres, but examination of residuals suggested the model poorly explained antibody responses at the upper end of the distribution. Linear quantile regression models were fitted to each 10th percentile of the distribution using the lqmm package in R to explore these relationships.
Results:
Parameter estimates for some villages varied across the distribution, suggesting that the majority of titres in these villages did not differ significantly from birds in the reference village. However, a greater proportion of birds with very high titres in these villages skewed parameter estimates based on mean regression. Parameter estimates in other villages were consistent across the distribution, suggesting a more widespread recent exposure of birds in these villages.
Conclusions
Differences betwen villages may be due to variation in the infecting serovars of *Salmonella*. Carriers of the *S.* Pullorum serovar may be more common in some villages, whereas widespread exposure to *S.* Enteritidis or *S.* Gallinarum may explain the raise in titres across the distribution in other villages.
Relevance
Quantile regression combined with use of the continuous data has proved useful in highlighting potential differences in the epidemiology of *Salmonella* in these areas, relevant to both chicken and human health. More work is needed on the relationship between the chicken antibody response and bacterial carriage in the village context, as this may not reflect the conditions under which most serological tests are developed.

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Veterinary hospital environmental contamination with Salmonella enterica - modeling a complex hospital ecology

Brandy A. Burgess[1], Paul S. Morley[2], [1]Virginia Tech, Blacksburg, VA, [2]Colorado State University, Fort Collins, CO, Contact: burgessb@vt.edu

Purpose: Healthcare-associated infections in veterinary hospitals are commonly attributed to Salmonella enterica and characteristically there is widespread environmental contamination identified during times of epidemic disease. The objective of this study was to determine a suitable analytic method to model the complex ecology of factors associated with environmental contamination of a veterinary hospital with S. enterica.

Methods: Environmental surveillance samples (N=5273) were collected from March 2003 through January 2013, as part of a long-term infection control program. Data on variables of interest were collected retrospectively from the electronic medical records database. Many variables that are easily measured (e.g., caseload) tend to be non-discriminatory in nature. While limited to these imperfect measures, use of alternative analytic methods, such as variable cluster analysis and principal components analysis, allows us to gain an understanding of the complex data structure and perspective on which variables really represent latent (unmeasured) factors that may be contributing to the overall ecology. After using these techniques, multivariable logistic regression was performed using generalized estimating equations to determine factors associated with environmental contamination with S. enterica.

Results: In general, the probability of detecting Salmonella in the hospital environment is associated with hospital and patient population characteristics; some of which are tangible such as hospital type or species and many that can be easily measured such as caseload and the number of days a hospitalized patient was shedding Salmonella.

Conclusions: Results of this study suggests that the probability of detecting Salmonella in the environment increases as the demand on personnel increases (i.e., a busy hospital).

Relevance: Veterinarians need to remain vigilant in the practice of infection control measures that we know empirically will mitigate the risk for widespread environmental contamination and sustained transmission among patients.

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Source attribution of human campylobacteriosis in Sweden

Thomas Rosendal[1], Anneli Carlander[2], Rikard Dryselius[3], Ingrid Hansson[4], Boel Harbom[4], Mia Holmberg[1], Elina Lahti[1], Hans Lindmark[3], Mattias Myrenås[4], Eva Olsson Engvall[4], Jonas Waldenström[5], Ann Lindberg[1], [1]National Veterinary Institute, Uppsala, Sweden; [2]Public Health Agency of Sweden, Stockholm, Sweden; [3]National Food Agency, Uppsala, Sweden; [4]National Veterinary Institute, Uppsala, Sweden; [5]Linnæus University, Kalmar, Sweden. Contact: thomas.rosendal@sva.se

Purpose:
Campylobacteriosis is the most reported zoonosis in EU and a reduction in incidence would be of great public health value. It is important to understand the relative impact of different sources of this infection in order to identify and prioritize control measures.

Methods:
Isolates of *C. jejuni* were collected from Swedish domestic human campylobacteriosis cases. Samples were also collected fromanimals, food and the environment and tested for *C. jejuni*. Isolates were genotyped by MLST and source attribution analysis using the asymmetric island model was done. The results of this model were evaluated by cross-validation.

Results:
The source attribution model indicated that important sources were poultry (41.3% of human cases) and imported poultry meat (19.4%). The proportion of cases attributed to water (2.0%) and wild birds (3.7%) was small as these sources were highly diverse and had only a small overlap with the human MLST types. The results of the proportion of cases attributed to sheep (27.6%) and cattle (5.9%) were different than has been described in previous source attribution studies. The cross-validation analysis indicated that the model did not accurately classify isolates into their source groups. None of the samples of true cattle origin were predicted to be of cattle origin; instead a majority (18/27) were predicted to be of sheep origin, and the rest were predicted to be poultry or poultry meat origin. Also, 50% of the true poultry observations were predicted to be of sheep origin.

Conclusions:
The study confirmed that Swedish cases of campylobacteriosis are primarily due to contact with poultry or poultry products. The research also shows that cattle and sheep play an important role in human cases but the relative importance of these cannot be determined. Misclassification of results by the model was identified by cross-validation and indicated that overlapping distributions of genotypes between sources is a challenge to this model and can lead to incorrect attribution.

Relevance:
This paper contributes to the understanding of *C. jejuni* epidemiology and highlights an important consideration in the interpretation of results from the asymmetric island model.

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SimInf; an R-tool for data-driven modelling of disease spread and control

Stefan Widgren[1], Pavol Bauer[2], Stefan Engblom[2], [1]National Veterinary Institute, Uppsala, Sweden; [2]Department of Information Technology Uppsala University, Uppsala, Sweden. Contact: stefan.widgren@sva.se

Purpose:
Livestock movements are important for the spread of many infectious diseases. European Union legislation requires all bovine animals to be registered in national databases. With this, the transport network is available together with population measurements of various granularity. The use of real population and event data enables disease spread modeling of the spatio-temporal dynamics due to age structures, trade patterns, population size and slaughter. However, performing detailed data driven simulations requires efficient algorithms to handle the complex network of herds and events. The aim of this study was to develop a computational modeling framework for data-driven simulations and analysis of infectious disease spread in large network of populations.

Methods:
In this work we present an innovative, efficient and flexible framework for spatio-temporal disease spread modelling. We have developed a discrete-event simulator, SimInf, that divide work among multiple processors available in standard computers. The model integrates infectious dynamics as continuous-time Markov chains and available data such as animal movements, births, slaughter or aging as externally defined events. The core simulator is implemented in compiled C code, called from R. This approach is a significant advancement to explore and study disease spread over spatio-temporal networks based on real data.

Results:
To demonstrate the usefulness of SimInf, we will present results of a simulation on national scale of VTEC O157 in the complete Swedish cattle population over 8.5 years. All reported cattle events (n = 18 649 921) during 2005-07-01 -- 2013-12-31 are included in the model, combined with a disease spread model in each holding (n = 37221).

Conclusions:
We conclude that SimInf is an efficient and flexible tool to incorporate available and real data in large-scale simulations of disease spread in spatio-temporal networks. The intention is to make SimInf available as an R-package at CRAN (http://www.cran.r-project.org/).

Relevance:
This new framework for disease spread modelling allows for inclusion of network contact data, which enables more realistic simulation models.

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Causal inference. Did we forget something?

Eystein Skjerve, Norwegian University of Life Sciences, Oslo, Norway. Contact: eystein.skjerve@nmbu.no

Purpose:
As a science of intervention, veterinary epidemiology relies heavily on our attemts to establish causal inference based upon assumed causal structures in our data. A causal model also underlies our strategies in reducing bias. This presentation aims at filling some gaps in our current understanding of causality in veterinary epidemiology.

Methods:
Based upon a causal inference diagram established using a Directed Acyclic Graph application (DAGitty) the causal structure is described. I then show how this can be incorporated in an intervention model using a Bayesian Network (BN) model, and show how the same causal structure can be used in a statistical model using a Structural Equation Model (SEM).

Results:
The use of a causal structure into a BN intervention model and the corresponding statistical model (SEM) demonstrates how causal graphs can be used in a wide variety of settings and help us in solving basic problems as confounding, colliders, intermediate variables and keep updating the causal model as we extract information from our data.

Conclusions:
The simple examples used shows how the graphical model, here as a DAG, can serve as a joint platform in many situations, from analysing observational studies to risk assessment and intervention models.

Relevance:
The tools presented may assist in identifying problematic feed-back structures in models, leading into other families of causal models. The DAGs represent stable causality, different from dynamic models also used in many studies in our field. Further steps away from stable causality include non- linear models, leading into the more esoteric field of complex systems and fractal epidemiology. We need more caution when we discuss our models, as we ultimately want our studies to be used in improving animal and public healh.

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Development of the STROBE-Vet statement: Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary extension.

Jan M. Sargeant[1], Ian Dohoo[2], Hollis Erb[3], Annette O'Connor[4], [1]Centre for Public Health and Zoonoses, Guelph, ON, Canada; [2]University of Prince Edward Island, Charlottetown, PE, Canada; [3]Cornell University, Ithaca, NY, [4]Iowa State University, Ames, IA, Contact: sargeanj@uoguelph.ca

Purpose: Transparency in reporting research is essential, and guidelines are available for many study designs. However, the reporting of observational studies in the veterinary literature presents challenges that are not adequately addressed in existing reporting guidelines. Therefore, our objective was to develop an extension of the human healthcare-oriented STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that specifically addresses unique reporting requirements for observational studies in animal-health, -production, -welfare, or food safety.

Methods: Seventeen experts attended a consensus meeting in May 2014 to discuss modifications to the STROBE statement. Prior to the meeting, experts were asked to indicate which of the 22 items of the STROBE statement should be modified, and if items should be added to address unique issues for observational studies in animal species with health, production, welfare or food safety outcomes. During the meeting, the results of the survey were provided and each STROBE item was discussed to determine whether re-wording or additions were warranted. Anonymous voting determined whether there was sufficient support for each change.

Results: Consensus recommendations included modifications or additions to 16 of the 22 STROBE items. The modifications included clarification on the term “participant” in animal studies, and recommendations for reporting issues related to non-independence in grouped animal populations, euthanasia as an outcome, key features of observational studies when the observational design does not specifically correspond to one of the common study types, putative causal assumptions, and details of questionnaire design, if applicable. The STROBE checklist item on funding was expanded to incorporate the broader concept of transparency in research.

Relevance: It is hoped that the use of this extension to the STROBE statement will improve the reporting of observational studies with animal-health, -production, -welfare, or food safety outcomes by recognizing the unique features of observational studies involving agricultural and companion animals.

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Estimation of the effect of F. hepatica infection on beef carcass performance using Bayesian statistics, adjusting for abattoir liver inspection imperfectness

Stella Mazeri[1], Gustaf Rydevik[1], Ian Handel[2], Mark Bronsvoort[1], Neil Sargison[2], [1]The Roslin Institute, Edinburgh, United Kingdom; [2]Royal (Dick) School of Veterinary Studies, Edinburgh, United Kingdom.
Contact: stella.mazeri@roslin.ed.ac.uk

Purpose: This study aims to estimate the effect of liver fluke on beef production and to investigate the use of diagnostic tests in a quantitative manner to aid control.
Methods: We used a Bayesian approach to build a regression model for the time to recorded slaughter weight, based on age, weight and the liver fluke status, taking into account breed and the random effect of farm. The model included sensitivity and specificity estimates of abattoir liver inspection for liver fluke. Using a subset of the data, fibrosis score (0-3) was included as a proxy for severity of fluke infection. Data used were collected at Scotland's leading red meat abattoir between 2012 and 2015.
Results: The posterior estimates indicated that cattle with liver fluke took 6.9%[1.2-12.7 95% credible interval] longer to reach slaughter weight, compared with healthy animals. Moreover, cattle with liver fluke took 7.1%[3.9-10.6%] longer for each unit increase of fibrosis score. Further preliminary results suggest that a serum antibody ELISA can be used to estimate the effect on growth rate, while faecal egg counts and a copro-antigen ELISA can be used to estimate parasite burden.
Conclusions:
Improved knowledge on the effect of F. hepatica infection on beef production in conjunction with the availability of diagnostic tests able to estimate production loss and parasite burden can inform targeted treatment management strategies and encourage more producers to adopt control measures, while reducing the establishment of anthelmintic resistance.
Relevance: Liver fluke, caused by F. hepatica is a multi-host parasitic disease affecting many countries worldwide. The infection in cattle mainly manifests as a sub-clinical disease, resulting in indirect production losses, which are difficult to estimate. The lack of obvious clinical signs results in these losses commonly being attributed to other causes such as poor weather conditions or bad quality forage. Moreover, due to the endemic nature of the infection in many countries, affected animals commonly have low levels of infection. To date it remains unclear at what levels parasite burden leads to production losses, or how the risk of losses can be measured using diagnostic tests.

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Keeping the Norwegian swine population free from LA-MRSA, is it possible?

Gry Grøneng, Anja B. Kristoffersen, Bjørn Lium, Carl Andreas Grøntvedt, Anne Margrethe Uhrdahl, **Madelaine Norström**, Norwegian Veterinary Institute, Oslo, Norway. Contact: madelaine.norstrom@vetinst.no

In 2014, a national survey of Livestock associated methicillin resistant Staphylococcus aureus (LA-MRSA) in Norwegian swine herds was performed, including testing of all herds with more than ten sows. The results were kept secret until all samples were analyzed, so that the Norwegian Food Safety Authorities (NFSA) could decide on which action to take based on the prevalence of positive farms. The NFSA decided to make socioeconomically analyses of different scenarios to support their decision making. In order to run these scenarios with probable prevalence´s of LA-MRSA during a ten year period, the Norwegian Veterinary Institute was requested to develop a transmission model of LA-MRSA in the Norwegian swine population. The model was based on an estimation that five, ten, 20 or 50 herds would be positive of LA-MRSA in the national survey, in combination with four different scenarios; ranging from a scenario initiated to eradicate LA-MRSA in the Norwegian swine herds and running a yearly surveillance program, to less ambitious scenarios and finally to a scenario where no further actions would be taken on detected positive herds. The simulation models included possible transmission routes; purchase from other farms, transport of animals between farms, human contacts or indirect transmission from the environment. We made assumptions of the probabilities of each of the transmission routes based on literature studies, a questionnaire to the Norwegian swine health service and expert opinions. However, more data regarding the probability of transmission of LA-MRSA from different sources are needed to improve the model further.
The most ambiguous scenario was the model with the lowest prevalence of LA- MRSA after a ten year period. However, herds with less than ten sows were not going to be tested in any of the scenarios if not detected as contact herds and thereby this population would remain a hidden source if not regularly included in the surveillance program. We recommended therefore to include all swine populations in the surveillance of LA- MRSA in the future, and to continue to slaughter out all detected farms with LA-MRSA in order to keep Norway free from this multi resistant agent.

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A systematic review and meta-analysis of on-farm methods for the detection of hyperketonemia in dairy cattle

Elise H. Tatone, Jessie Hubbs, Jessica L. Gordon, Todd F. Duffield, University of Guelph, Guelph, ON, Canada. Contact: etatone@uoguelph.ca

Purpose:
Several methods have been validated for the detection of hyperketonemia (serum beta-hydroxybutyrate (BHB) > 1.2 mmol/L) in dairy cattle on-farm, however the reported sensitivity and specificity of each method varies and no single study has compared them all. The objective of this work was to perform a systematic review and meta-analysis to determine the method with the highest combined sensitivity and specificity, and the optimal threshold for each method.

Methods:
A comprehensive literature search resulted in 5,196 references. After removing duplicates and performing relevance screening, 23 studies were included for the qualitative assessment and 16 for the meta-analysis. Index tests included in the meta-analysis were the Precision Xtra® handheld device that measures BHB concentration in whole blood, Ketostix® and KetoTest® semi-quantitative strips that measure the concentration of acetoacetate in urine and BHB in milk, respectively.
The diagnostic accuracy of the 3 tests was compared using the hierarchical summary receiver operator characteristic (HSROC) method. Threshold and accuracy were included as random effects by study, and variables were included to control for test type, accuracy, positivity threshold and the shape of the HSROC curve. Subgroup analysis was conducted for each index test to examine the accuracy at different thresholds.

Results:
The Precision Xtra® device had the highest summary sensitivity (95%) and specificity (99%). The threshold employed (1.2-1.4 mmol/L) did not significantly impact the diagnostic accuracy of the test. The Ketostix® and KetoTest® strips were not significantly different in overall diagnostic accuracy and both methods had the highest summary sensitivity and specificity when the trace and weak positive thresholds were used.

Conclusions:
The Precision Xtra® had the best overall test accuracy of the on-farm methods included in the meta-analysis. The large variation in individual study results reinforces the need for diagnostic test accuracy meta-analysis.

Relevance:
Meta-analysis of diagnostic test accuracy in human medical literature is becoming more common; however, to date this is the first veterinary example.

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Cost-effectiveness of mass dog vaccination campaigns against rabies in Flores Island, Indonesia

Ewaldus Wera[1], Monique C. M. Mourits[2], Maria M. Siko[3], Henk Hogeveen[2], [1]Kupang State Agricultural Polytechnic, West Timor, Indonesia; [2]Wageningen University, Wageningen, Netherlands; [3]Husbandry and Animal Health Department, Sikka, Flores, Indonesia. Contact: ewaldus.wera@wur.nl

With 19 reported fatal human cases annually, Flores Island has one of the highest incidences of rabies of all islands in Indonesia. Since 2000, the local government has been applying annual mass dog vaccination using both short- and long-acting vaccines. Insight in the effectiveness of these vaccination campaigns in Flores is, however, lacking.

The objective of this study is to evaluate the cost-effectiveness, defined as the costs per dog rabies case averted, of different mass dog vaccination strategies in Flores Island. Different vaccination strategies are based on the different types of vaccines licensed in Indonesia and currently used in Flores Island in combination with the proportion of the dogs that is vaccinated. Based on the immunity duration of the vaccines, vaccines are categorized as short- (<1 year) or long-acting rabies vaccines (≥1years). The hypothetical vaccination strategies are: 1) no vaccination; 2) vaccination using a short-acting vaccine without booster, and 3) vaccination using a long-acting rabies vaccine. A SEIV simulation model is developed to determine the impact of the strategies on the number of rabies cases over a period of 1 year within a typical village on Flores Island of 1500 inhabitants with an average dog population of 400. Without any vaccination, introduction of the virus resulted in 81 cases of dog rabies in a year. A vaccination campaign reaching 30%, 50% or 70% of total dog population within a village using a short-acting vaccine without booster prevented 50%, 70%, and 82% of cases per year while costs per dog rabies case averted were US$9.28, US$11.08, and US$13.23, respectively. With the long-acting vaccine, annual vaccination of 30%, 50%, 70% of dog population prevented 58%, 77%, and 87% of cases with costs per dog rabies case averted of US$10.56, US$13.30, and US$16.52, respectively.

Vaccination of 70% of total dogs using a long-acting vaccine is the most effective strategy in reducing the rabies cases. This strategy also has the highest costs. In a next step of our research we will compare the costs of the vaccination campaigns with the benefits in saved human life years and post exposure treatments.

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Application of capture-recapture model to assess the sensitivity of equine viral arteritis surveillance in French equine breeding stock by estimating the number of outbreaks

Jean-Philippe AMAT[1], Timothée VERGNE[2], Jackie TAPPREST[3], Bénédicte FERRY[4], Aymeric HANS[3], Sandrine VINATIER[5], Pascal HENDRIKX[6], Barbara DUFOUR[7], Agnès LEBLOND[8], [1]ANSES & INRA, Dozulé, France; [2]Royal Veterinary College, London, United Kingdom; [3]ANSES, Dozulé, France; [4]French horse and riding institute (IFCE), Saint-Ouen-de-Thouberville, France; [5]French horse and riding institute (IFCE), Pompadour, France; [6]ANSES, Lyon, France; [7]Veterinary School of Maisons-Alfort (ENVA), Maisons-Alfort, France; [8]INRA, Saint-Genès-Champanelle, France. Contact: jean-philippe.amat@anses.fr

Purpose
Equine viral arteritis (EVA) is a cause of abortion in mares and neonatal deaths. In France, surveillance of EVA is based mostly on serological testing of all or part of the breeding horses, depending on the studbooks' regulations. Hence, EVA prevalence is not precisely known in the overall breeding population. The objective was to assess the surveillance sensitivity by estimating the number of outbreaks that occurred in French breeding stock between 2006 and 2013 using the capture-recapture methods.
Methods
Data from breeding mares which exhibited at least one positive test in serology using viral neutralization test between 2006 and 2013 were used for analysis (n=1645). Data consisted of the annual antibody titers and the location of the mare. Seroconversion was defined as a change in antibody titer from negative to positive or a three-fold increase. The number of seroconversions was counted for each holding and modeled using unilist zero-truncated capture-recapture methods with R. Three different models were used: a negative binomial model and two Poisson models with or without covariate. The covariate was the number of horses tested in each infected location.
Results
From 2006 to 2013, 226 cases of seroconversion located in 174 holdings were identified. Using the Akaike information criterion, the Poisson model with covariate appeared to be the most appropriate model. During the period considered, the number of outbreaks in breeding stock was estimated to be 226 ($CI_{95\%}$ 212-244). Consequently, the number of outbreaks not detected was estimated to be 52 ($CI_{95\%}$ 38-70) and the estimated sensitivity of the surveillance at holding level was around 77% ($CI_{95\%}$ 71%-82%).
Conclusions and Relevance
This study is the first in France to estimate the number of EVA outbreaks in breeding stock and to assess quantitatively the surveillance sensitivity. The definition of seroconversion used in this study may be used to analyze other surveillance datasets based on serology even in other animal species. The results revealed a significant number of outbreaks in breeding stock. The sensitivity of the surveillance could be improved by including more breeding horses in the active surveillance.

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Veterinary race-day events experienced by flat racing Thoroughbreds in Great Britain (2000 to 2013).

Sarah M. Rosanowski[1], Yu-Mei Chang[2], Anthony J. Stirk[3], Kristien L. P. Verheyen[1], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]Royal Veterinary College, London, United Kingdom; [3]British Horseracing Authority, London, United Kingdom. Contact: srosanowski@rvc.ac.uk

Purpose: Injuries are an inevitable risk in any sport involving elite, high performance athletes. The racing industry is committed to improving the safety of racehorses to reduce injury incidence and enhance equine welfare. Before implementing interventions to initiate effective change, the occurrence of race-day veterinary events must be quantified. The objective of this study was to describe events experienced by flat racing Thoroughbred racehorses in Great Britain.
Methods: A 14-year retrospective cohort study was conducted, using all veterinary events reported by race-day veterinarians and stored in a custom-designed database. Veterinary events were described by type of event, structure affected and whether the event had a fatal outcome.
Results: A total of 7,993 veterinary events occurred in 6,727 horses (median age 4; range 2 to 15 years; 67.0% male). In 1,926 (24.1%) events the skin and/or muscles were affected; 69.9% of these were wounds or lacerations. The respiratory system was affected in 1,678 (21.0%) events, of which 1,018 (60.7%) were epistaxis. Nearly 20% (n=1,532) of events were gait observations including non-specific lameness. Of the events, 1,223 (15.3%) affected bones and joints and 87.2% of these were fractures; 492 (6.2%) affected tendons and ligaments. A total of 628 (7.9%) fatal events occurred, including 499 (79.5%) fractures, 54 (8.6%) tendon injuries, 64 (10.2%) vascular collapse cases and 8 (1.3%) epistaxis events. Most fractures (648; 60.8%) occurred in the distal limb, 332 (31.1%) in the proximal limb. Third metacarpal or metatarsal fractures were the most common fracture (242; 22.7%), followed by fractures of the pelvis (223; 20.9%) and the proximal phalanx (175; 16.4%). Most tendon or ligament injuries were to the superficial digital flexor tendon (68.5%) or suspensory ligament (16.2%).
Conclusion and relevance: This large-scale study has provided a description of veterinary events experienced on race day in flat racehorses in Great Britain. The findings of this study will be used to identify outcomes for which modifiable risk factor analysis will be conducted. Results also provide a baseline for monitoring the effectiveness of future interventions.

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A case-control study to determine the causes of respiratory disease in the working equids of Ethiopia.

Gabrielle Laing[1], Rob Christley[1], Andrew Stringer[1], Alan Radford[1], Nigatu Aklilu[2], Richard Newton[3], Gina Pinchbeck[1], [1]University of Liverpool, Liverpool, United Kingdom; [2]Society for the Protection of Animals Abroad (SPANA), Debre Zeit, Ethiopia; [3]Animal Health Trust, Newmarket, United Kingdom. Contact: gabrielle.laing@liverpool.ac.uk

Previous research and clinical case data from SPANA Ethiopia has demonstrated that respiratory disease, particularly coughing and nasal discharge are a major reason for clinic attendance and are consistently ranked in the top-three health concerns for working equid owners. However, there is little existing literature on the possible aetiology. **Purpose:** Case-control study to determine risk factors for respiratory disease.

Method: Cases and controls were recruited from horses attending SPANA clinics in central Ethiopia. Cases were all horses presenting to the clinic for respiratory signs i.e. coughing, nasal discharge or dyspnoea. Unmatched controls were randomly selected from horses without respiratory signs. All animals underwent full clinical examination, serology & basic haematology. Endoscopic examination of respiratory tract was performed up to the level of the carina, including tracheal mucus score (0-3). Tracheal wash samples underwent cytological evaluation and PCR identification of the major respiratory pathogens: equine influenza virus, equine herpesvirus 1/4, equine arteritis virus, equine rhinitis virus A/B, *Streptococcus equi* subsp. *equi* and *Streptococcus zooepidemicus.* Additional data were collected by questionnaire.

Results: 108 cases and 92 controls were examined. Over one-third of cases presented with coughing (36%) and nearly half had a nasal discharge (43%). Case horses were more likely to cough on endoscopy (84% compared to 16% controls) and have abnormal findings on thoracic auscultation (54/63). Increased tracheal mucus (≥2/3) was seen in 28% of case horses. PCR on tracheal wash samples detected *S equi* in 5 animals, 1 case with EHV-1 and 33 with *S zooepidemicus* present. Significantly ($p<0.001$) more cases were positive for *S zooepidemicus* than controls. A dual ELISA for antibodies to *S equi* showed 25% seropositive, of which 68% were cases. Cytology results will also be presented.

Conclusion & Relevance: Horses commonly presented with clinical signs of respiratory disease and the majority of cases had evidence of lower respiratory tract disease. The role of *Streptococcus* species in respiratory disease in this population should be further considered.

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Idiopathic focal eosinophilic enteritis (IFEE), an emerging cause of abdominal pain in horses: the effect of age, time and geographical location on risk.

Debra Archer[1], Deborah Costain[2], Chris Sherlock[3], [1]University of Liverpool, Neston, United Kingdom; [2]Lancaster University, Lancaster, United Kingdom; [3]Lancaster University, Lancaster, United Kingdom.
Contact: darcher@liv.ac.uk

Purpose: Idiopathic focal eosinophilic enteritis (IFEE) is an emerging cause of abdominal pain (colic) in horses that frequently requires surgical intervention to prevent death. The epidemiology of IFEE is poorly understood and it is difficult to diagnose pre-operatively. The aetiology of this condition and methods of possible prevention are currently unknown. The aims of this study were to investigate temporal and spatial heterogeneity in IFEE risk and to ascertain the effect of horse age on risk.
Methods: A retrospective, nested case-control study was undertaken using data from 85 IFEE cases and 848 randomly selected controls admitted to a UK equine hospital for exploratory laparotomy to investigate the cause of colic over a 10-year period. Generalised additive models (GAMs) were used to quantify temporal and age effects on the odds of IFEE and to provide mapped estimates of 'residual' risk over the study region.
Results: The relative risk of IFEE increased over the study period ($p=0.001$) and a seasonal pattern was evident ($p<0.01$) with greatest risk of IFEE being identified between the months of July and November. IFEE risk decreased with increasing age ($p<0.001$) with younger (0 - 5 years old) horses being at greatest risk. The mapped surface estimate exhibited significantly atypical sub-regions ($p<0.001$) with increased IFEE risk in horses residing in the North-West of the study region.
Conclusions: IFEE was found to exhibit both spatial and temporal variation in risk and is more likely to occur in younger horses.
Relevance: This information may help to identify horses at increased risk of IFEE, provide clues about the aetiology of this condition and help to identify areas that require further research.

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Risk of entry and transmission for two Culicoides-borne diseases in horse: comparison of African horse sickness and Equine encephalosis for France

Céline Faverjon[1], **Agnès Leblond**[1], Sylvie Lecollinet[2], Aline de Koeijer[3], Rene Bodker[4], Egil A. J. Fischer[5], [1]INRA, Lyon, France; [2]ANSES, Maisons Alfort, France; [3]CVI, Lelystad, Netherlands; [4]DTU, Copenhaguen, Denmark; [5]Utrecht university, Utrecht, Netherlands. Contact: agnes.leblond@vetagro-sup.fr

Purpose:
Providing updated information on the spatiotemporal risk of diseases entry and transmission may help to hierarchize the risk for diseases with similar epidemiology and transmission patterns. We combined a model on risk of disease entry with a model on potential for transmission in order to rank the risk for two vector-borne diseases, African horse sickness (AHS) and Equine encephalosis (EE). AHS is one of the most devastating diseases in equidae while EE presents few symptoms, but both diseases affect only equidae, are transmitted by the same vectors (Culicoides) and have the same geographical distribution.
Methods:
The risk of entry was assessed based on a stochastic spatiotemporal model of virus entry for two entry pathways; importation of animals and vectors. The risk of virus transmission was estimated using a deterministic model which calculates a cumulative number of infectious bites per time period. Analyses were performed for three consecutive years (2010-2012) in France.
Results:
Seasonal variations in virus entry were the same for both diseases (high risk from July to December), but with an overall risk higher for EE (e.g. median annual probability of entry through an infectious host equals 9x10-1 for EE and 3x10-3 for AHS). However, the spatial patterns of the probability of entry were different (e.g. 'Limousin' at risk for EE but not for AHS). Comparison of diseases transmission also shows spatial and temporal variations with a greater risk for EE. Differences between diseases are mainly due to the longer viraemia for EE associated with very little control measures of EE during importation procedures and with poor clinical detection of EE due to sporadic and unspecific symptoms, whereas AHS will be detected and has an only short viraemia ending in death of the equid.
Conclusions:
Our study shows that the risk posed by similar viruses can be ranked using a quantitative combination of models on diseases entry and transmission. In our study, the overall risk for EE was higher, the differed for EE and AHS in different regions. Results can be used to implement specific risk based surveillance.

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Drivers and barriers for the uptake of a new Hendra virus vaccine for horses in Australia

Navneet K. Dhand[1], Nicole Schembri[2], Anke Wiethoelter[1], Jenny-Ann L. M. L. Toribio[1], Nina Kung[3], Barbara Moloney[4], Kate Sawford[1], Therese Wright[5], Hume Field[6], Melanie Taylor[2], [1]The University of Sydney, Camden, Australia; [2]University of Western Sydney, Sydney, Australia; [3]Queensland Department of Agriculture, Fisheries, and Forestry, Brisbane, Australia; [4]NSW Department of Primary Industries, Orange, Australia; [5]NSW Department of Primary Industries, Orange, Australia; [6]EcoHealth Alliance, New York, NY, Contact: navneet.dhand@sydney.edu.au

Purpose:
Hendra is an emerging zoonotic disease transmitted from flying foxes to horses and from horses to humans. This study was conducted to identify trends, drivers and barriers for the uptake of a new Hendra vaccine for horses since its launch in November 2012.
Methods:
Five online surveys were administered to horse owners at six monthly intervals between November 2012 and December 2014. Data from each survey were stacked and a binary outcome variable created based on the question 'Have any of your horse(s) been vaccinated against Hendra virus?'. Respondents who were not responsible for making decisions regarding vaccination were excluded. Generalized linear mixed models were built to evaluate association of demographic, management and behavioural variables with the outcome, after including respondent ID as a random effect to adjust for multiple observations for some respondents over time.
Results:
The numbers of participants in the five online surveys ranged from 720 to 1195, including 341 respondents who participated in each survey. Overall, 56% of them were aged between 35 and 54 years and 90% were female. Proportion of respondents who had vaccinated their horses increased from 11% at the first to 28% at the second and 56% at the third survey and then hovered around this value. Respondents who thought that a Hendra case was 'moderately' and 'very/extremely' likely in their area had 2.7 and 8.2 times odds of getting their horses vaccinated than those who thought that a case was not likely to occur ($p<0.001$). Respondents were more likely to get their horses vaccinated if they were worried about themselves or their family members getting Hendra virus or if they agreed with the establishment of a national horse registration system to assist with disease control and horse movements. Owners reporting a good sense of control over the risk of Hendra virus were also more likely to have vaccinated their horses.
Conclusions:
Horse owners made their decisions by considering both threat appraisal (severity and vulnerability) and coping appraisal (response efficacy and self-efficacy).
Relevance:
The study has implications for making policy decisions about encouraging uptake of the vaccine.

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Combating Hendra - Biosecurity practices and risk perceptions of Australian horse owners.

Nicole Schembri[1], Navneet K. Dhand[2], **Anke Wiethoelter**[1], Jenny-Ann L. M. L. Toribio[2], Hume Field[3], Barbara Maloney[4], Kate Sawford[2], Nina Kung[5], Therese Wright[4], Melanie Taylor[1], [1]University of Western Sydney, Sydney, Australia; [2]University of Sydney, Camden, Australia; [3]Jeppesen Field Consulting, Brisbane, Australia; [4]NSW Department of Primary Industries, Orange, Australia; [5]Queensland Department of Agriculture, Fisheries and Forestry, Brisbane, Australia. Contact: anke.wiethoelter@sydney.edu.au

Purpose: Discovered in Australia in 1994, Hendra virus (HeV) is an endemic zoonotic disease caused by spillover from flying foxes to horses and horses to people. Moderate uptake of the HeV horse vaccine reiterates the need for continued biosecurity measures. This study aims to quantify horse owner's level of biosecurity in association with property-based measures, their HeV risk perceptions and preparedness.
Methods: An online, self-administered longitudinal survey of horse owners was conducted over two years from November 2012 with five surveys distributed at six-monthly intervals. Descriptive and multivariable ordinal logistic regression analyses were undertaken on data from the second survey to determine participant level of biosecurity and associated factors. Level of biosecurity (low, medium or high) was based upon responses to 19 preventive measures involving contact with both healthy and sick horses that were carried out 'rarely, 'sometimes' or 'often'. Preventive measures were converted into binary variables, with a proportion of the 19 practices estimated for each individual giving an overall biosecurity rating. Low biosecurity individuals undertook <34% of practices, medium, up to 67% of practices and high biosecurity individuals undertook >67% of practices.
Results: Over a quarter of the 713 survey participants (N = 198) were classified as having a high biosecurity rating. Around 60% of these participants lived within 50km of a known HeV case, with 51% strongly agreeing that they had a good sense of control over *their* HeV risk. A greater proportion of high-level biosecurity participants "always" covered feed/water and limited horse access to trees at night ($P<0.05$), were "very likely" to suspect HeV in a sick horse, contact their veterinarian to discuss or examine changes in their horse(s); and had access to a greater range of personal protective equipment ($P<0.05$).
Conclusion and relevance: Gaps identified in horse owner biosecurity practices will assist government, veterinarians, and horse industry groups in prioritising and developing targeted risk and prevention communication strategies to protect horse owners and the general public against HeV.

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Intervention to mitigate *Trypanosoma evansi* in equids in Qalander community in India: A retrospective study

Dinesh S. Mohite[1], Saurabh Singh[2], Sanjay Sharma[2], Amit Kumar[2], [1]Brooke Hospital For Animals (India), Ghaziabad, U.P., India; [2]Brooke Hospital For Animals (India), Ghaziabad, U.P., India. Contact: mohite@thebrookeindia.org

Purpose

Qalander is a poor tribal community residing along riverbanks in Uttar Pradesh who earn their livelihood breeding equids for sale. Grazing equids with buffalo near stagnant water exposes stock to *T evansi* (Surra), a high equine mortality vector-borne protozoal disease prevalent mainly in spring and autumn, for which buffalo act as a reservoir. The community's preference to resolve adversity through social meetings, their reluctance to involve outsiders and their remote location make government veterinary service and Non Governmental Organisation engagement difficult. Some inappropriate knowledge can lead to misdiagnosis of equine disease, inappropriate administration of toxic antiprotozoal drugs and misuse of antibiotic. Surra results in high economic loss for Qalander. Since simple changes to husbandry practices can enhance disease management and improve equine welfare is a priority disease for the Brooke, an international equine welfare NGO. The aim of this study was to trial and assess an intervention to reduce Surra in Qalander-owned equids.

Method

Brooke interventions comprising liaising with community leaders, demonstrating disease diagnosis and treatment, carrying out awareness camps and linking communities with local service providers were delivered to 16 Qalander sites between 2012 and 2014. Clinical records logged each new, field diagnosed Surra infection during months of high prevalence (April-November). Total equine population was recorded.

Result

In year one, 13% (95% CI 11-14%) of the total equine population presented at clinics with confirmed Surra infection. This remained at 13% (95% CI 12-15%) in year two. In year three, 7% (95% CI 6-8%) of the total equine population presented at clinics with confirmed Surra infection. There was a significant differences between year one and year three (p=0.0001).

Conclusion

The decline in Surra prevalence in the Qalander community during the intervention period suggests that the community engagement-based approach may be beneficial for its mitigation.

Relevance

Policy makers have not considered Qalander community in Surra control policy, these findings suggest potential for successes should they be included.

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Current status of bovine brucellosis in small livestock farms in Southern Nariño, Colombia.

Bibiana Benavides Benavides[1], Catalina Garzón[2], Alvaro Ortiz[1], [1]Universidad de Nariño, Pasto, Colombia; [2]Instituto Colombiano Agropecuario ICA, Pasto, Colombia. Contact: bibibenavides@gmail.com

Background: The Colombia bovine brucellosis (BB) control program was implemented in 2002 and, in 2009, the Department of Nariño was classified as an area of high prevalence of brucellosis (i.e., herd prevalence > 5%). The control program in Nariño targets medium and large dairy herds with more than 20 and 100 animals, respectively, because they are required to be brucellosis free in order to sell milk to local milk processing plants. In Nariño, 80% of all dairies are small herds. In 2014, a novel project (Contrato Plan Nariño CPN) was implemented in 23 municipalities. This project targets small herds (≤ 20 animals) which are considered an important source of infection to medium and large dairies.
Purpose: The aims of this study were to estimate the seroprevalence of BB in small herds in Nariño during September 2014 - February 2015, and to identify time-spatial clusters of seropositive herds.
Methods: Blood serum samples were collected from cows > 24 month old and intact male calves > 8 months old for detection of B abortus antibodies by using the fluorescence polarization assay as a screening test, followed by a competitive ELISA as confirmatory test. Spatial or space-time disease clusters were identified using SaTScan software.
Results: The herd seroprevalence of BB was 59/5111 or 1.2% (95% CI = 0.9, 1.4%). The animal seroprevalence was 71/24018 or 0.29% (0.22, 0.36%). The herd seroprevalence of BB was higher (1.3 to 2.4%) in the three municipalities with the largest number of dairy herds in Nariño. In addition, we identified clusters of seropositive herds within these three municipalities ($p < 0.05$).
Conclusion and relevance: This study is relevant because it provides new baseline seroprevalence data of BB in small dairy herds in Nariño. Study results suggest the disease burden in Nariño is lower, compared to that in medium and large herds in Nariño reported in previous years.

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Leptospirosis in subsistence pigs in Mato Grosso do Sul state, Brazil - preliminary analysis

Gabriela Tjhio César Pestana Barros[1], Rita de Cássia da Silva Paes[2], Aline de Oliveira Figueiredo[2], Jacqueline Marques de Oliveira[2], Nathalia Trindade Azevedo Marques[1], Vitória Machado Neres[1], Juliana Arena Galhardo[1], [1]Universidade Federal de Mato Grosso do Sul, Campo Grande-MS, Brazil; [2]Agência Estadual de Defesa Sanitária Animal e Vegetal de Mato Grosso do Sul, Campo Grande-MS, Brazil.
Contact: gabipestanabarros@gmail.com

Purpose: The aim of this study was to determine the prevalence of anti-*Leptospira* spp. antibodies in unvaccinated domestic pigs living under subsistence production system, the prevalence of positive properties and the risk areas for leptospirosis in the state.
Methods: Were analyzed 1,082 pig serum samples from 307 properties, collected in 2012 by the State Bureau of Animal and Plant Health Protection (IAGRO) for seroepidemiological survey of classical swine fever. Diagnosis was made at the Animal Diseases and Food Microbiology Laboratory using microscopic agglutination test for the serovars *Leptospira bratislava*, *L. canicola*, *L. grippothyphosa*, *L. hardjo*, *L. icterohaemorrhagiae* and *L. pomona*. Animals were considered positive when presenting titer of ≥100 for any of the serovars and the property was considered positive when presented at least one positive animal. For analytical purposes, the state was divided into 11 strata. For distribution analysis of properties and determination of risk areas, was designed a geographic information system using QGIS 2.8.1 software.
Results: A prevalence of 48.7% (527/1082) of seropositive pigs was observed and the prevalence of seropositive animals per strata ranged from 22.4% to 88.0%. Regarding to properties, it was observed a prevalence of 53.4% (164/307), distributed in all strata. Risk areas were observed throughout the territory, with a higher concentration in the south strata of the state.
Conclusions: Prevalence rates of leptospirosis are high in subsistence pigs and properties of Mato Grosso do Sul. Infection is widespread in the state and at the southern region agriculture is the predominant activity, which may enable the maintenance of reservoirs, particularly rodents, and the transmission of leptospirosis in these areas.
Relevance: Leptospirosis is considered the most widely distributed zoonosis in the world and epidemiologically relevant in urban and rural areas due to the diversity of synanthropic and wild reservoirs. In Mato Grosso do Sul state, Brazil, the subsistence production is present in rural and peri-urban areas and usually presents unsatisfactory sanitary conditions, favoring the spread of leptospirosis.

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An estimation of Mycoplasma bovis herd-level transmission probabilities with diagnostic uncertainty by Bayesian Hidden Markov Model.

Per K. Nielsen[1], Liza Rosenbaum Nielsen[2], Tariq Halasa[1], Nils Toft[1], [1]Technical University of Denmark, Frederiksberg C, Denmark; [2]University of Copenhagen, Frederiksberg C, Denmark. Contact: pkani@vet.dtu.dk

Purpose:
Mycoplasma bovis (M. bovis) causes disease in cattle worldwide. Common clinical signs include mastitis and arthritis in adults and pneumonia and otitis media in young stock leading to a significant economic impact. Infected animals can carry this pathogen asymptomatically for prolonged periods which leads to an on-going latent infection in farms. The subclinically infected animals will influence herd-level diagnostics, and this may lead to false negative or false positive diagnosis of farms. This is further complicated by the use of non-perfect diagnostic tests.
The objective of this study was to obtain knowledge about progression of herd-level M. bovis infections given imperfect diagnostic tests.
Method:
The study was based on 4 nation-wide screenings of bulk tank milk samples from all dairy herds for M. bovis. Data were collected from 3241 Danish dairy cattle farms during 2013 and 2014, at approximately 4 month intervals. All samples were tested with an indirect M. bovis antibody detecting ELISA (Bio-X Diagnostics, Jemelle, Belgium). A Bayesian Hidden Markov Model with binary latent states was developed. Prior knowledge about the test sensitivity/specificity from a previous diagnostic test evaluation study was placed on the observed states and prior knowledge about the true prevalence was used as the initial latent state. We used vague priors on the transmission probabilities.
Preliminary results:
The median probability of becoming latent infected given a previous non-infected state was 2.5% (1.8-3.3% 95% Credibility Interval) and the median probability of becoming latent non-infected given a previous infected state was 98.5% (91.9-99.9% 95% CI).
Conclusion:
Infected farms tended to become non-infected while non-infected farms remained non-infected. This suggests another mechanism for the spread of M. bovis. The study will, prior to ISVEE 2015, explore the effects of cattle movement on the transmission probabilities and the implications for the latent infection states.
Relevance:
This work will contribute to the understanding of the epidemiology of M. bovis with respect to reducing the infection burden for both the individual farmer and on a population level.

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Mycoplasma bovis in Australian feedlot cattle: risk factors for seroconversion and association with bovine respiratory disease

Meghan L. Schibrowski[1], Timothy J. Mahony[1], Justine S. Gibson[2], **Tamsin S. Barnes**[2], [1]University of Queensland, Brisbane, Australia; [2]University of Queensland, Gatton, Australia. Contact: t.barnes@uq.edu.au

Purpose:
There is minimal information on the epidemiology of *Mycoplasma bovis* in feedlot cattle in Australia and it is not known whether the organism can act as a primary initiator of bovine respiratory disease (BRD) in these populations. The objectives were to estimate the incidence of and identify risk factors for seroconversion to *M. bovis*, and assess its association with BRD in feedlot cattle.
Methods:
Paired sera from 1,354 randomly selected cattle were sourced from a larger Australian parent study (n=35,160). Sera were collected at induction at feedlots (n=14) and approximately six weeks later, and tested using the commercially available *M. bovis* enzyme-linked immunosorbent assay (Bio-X Diagnostics®). The total effects of risk factors for seroconversion were estimated using a causal diagram-informed process to determine minimal sufficient adjustment sets to include in separate multilevel models for each risk factor of interest. DAGitty software was used to produce directed acyclic graphs to aid this process. Four-level multivariable logistic regression models were fitted using Stata®. A similar approach was used to assess the association between seroconversion and the occurrence of BRD during the first 50 days at the feedlot.
Results:
3.5% (95% CI 2.0 - 5.0%) of animals were seropositive at induction and 24.3% (95% CI 20.8 - 27.7%) of seronegative animals had seroconverted by the second sampling. Risk factors that were found to be associated with risk of seroconversion were breed (Herefords at greatest risk), number of cattle in the arrival group (larger groups at decreased risk) and access to water shared with another pen of animals (increased risk compared to not shared). Seroconversion to *M. bovis* was strongly associated with the development of BRD (OR 3.1, 95% CI 2.1 - 4.7) during the early feeding period. This association was stronger than that between seroincrease to each of four common respiratory viruses and BRD identified in the parent study.
Conclusions:
Seroconversion to *M. bovis* is common in feedlot cattle and strongly associated with BRD.
Relevance:
These findings suggest that *M. bovis*-targeted control measures could help reduce the incidence and economic impact of BRD.

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The influence of milking machine status and milking routine on bulk tank somatic cell count in Uruguayan herds

Claudina Vissio[1], Mette Bouman[2], Alejandro Larriestra[1], [1]Universidad Nacional de Río Cuarto, Río Cuarto, Argentina; [2]LDS Uruguay, Cosmopolita, Uruguay. Contact: cvissio@ayv.unrc.edu.ar

Approximately 65% of Uruguayan milk production is exported. The economic value of the dairy exports is only surpassed by beef and soy bean. No large-scale study has been carried out so far to characterize udder health management and its level of effectiveness. Purpose: the aim of this study was to assess the influence of milking machine status and the milking routine on bulk milk somatic cell count (BMSCC) in Uruguayan herds. Methods: between 5 April 2006 and 6 September 2012 one of the authors made 1560 visits to 1023 farms. Each visit involved a static machine test according to modified ISO recommendations and observation of the milking process, during which the use of blanket dry cow therapy was also recorded. Nine hundred fifty six visits to 678 farms had a full dataset and were used for this analysis. The log transformed BMSCC (lnBMSCC) was the response study variable. Univariate analysis was applied to reduce the number of predictors to be included in the multivariate model. A linear mixed regression model considering year and season as a random effect was fitted. Results: the median BMSCC over the years was 400000 cells/mL (interquartile range =250000-500000 cells/mL). There was a clear seasonal trend, with the highest InBMSCC during the summer. The final model showed a net reduction of BMSCC for herds that did not use water for teat preparation (-58773 cells/mL), used post-dip (-52784 cells/mL) and avoided over-milking (-42953 cells/mL). Herds that milked with a correct working vacuum, sufficient effective reserve and pulsation that complied with ISO standards showed a net BMSCC reduction of 23583 cells/mL. A correctly sized and installed milk line reduced BMSCC in an additional 24000 cells/ml. A high proportion of farms in this study reported dry treating all cows (91%); this variable resulted in lower BMSCC in the univariable analysis but disappeared in the multivariable analysis. Conclusion and relevance: this research has shown quantitative evidence of the effectiveness of several milking practices and the status of the milking machine under Uruguayan conditions, which is relevant information for a dairy industry that needs low BMSCCs to compete on the world market.

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A systematic review and meta-analysis of vaccine efficacy to prevent urinary shedding of Leptospira in cattle, sheep and deer

Juan M. Sanhueza, Cord Heuer, Peter R. Wilson, Jackie Benschop, Julie M. Collins-Emerson, Massey University, Palmerston North, New Zealand. Contact: j.m.sanhueza@massey.ac.nz

Purpose:
Leptospirosis is endemic in New Zealand's largely unvaccinated pastoral dry stock populations (beef cattle, sheep, deer). Around 80% of human notified cases are from occupationally exposed people such as abattoir workers and farmers. Vaccinating animals against Leptospira is regarded as the most effective way to reduce human exposure. The objective of this study was to estimate vaccine efficacy to prevent urinary shedding of Leptospira in cattle, sheep and deer and to assess heterogeneity.
Methods:
A systematic literature review was conducted to select articles evaluating the efficacy/effectiveness of commercial vaccines against Hardjobovis or Pomona (serovars most common in New Zealand livestock) to prevent urinary shedding in cattle, sheep or deer. Data from eligible articles with sufficient information were included in a random effect meta-analysis. Outcome parameter was the natural logarithm of relative risk of shedding in vaccinated versus control animals. Heterogeneity between studies was quantified (I2 statistic) and further explored through meta-regression. Covariates included were species, age at vaccination, shedding evaluation method, vaccine type (monovalent/polyvalent), Leptospira serovar used for challenge, and type of challenge (artificial/natural).
Results:
Systematic literature search identified 1237 articles of which 113 were eligible based on title and/or abstract, and 22 presented sufficient data for the meta-analysis. Overall vaccine efficacy was 61.9%. Substantial heterogeneity was observed in the meta-analytic model (I2=79.8%). Reasons for heterogeneity and adequacy of pooled effect will be presented and discussed.
Conclusions:
Vaccination was generally efficacious and an important tool to prevent urinary shedding. Tests used to measure shedding, and age at vaccination accounted for heterogeneity.
Relevance:
The possibility of suboptimal vaccine effectiveness may be reduced but the on-farm significance of factors should be further explored.

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Rethinking Mycobacterium avium subsp. paratuberculosis infection dynamics in cattle: a new modeling approach

Rebecca L. Smith[1], Ynte H. Schukken[2], Yrjo T. Grohn[3], [1]University of Illinois, Urbana, IL, [2]GD-Animal Health, Deventer, Netherlands; [3]Cornell University, Ithaca, NY, Contact: rlsdvm@illinois.edu

Purpose: Models of *Mycobacterium avium* subsp. *paratuberculosis* (MAP), a chronic infectious agent of cattle, are used to identify effective control programs; these models assume that infections occur before 1 year of age and that all infected animals follow the same path. However, new biological findings show that adult infections likely do occur and that infected animals can be separated into 2 paths: animals that will become high-shedding and, eventually, experience clinical disease (high-path); and animals that will shed only small quantities of MAP and will remain subclinical (low-path). We propose a new model of MAP that accounts for both calf and adult infection and that allows for dual-path infection.
Methods: A stochastic model using Gillespie's direct algorithm was adapted from Mitchell et al. (2008) to include adult infections and 2 infection pathways. The model was parameterized from a longitudinal study of 3 dairy herds in the United States.
Results: Survival analysis of disease progression rates, using Kaplan-Meier estimates, found that high-path animals progress more quickly than previously believed, moving from latency to shedding at almost 3 times the rate of low-path animals and progressing from low to high shedding at twice the rate previously assumed. Analysis of the stochastic model showed that adult infection may play an important role in MAP dynamics on a dairy farm, depending on the relative susceptibility of calves and adults. Global sensitivity analysis found that the increased rate of progression for high-path animals would increase both the prevalence and the persistence of MAP on a dairy farm.
Conclusions: The model predicted that elimination of MAP would be difficult and would require more than 25 years in most cases.
Relevance: This new model will be able to determine more accurately the effectiveness of MAP control programs.

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Influences on dairy farmers' participation in a voluntary Johne's disease control program in Canada

Caroline Ritter[1], Grace P. S. Kwong[1], Robert Wolf[1], Charlotte Pickel[1], Mike Slomp[2], Jodi Flaig[2], Steve Mason[1], Cindy L. Adams[1], David F. Kelton[3], Jolanda Jansen[4], Karin Orsel[1], Jeroen De Buck[1], Herman W. Barkema[1], [1]University of Calgary, Calgary, AB, Canada; [2]Alberta Milk, Edmonton, AB, Canada; [3]University of Guelph, Guelph, ON, Canada; [4]St. Anna Advies, Nijmegen, Netherlands. Contact: cmnritte@ucalgary.ca

Introduction/Purpose: The Alberta Johne's Disease Initiative is a voluntary management-based control program to reduce the prevalence of Mycobacterium avium subsp. paratuberculosis in Alberta dairy herds. Despite extensive communication strategies to promote participation and low cost to the producer, approximately 35% of Alberta dairy farms never enrolled in the AJDI. The purpose of this study was to identify reasons for non-participation.
Methods: Face-to face interviews were conducted with 163 AJDI non-participants and 61 AJDI participants using standardized questionnaires. The groups were compared in regards to their 1) general farm characteristics, 2) attitudes, norms and beliefs towards Johne's disease (JD) and the AJDI, 3) main farm goals and constraints, 4) self-assessed knowledge of JD, and 5) use of information sources and their impact on AJDI enrollment.
Results: The most distinct differences between groups were that AJDI participants had a larger herd size, a higher self-assessed knowledge of JD, and a better understanding of AJDI details prior to participation. This group also used the veterinarian more often compared to non-participants. In contrast, non-participants perceived time as greater constraint on their farms and they perceived management changes associated with AJDI participation as too time consuming. To non-participants it was more important that the program has worked on other farms before they enroll.
Conclusion/Relevance:
This study will help to make knowledge transfer and communication to dairy producers more efficient. Communication to non-participants should take the individual situation of each producer into account. Educating non-participants about the details of the AJDI and emphasizing that many management changes do not necessarily take more time will help to increase their motivation to enroll. The herd veterinarian or other producers that can report positive AJDI experiences are ideal mediators to induce participation.

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Identifying effective treatment criteria for use in targeted selective treatment programs to control type II haemonchosis in recently-lambed ewes in Ontario, Canada

Trisha Westers[1], Andria Jones-Bitton[1], Paula Menzies[1], John VanLeeuwen[2], Andrew S. Peregrine[1], [1]University of Guelph, Guelph, ON, Canada; [2]University of Prince Edward Island, Charlottetown, PE, Canada. Contact: twesters@uoguelph.ca

Purpose: Type II haemonchosis is often associated with late gestation and parturition in ewes in Canada. Due to widespread anthelmintic resistance (AR), targeted selective treatment (TST), where individual animals are treated rather than the entire flock, is a possible strategy to control clinical signs in recently-lambed ewes while still maintaining parasite refugia. Performing fecal egg counts (FEC) on individual animals is often cost-prohibitive, so indicators that identify ewes with high FEC are essential for TST programs. The study objective was to evaluate the ability of four TST indicators to predict FEC in recently-lambed ewes.

Methods: A field study was conducted during the 2013 and 2014 lambing seasons (February-May) on three client-owned farms in Ontario with documented AR and problems with type II haemonchosis. All ewes were examined within three days of lambing and selected for treatment with oral closantel (10 mg/kg), a novel anthelmintic to Canada, if they met at least one of four criteria: a) the last grazing season was their first grazing season; b) body condition score (BCS) <2; c) Faffa Malan Chart (FAMACHA) score >3; and/or d) three or more lambs at foot. Fecal samples were collected per rectum on the treatment day from each of 20 randomly selected treated and untreated ewes on each farm.

Results: *Haemonchus* sp. percentages on each farm, as determined by coproculture, ranged from 77% to 97% of total fecal trichostrongyle-type egg counts. Mean FEC were significantly higher in treated ewes (n=138) than in untreated ewes (n=104) over both years of the study ($p=0.0003$). Univariable analyses found that FAMACHA score ($p<0.0001$) and BCS ($p=0.006$) were associated with FEC. A general linear mixed model was subsequently fit with logarithmic-transformed FEC as the outcome variable, the indicators as fixed effects, and year and farm as random effects. FAMACHA score was the sole indicator to remain significantly associated with FEC ($p=0.001$).

Conclusions: FAMACHA score is the most useful predictor of FEC in ewes immediately post-partum on farms with type II haemonchosis.

Relevance: FAMACHA should be included in TST programs to identify individuals requiring treatment.

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A method to visualise natural infection patterns of Leptospira serovars Hardjo and Pomona micro-agglutination test titres in sheep and cattle on New Zealand farms

Emilie Vallée[1], Cord Heuer[1], Julie Collins-Emerson[2], Jackie Benschop[2], Peter Wilson[3], [1]Massey University, Palmerston North, New Zealand; [2]Massey University, Palmerston North, New Zealand; [3]Massey University, Palmerston North, New Zealand. Contact: E.Vallee@massey.ac.nz

Purpose:
Leptospiral infection with serovars Hardjo (H) and Pomona (P) is widespread in New Zealand (NZ) sheep and beef cattle with up to 97% of flocks and herds seropositive. However, little is known about the epidemiology of H and P in these species on NZ farms.

Methods:
To explore exposure patterns a longitudinal study was conducted on 9 farms with 2260 ewe lambs enrolled when around 1 month old, 851 heifers enrolled at around 15 months old and 1174 calves enrolled between 2 and 6 months of age. Up to 7 blood samples in 27 months for sheep and up to 6 samples in 20 months for cattle were collected and tested by microscopic agglutination test (MAT) for H and P.
Zero-inflated Poisson models were used to model the log-transformed MAT titres as a function of age. A fixed effect for farm and a quadratic term for age were included. Predicted values and their confidence intervals were extracted and plotted as a function of age. The produced plots could be interpreted as adjusted farm-level geometric mean titres.

Results:
All the sheep flocks and cattle herds were exposed to H and 3 sheep flocks and 1 cattle herd had exposure to P during the study period. Maternal antibodies to H were identified, declining over 7 months in cattle and 3 months in sheep. A subsequent titre increase was consistent across the farmsbetween 10 to 20 months for all serovars in each species. A decrease after a peak was observed on some farms with a long follow-up period. More between-farm variation in pattern was observed for P than for H, and for cattle than for sheep.

Conclusions and relevance:
This method allowed ready visualisation of exposure patterns on individual farms, and collectively, without the need to choose a cut-point or define seroconversion. It can also be used in analytical studies to compare titres between groups and identify risk factors for exposure to *Leptospira*.

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The effect of *Leptospira* serovars Hardjo and Pomona on sheep growth and reproduction, and cost effectiveness of vaccination

Emilie Vallée[1], Cord Heuer[1], Julie Collins-Emerson[2], Jackie Benschop[2], Peter Wilson[3], [1]Massey University, Palmerston North, New Zealand; [2]Massey University, Palmerston North, New Zealand; [3]Massey University, Palmerston North, New Zealand. Contact: E.Vallee@massey.ac.nz

Purpose:
Leptospirosis causes clinical disease in sheep and is an important occupational disease in New Zealand (NZ). Up to 97% of NZ sheep flocks are seropositive to *Leptospira* serovars Hardjo (H) and/or Pomona (P), yet vaccination is rare. This study evaluated the impact of H and P on growth and reproduction and the cost-effectiveness of vaccination.

Methods:
A split-herd vaccination trial involved a bivalent H and P vaccination programme for 1/3 of 2260 ewe lambs on 8 farms starting at 1 month of age. Repeated blood samples were taken over 1 (n=6 farms, mated as hoggets) or 2 (n=2 farms, mated as 2-tooths) years for microscopic agglutination test to assess exposure to H and P. Weight and pregnancy, docking and weaning data were recorded.

Results:
All farms became positive for H at around 10 - 15 months and 3 became positive for P at around 8 - 15 months.
Preliminary results show that on the single farm where H infection was evident from 3 months of age, vaccinated lambs were 1 kg heavier at 12 months ($p < 0.05$). No other weight difference and no difference in reproduction outcomes were observed between vaccinated and control groups. However, when individual animal exposure status was analysed, control 2-tooths with P titres ≥192 were less likely to keep a lamb between docking and weaning (OR=0.20, 95% CI: 0.05-0.87, adjusted for farm and mating weight), for a difference in weaning rate of 0.19 percentage points between seropositive and seronegative sheep, on one farm with P exposure.

Conclusions and relevance:
A 1kg improvement in weight equates to an additional NZD2.5 income, less than the cost of a vaccination program. In the absence of reproduction effects, vaccination appears unlikely to be cost-effective on NZ sheep farms when related to animal production, on farms with exposure patterns similar to those observed in this study.

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Risk factors for ovine enzootic abortion in eastern region, Saudi Arabia

Ahmed M. Elmoslemany[1,2], Mahmoud Fayez[3], [1]King Faisal University, AL-Hasa, Saudi Arabia; [2]Kafrelsheikh University, Kafrelsheikh, Egypt; [3]Veterinary Serum and Research Institute, Cairo, Egypt. Contact: aelmoslemany@gmail.com

Purpose: *Chlamydophila abortus*, is the causative agent of ovine enzootic abortion, a disease primarily affects sheep and goats causing considerable reproductive losses worldwide. This study was conducted to investigate factors associated with ovine chlamydiosis in sheep in the eastern region of Saudi Arabia.
Methods: Blood samples were collected from 1717 ewes from 21 flocks located in the eastern region of Saudi Arabia over one year period. Serum samples were evaluated for antibodies against *C. abortus* using indirect ELISA (IDEXX Chlamydiosis Total Ab Test). Data on flock and animal levels risk factors were collected via questionnaire (with closed ended questions on management and biosecurity aspects) filled by the investigators during farm visits. The association between management practices and chlamydiosis in ewes was determined using mixed effect logistic regression (xtmelogit, stata 13) with random effect for flock.
Results: Univariable analyses ($P < 0.20$) indicated association between serological status for chlamydiosis and (flock size, age of ewes, adding new sheep into the flock, hygiene score of the farm and allowing ewes in or out farm during breeding season). The final multivariable model ($P < 0.05$) retained the following factors: large size flocks (>400) had higher odds of being sero-positive (OR=2.7) compared to small ones (<100). Ewes at 1.5-3 years had higher risk (OR=1.86) than younger ones. Flocks buying new animals from other flocks had higher odds (OR=3) compared to closed ones. Additionally, flocks allowing female in (OR=2.9) or female out (OR=2.5) were at higher risk of infection compared flocks with closed breeding system.
Conclusions: This study, highlights some important management factors that should be considered for prevention and control of ovine chlamydiosis in Saudi Arabia.
Relevance: Results from this study should be relevant to sheep producers using similar management practices in Saudi Arabia.

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Sero-epidemiological study on brucellosis in sheep and goats in Al-ahsa province, Saudi Arabia

Abdulmohsen Alnaeem, Abd-Alkareem Al-Bokair, King Faisal University, AL-Hasa, Saudi Arabia. Contact: aaalnaeem@kfu.edu.sa

Brucellosis is a major zoonotic disease affecting wide range of domestic and wild animals and caused Brucella Spp. The disease has both public health and economic significance worldwide. Therefore, the objectives of this study were to estimate prevalence of brucellosis in sheep and goats in AL-Hasa province, Eastern Region of Saudi Arabia, and to identify factors associated with small ruminant Brucellosis under local management and environmental conditions.
Blood samples were collected from 1472 animals (923 goats and 549 sheep) from 87 flocks located in the eastern region of Saudi Arabia over one year period. Serum samples were initially screened using Rose Bengal Plate Test (RBT) and positive samples were confirmed using indirect ELISA. Data on flock and animal levels risk factors were collected via questionnaire (with closed ended questions on management and biosecurity aspects) filled by the investigators during farm visits. Data on risk factors were analyzed using multivariable logistic regression.
The results showed that flock level prevalence of brucellosis was 23.88 % in both species, whereas animal level prevalence was 1.4% in goats and 0.94% in sheep. Univariable analyses ($P < 0.25$) indicated positive association between flock level prevalence and (flock size, mixed sheep and goat flocks, and grazing in a communal pasture), whereas having veterinary service was protective. The final multivariable model ($P < 0.05$) showed that large size flocks had higher odds of being sero-positive (OR=8.4653) compared to small ones. Additionally, flocks grazing in a communal pasture were associated with increased risk of brucellosis prevalence (OR=4.3152). In conclusion, this study, highlights some important factors that should be considered for prevention and control of small ruminant brucellosis in Saudi Arabia.

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What is the best date to vaccinate Sahelian sheep against peste des petits ruminants to get optimal immunity coverage?

Pachka Hammami, Renaud Lancelot, Matthieu Lesnoff, CIRAD, Montpellier, France. Contact: pachka.hammami@cirad.fr

According to FAO, >100 million sheep and goats (shoats) are reared in Sahelian Africa. Causing major losses, peste des petits ruminants (PPR) is the most serious infectious viral disease affecting shoats in this region. An existing vaccine provides a lifelong immunity after a single injection. A global PPR control strategy has been defined by OIE and FAO, relying on mass vaccination campaigns coordinated at the regional level. In Sahelian Africa, shoat reproduction is strongly seasonal according to available forage resources. Moreover, high offtake rates are met in lambs before the Tabaski feast (Aïd El Kebir), whose date is moving forward each year. These features result in seasonal variations in population structure and size.

This work aimed to find the best date to implement PPR vaccination campaigns in sheep. A matrix population model was built using monthly Leslie projection matrices. Demographic parameters were estimated from herd follow-up data collected in northern Senegal. We simulated vaccination campaigns assuming 100% of sheep > 3 months old were hit. Overall, 144 combinations of 12 offtake patterns (varying Tabaski month) with 12 vaccination months were assessed with 3 indicators: i) number of months with immunity coverage > 80%, ii) residual immunity 1 year post vaccination, and iii) mean annual immunity coverage. The figures below are given together with their 95% confidence intervals in brackets.

The Tabaski month weakly influenced the post-vaccination immunity decay. The highest number of protected months (9 [9 ; 9]) was reached for sheep vaccinated from May to July, and the lowest (3 [3 ; 4]) for vaccination in April. One year after vaccination, immunity rate ranged from 61% [61 ; 61] (vaccination in Aug.) to 72% [71 ; 72] (vaccination from Feb. to May). Mean immunity rate ranged from 88% [88 ; 88] (vaccination in July) to 77% [76 ; 77] (vaccination in Jan.).

Other criteria must be considered to choose the date of vaccination. For instance, farmers must be able to afford vaccination and sheep must be in good physiological status. For Sahelian sheep the best trade-off might be to implement vaccination between Sept. and Nov. We intend to use this method for goats and other agro-eco systems.

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The effect of morbidity on weaning weight of beef calves

Liesel G. Schneider, David R. Smith, Mississippi State University College of Veterinary Medicine, Mississippi State, MS, Contact: ljg103@msstate.edu

Purpose: Weaning weight is an economically important outcome to beef cow-calf operations. The objective of this study was to quantify the effects of pre-weaning illnesses on the weaning weight of beef calves.
Methods: Birth to weaning health and performance data from 14,798 steer calves over a 14 year period (1993-2006) at the US Meat Animal Research Center were analyzed. The effect of morbidity on weaning weight was tested using a generalized linear mixed model with a random effect of year. Calves were categorized as diseased or not and by the age of disease diagnosis: no disease; early (0d to 60d); middle (61d to 120d); and late (121d until weaning). Statistical significance was set at $\alpha \leq 0.05$.
Results: The average age and weight at weaning was 185 (std dev = 26) days and 221 (std dev = 35) kg respectively. The average number of calves weaned per year was 1057 (std dev = 228). Weaning weight increased by 0.76 kg for every one day increase in age at weaning. The total number of calves diagnosed over the 14 year period with bovine respiratory disease (BRD) was 1105 (7%), 615 (4%) with eye lesions, 251 (2%) with diarrhea, and 263 (2%) with lameness. Calves diagnosed with BRD or eye lesions at any age prior to weaning were significantly lighter weight at weaning than calves without. Compared to calves without BRD, calves with early BRD were 25 kg lighter at weaning, and calves with BRD in the middle and late ages were 8 kg lighter. Compared to calves without eye lesions, calves with early, middle, or late eye lesions were 28, 10, and 7 kg lighter at weaning, respectively. Calves with diarrhea in early or middle periods were approximately 23 kg lighter weight at weaning than calves without enteric disease. Calves with lameness in the middle or late age periods were 6 kg and 8 kg lighter at weaning, respectively, than calves with early or no lameness.
Conclusions: Morbidity in the first 60 days of life had the most detrimental effect on growth performance, with the exception of lameness in which the greatest effect was seen if it occurred after 60 days of age.
Relevance: Both if calves experience disease and the age of occurrence of specific diseases negatively affects weaning weight.

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Calf management practices and associations with herd-level morbidity and mortality on beef cow-calf operations in Western Canada

Christine F. Murray[1], Laura J. Fick[1], Edmond A. Pajor[1], Herman W. Barkema[1], Murray Jelinski[2], **M. Claire Windeyer**[1], [1]University of Calgary Faculty of Medicine, Calgary, AB, Canada; [2]Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, Canada. Contact: c.windeyer@ucalgary.ca

Purpose: The objectives of this study were to investigate management practices on cow-calf operations and to determine their association with herd-level morbidity and mortality of pre-weaned calves.
Methods: A survey about health management practices, morbidity, and mortality was administered by distributing paper surveys by mail and at conferences, and by circulating an online link through social media and in producer magazines. The survey was completed by 267 producers. Data were analyzed with descriptive statistics and multivariable linear regression.
Results: Most herds (37%) began calving in March. Herds that began calving in April had lower calf mortality from d 7 to weaning compared to those that began in January or February (P=0.02). Herds with a shorter calving season had lower mortality from d 7 to weaning (P=0.007). Over 86% of producers reported checking if a calf received colostrum by observing it suck. Also, 86% intervened if a calf did not consume adequate amounts of colostrum. Intervening with colostrum after assisted calving was associated with reduced mortality from d 7 to weaning (P=0.02). Herds that castrated calves by small elastrator band had a greater incidence of pre-weaning diarrhea (P=0.002) and death from d 1 to 7 (P=0.02). Only 4.4% of producers used pain medication at castration. Most producers (91%) used an antiparasiticide on cows, whereas less than 70% used it on calves, most commonly in the fall. The average herd-level mortality within the first 24 h of life, from d 1 to 7, and d 7 to weaning were 2.3, 1.1, and 1.4%, respectively. Average herd-level treatment for pre-weaning diarrhea and bovine respiratory disease (BRD) were 4.9 and 3.0%, respectively. Herds with a greater incidence of BRD had greater mortality from d 7 to weaning (P=0.001).
Conclusions: Calf diarrhea was associated with band castration, while mortality was associated with calving season, colostrum management, band castration, and BRD.
Relevance: Assessing the association of health management practices to the incidence of calfhood morbidity and mortality is an important step towards establishing evidence-based management to improve the health and survival of beef calves.

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An assessment of the farm-level impact of the *Theileria orientalis* (Ikeda) epidemic of cattle in New Zealand, 2012 - 2013: a mixed methods approach.

Daan Vink[1], Kevin Lawrence[2], Andrew M. J. McFadden[1], Paul Bingham[1], [1]Ministry for Primary Industries, Upper Hutt, New Zealand; [2]Massey University, Palmerston North, New Zealand. Contact: Daan.Vink@mpi.govt.nz

Background: *Theileria orientalis* (Ikeda), a tick-borne protozoan disease, was first identified in New Zealand in 2012. It has subsequently spread epidemically, and poses a significant challenge for the cattle production industries.
Objectives: To determine within-herd frequency and spatiotemporal spread of clinical theileriosis during the early phase of the epidemic.
Methods: A mixed methods approach was taken to integrate information derived from different sources. A detailed questionnaire was carried out on 18 dairy case farms. Subsequently, a telephone questionnaire eliciting information on measures of disease frequency was performed for an additional 139 case farms. Finally, data were extracted from a Ministry for Primary Industries (MPI) database for a further 42 case farms. Analysis consisted of calculation of disease frequency measures, and description of temporal and spatial spread. Triangulation of the data sources was carried out to assess the validity of making inferences.
Results: Data were analysed from 196 farms; this represented 74% of known case farms at the time. These farms contained 99,505 cattle; 2,856 animals were reported with clinical disease, and a further 590 animals were recorded as having died from theileriosis. The within-herd incidence risk, cumulative mortality and case fatality rate were estimated at 0.97%, 0.23% and 16.67%, respectively. There was substantial variability in the level of impact, with approximately 10% of farms severely affected. The reported temporal and spatial spread of disease was highly comparable with other reports.
Conclusions: The results from this study represent the best estimate of within-herd measures of disease frequency on cattle farms during the emergence and early spread of the disease. The inclusion of the majority of farms known to be affected at the time implies that the information is likely to be representative.
Relevance: In the absence of systematically-collected data from the early phase of an epidemic, retrospectively quantifying the impact of disease can be challenging. The mixed methods represents a flexible framework for integrating data from disparate sources, and making inferences.

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Using multiple streams of surveillance to monitor the epidemic of theileriosis (Ikeda) in cattle in New Zealand

Andy M. J. McFadden, Daan Vink, Ministry for Primary Industries, Lower Hutt, New Zealand. Contact: andrew.mcfadden@mpi.govt.nz

PURPOSE: To describe methods of past and current surveillance of the Theileria associated bovine anaemia (Ikeda; TABA) epidemic in New Zealand and the resulting inferences made from the spatial and temporal patterns of outbreaks observed.
METHODS: Over the three year period of the TABA epidemic a portfolio of surveillance methods have been used: case reporting (with subsidised PCR testing), syndromic surveillance, sentinel surveillance, serological surveillance as well as specific active surveillance initiatives to understand the tick vector distribution.
RESULTS: Surveillance data has shown that the number of affected cattle herds has continued to increase over time with seasonal peaks in autumn and spring coinciding with peak activity of nymph and adult ticks. In spring 2014, the epidemic extended south into areas that were previously considered to be of low tick risk. As a result a survey of the tick vector was initiated that showed that ticks were present in areas outside of the known distribution.
Target surveillance of pooled blood samples from cattle herds across New Zealand showed there still remained a significant percentage of herds where non-Ikeda types only were present indicating that these herds were at risk of future Ikeda outbreaks. For some regions there had been a noticeable increase in the percentage of herds infected, yet with only a small increase in the number of outbreaks reported from the previous year. Thus, outbreaks have gone unobserved or haven't been confirmed by testing. In these regions extensive low input beef farming could explain the non-detection observed.
There was a close relationship between the number of syndromic reports of anaemia and the number of confirmed cases of TABA (Ikeda), ($P<0.01$, Adjusted R-squared= 0.74).
CONCLUSIONS: Active monitoring of the epidemic for a three period has provided valuable insight into seasonal nature of the disease and its continuing impact.
RELEVANCE: The use of a portfolio of novel surveillance methods provides a case study of how methods of surveillance can be changed over time to accommodate for changing available resources and objectives.

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Use of routine herd data to estimate claw health in dairy herds

Henriette Brouwer[1], Thomas Dijkstra[2], Heleen Worm[2], Yvonne van der Vorst[3], **Gerdien van Schaik**[1], [1]GD Animal Health, Deventer, Netherlands; [2]GD Animal Health, Deventer, Netherlands; [3]Dairy Co-operative Royal FrieslandCampina, Amersfoort, Netherlands. Contact: g.v.schaik@gddiergezondheid.nl

Purpose:
Lameness in dairy cattle is an important issue. For sustainable dairy production, claw health should be improved. The claw health status of a herd can be assessed by clinical observation of individual cows, which is time consuming. The objective of the study was to develop an empirical model on routine herd data that could classify herds with a below or above average claw health.
Methods:
Two hundred dairy herds were visited by a veterinarian to determine the percentage of lame cows, the percentage of cows with visible hock or knee lesions and an overall grade for claw health. Routine herd data were obtained and transformed into cattle health parameters (CHP). Principal component analysis was used to combine the claw health parameters into a continuous observed claw health score. Herds were classified as herds below (score<0) or above average (score≥0) for claw health. The dataset was randomly divided in a test group of 150 herds to develop a predictive model and a group of 50 herds for validation of the model. Multivariable linear regression with a backward elimination procedure was carried out on routine herd data of the test group to find the best predictive model for claw health. With the final predictive model, the claw health status of the 50 validation herds was estimated. The agreement between the predicted relative to the observed claw health score was obtained with a two-by-two table.
Results:
The final predictive model explained 27% of the variance in the observed claw health score and contained cattle mortality, non-ear tagged calf mortality, replacement rate, no. of inseminations per cow, open or closed herd and the herd status for BVD, salmonella and IBR. The model correctly classified the claw health status for 72% of the validation herds with a sensitivity of 77% (95% CI 46-95%) and specificity of 76% (95% CI 57-90%).
Conclusions & Relevance:
The study showed that there is merit in estimating claw health of dairy farms using routine herd data. This provides the opportunity to monitor claw health in a population and classify individual herds for claw health. The claw health status of herds combined with a benchmark may stimulate herd owners to improve claw health in their herds.

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Randomized longitudinal study to test the effect of pre-calving vaccination of range beef cows and other factors on the incidence of calf pneumonia

David R. Smith[1], Amelia Woolums[1], Dale Grotelueschen[2], [1]Mississippi State University, Mississippi State, MS, [2]University of Nebraska-Lincoln, Clay Center, NE, Contact: david.smith@msstate.edu

Purpose:
The objective of this study was to test the effect of pre-calving vaccination of beef cows and other factors on the incidence of bovine respiratory disease (BRD) among calves in a ranch with a history of BRD incidence greater than 10%.

Methods:
Beef cows (n=430) in late-gestation were randomly assigned, using spreadsheet software, to two treatments: (1) pre-calving vaccination with a killed virus vaccine directed against BHV-I, BVDV types 1 and 2, PI-3 virus, and BRSV; or (2) no pre-calving vaccination. At treatment cattle body condition score, cow ID, and age were recorded. Calving dates, calving group, gender, birth weight, and date of first BRD treatment were recorded. Calves were observed for BRD from birth through backgrounding. Personnel who observed, diagnosed, and treated calves, were blinded to the treatment status of the dam.

Results:
Records from 388 calves were available for analysis. Associations between cumulative incidence of calf BRD and cow vaccination or other factors were tested in a GLMM logistic regression model with calving group as a random effect. The median days from vaccination to calving was 36 (mean 40, range 69) days. BRD was diagnosed in 45 calves (12%) ranging in age from 38 to 154 (median 64, mean 70) days of age. Twenty-three of 177 calves (13%) born to unvaccinated dams and 22 of 211 (10%) calves born to vaccinated dams developed BRD. Incidence of BRD was not significantly reduced by vaccine treatment (OR= 0.8, p=0.54) or by dam's body condition or age, calf birth weight, or when calves were born in the calving season. Male calves had a significantly greater incidence of BRD (OR = 2.0, p= 0.04). There was no evidence that the study design induced herd immunity because incidence of BRD was similar in other groups on the same ranch that did not receive pre-calving vaccination.

Conclusions:
Vaccination of late gestation cows did not reduce BRD incidence of calves. This study contributes to the evidence that male gender is associated with increased risk for calf BRD.

Relevance:
This study reveals that male calves may have greater risk for BRD and raises questions about the effectiveness of vaccinating cows against viral BRD pathogens prior to calving.

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The Effect of Group Size on the Respiratory Diseases and Work Load in Calf Rearing Unit- a Clinical Trial

Tuomas J. Herva[1], Timo Soveri[2], Reetta Palva[3], Sari Morri[4], [1]Atria Ltd., OULU, Finland; [2]University of Helsinki, Helsinki, Finland; [3]TTS - Work Efficiency Institute, Rajamäki, Finland; [4]TTS - Work Efficiency Institute, RajamäkiOULU, Finland. Contact: tuomas.herva@atria.fi

Control of respiratory diseases in calf rearing units is an important way to support animal welfare (AW) and limit usage of antibiotics and work load as well.
The objective was to study the effect of group size on respiratory diseases and work load. Two of six milk feeding compartments in a calf rearing unit with 1440 calves were randomly divided to one group with 40 calves and four groups of 10 calves. Three groups of 80 calves were reared and studied in both compartments. Clinical signs of calves, viral antibodies (PI3, BCV, BRSV), inflammation mediators and protein levels in blood sample were studied three times by two veterinary surgeons, on arrival, three weeks later and after weaning before moving calves to the following compartment.
All medications given according to the instructions of the unit veterinarian and the daily working time per each group were recorded by regular workers of the unit. Additionally, working time was measured by external audits once in the beginning of rearing and in the end of rearing.
Viral antibodies were found in most calves. There were not differences between small and big groups. Calves were healthier in small groups, although most calves (71% vs. 84%) had some respiratory signs in both groups. At the third examination, clinical signs of calves in bigger groups exceeded medication limits two times more often than calves in smaller groups. There were many antibiotic treatments in both groups. There was a trend towards increased treatments in big groups, but the difference was not significant. Serum amyloid A (SAA) levels were highest in young calves. The associations between group size, protein levels, clinical signs, SAA and haptoglobulin will be studied with more advanced methods.
Health inspections and medical treatments took 49-87% of all working time. Treatment incidence was a major factor affecting the work requirement. Working routines were well designed and daily work was efficient. Group size did not affect work requirement for other tasks than health inspections and medical treatment.
Group size was found to decrease incidence of respiratory disease and work load in calf rearing, which have important effect on AW and profitability of calf rearing.

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Somatic Cell Count in Milk from Dairy Cattle: The Dilution Effect Matters

Kaare Græsbøll[1], Carsten Kirkeby[1], Søren S. Nielsen[2], Tariq Halasa[1], Nils Toft[1], Lasse E. Christiansen[3], [1]Technical University of Denmark, Frederiksberg C, Denmark; [2]University of Copenhagen, Frederiksberg, Denmark; [3]Technical University of Denmark, Kgs. Lyngby, Denmark. Contact: kagr@dtu.dk

Background:
Danish dairy farmers receive a milk price depending on the somatic cell count (SCC) in the bulk tank. Therefore there is a large incentive to correctly identify and cull cows with persistently elevated levels of SCC. However, the SCC displays large variance between measurements and varies over lactations, which makes analysis difficult. Traditionally, SCC has been modelled without a dilution effect, unrelated to the amount of milk produced.

Purpose:
Using data from 610 Danish farms with a total of >290,000 Holstein cattle over a period of 13 years, we investigated several transformations of the SCC measure from each cow. The aim was to determine the most robust estimate in terms of normality of residuals and variance of the estimate.

Methods:
We used different log transformations and included the dilution factor by looking at not only the SCC per mL milk, but also the total count of bacteria in the milk. Normality was tested by Q-Q plots. Furthermore, we tested correlations between milk yield and the SCC.

Results:
All tested transformations of the SCC using the total count reduced the variance of the residuals of the model by a factor of two. A double log transformation of the SCC gave the best normality of residuals. Analysis of the correlations showed positive correlation of SCC with the milk yield, when using the total count of SCC.

Conclusions:
The level of SCC for a dairy cow is best determined using the total count of SCC in the milk. We therefore conclude that the dilution effect is an important factor in dairy production.

Relevance:
Determining the most robust method of predicting the SCC is economically important for farmers that need to take decisions on which cows are most valuable. Therefore, the dilution effect should be taken into consideration when estimating the SCC level of each cow. Furthermore, for a robust estimate when simulating dairy farms or predicting future values of dairy cows, the dilution effect should also be included.

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Drinking water management to reduce E. coli O157:H7 shedding in finishing cattle: Intervention trial

Renata Ivanek[1], Melissa Bean[2], Elena Gart[2], Kallie McWhinney[2], Glenn Lahodny[2], Karina Baumgarten[2], Sara Lawhon[2], Kendra Nightingale[3], Pablo Pinedo[4], [1]Cornell University, Ithaca, NY, [2]Texas A&M University, College Station, TX, [3]Texas Tech University, Lubbock, TX, [4]Texas A&M AgriLife Research, Amarillo, TX, Contact: ri25@cornell.edu

Purpose: Previous studies identified drinking water as a pathway of Escherichia coli O157:H7 (ECO157) transmission in feedlots, with drinking water-to-cattle ratio as a suspected modulator of the process. Water-to-cattle ratio is estimated by dividing the volume of standing water in water-troughs in a pen with the number of heads in the pen. An automatic system refills water as cattle drink; with lower water-to-cattle ratio cattle drink fresher water. The objective was to conduct a randomized intervention trial to test if altering water-to-cattle ratio can control ECO157.
Methods: The trial was conducted in summer 2014 in a Texas feedlot. ECO157 detection was based on the culture with enrichment. All 192 feedlot pens were tested with boot swabs and 23 were positive. Of these, 19 pens were enrolled into the trial after blocking on days in feeding. In each pen 40 fresh fecal pats were tested for ECO157. Drinking water samples were tested for ECO157 and to enumerate generic E. coli and Coliforms. The intervention consisted of reducing the volume of water in drinking troughs to 1/2 of the original value in 10 of the enrolled pens (intervention pens) while no changes were made in the other 9 pens (control pens). Fecal and water samples were tested before and 3 weeks after the start of the trial. A total of 1,519 fecal and 38 water samples were tested. Analysis accounted for repeated measures and pen clustering.
Results: Fecal pats in treatment pens (with lowered water-to-cattle ratio) had increased odds of being ECO157 positive compared to control pens (Odds Ratio (OR) = 1.5; 95% Confidence Interval (CI) = 1.06 - 2.10). For every additional gallon of water available per head the odds of a fecal pat being positive reduced 7.5 times (OR = 0.13; 95% CI = 0.03 - 0.7). The levels of generic E. coli and Coliforms were higher in the treatment compared to control pens.
Conclusions: Results suggest a protective dilution effect of a higher water-to-cattle ratio and that lowering water-to-cattle ratio may facilitate the spread of ECO157. The intervention trial is repeated in summer 2015 to test repeatability of findings.
Relevance: Increasing water volume in water-troughs may serve as a novel strategy to control ECO157 in feedlots.

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Close proximity contact network and activity patterns for Digital dermatitis and Escherichia coli O157 (EHEC O157) shedding in beef cattle

Dorte Dopfer, UW-Madison, School of Veterinary Medicine, Madison, WI, Contact: dopferd@vetmed.wisc.edu

Purpose
The dynamics of infectious diseases depends on the contact structure of susceptible individuals with infected individuals in a closed population. At the same time, it is likely that infectious diseases affecting locomotion in cattle will modify contact patterns and therefore shedding patterns of other pathogens. From pilot studies in the field, we have found that Digital dermatitis (DD), and shedding of EHEC O157 are negatively associated and set out to confirm this in a larger group of cattle.
Methods
Wearable motes transmitting radio signals together with accelerometers were attached to140 beef cattle housed in one US Midwestern feedlot pen for five days. Ten stationary radio loggers were evenly spaced and attached to the pen perimeter. Data were recorded once every minute. Fecal grab samples, locomotion scoring, Foot Rot and DD stages were recorded before and after the 5-day period. Contact structures and activity patterns of the cattle were analyzed using a network approach in R 3.2.1. Video cameras recorded cattle movements and contacts every 30 seconds, while cattle had a color code on their backs for identification.
Results
The data set sheds light on the dynamics of EHEC O157 shedding patterns in relation to lameness, IP presence, DD stages and the cattle's contact patterns over time. Activity patterns for cattle with and without DD are different depending on the clinical stage of DD or IP and they are related to shedding patterns of EHEC O157.
Conclusions
Accerlerometers will confirm that cattle with DD will stand for longer periods of time, lay down for longer periods of time and overall not change their movements if they can avoid it due to pain. At the same time, cattle that do not move much will become infected with EHEC O157 as often and consequently not shed the pathogens as often as the ones that move freely within their pens.
Relevance
Using close proximity contact networks and activity patterns of populations of animals or humans, the transmission dynamics of infectious diseases can be studied and parameters for transmission models of infection estimated. The current example will result in the data analysis routines for similar data sets from other infections and populations.

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Modeling variability associated with estimating concentrations of six non-O157 E. coli serogroups in cattle feces based on a multiplex quantitative PCR.

Pius S. Ekong, Michael W. Sanderson, Pragathi B. Shridhar, Jianfa Bai, T. G. Nagaraja, Kansas State University, Manhattan, KS, Contact: pekong@k-state.edu

Purpose
The concentration of non-O157 STEC in the cattle production system is necessary for quantitative microbial risk assessment, but values are difficult to obtain. In order to provide an estimate of the concentration of non-O157 STEC detected in cattle feces and the variability around the concentration estimate, we developed a Monte Carlo simulation model in @RISK based on multiplex quantitative PCR (mqPCR) cycle threshold (C_T) values.
Methods
We utilized mqPCR assays that targeted serogroup-specific genes to detect and quantify the six major non-O157 STEC in cattle feces. A linear equation was fit based on data from post enrichment C_T values and pre-enrichment colony counts (CFU/g) in fecal samples spiked with ten-fold serial dilutions of pooled pure cultures of O26, O103 and O111; and O45, O121 and O145 serogroups. Distributions were fitted to intercept and slope parameters of the linear equations and using a uniform distribution of C_T values, estimates of variability around the calculated concentrations were generated. Distributions of C_T values for each serogroup obtained from feces of 576 naturally-shedding cattle (observed C_T 20.57 - 38.04) were used in the resulting model to predict the field distribution of fecal concentrations and their variability estimates.
Results
Variability around the concentration estimate was similar across the range of positive C_T values. At a C_T of 25, the models predicted a log count of 5.33 CFU/g for O26, O103 and O111 serogroups, (95% prediction interval ±0.66 log), and for O45, O121 and O145 serogroups predicted log count was 5.12 CFU/g, ±0.88 log. Estimated mean log concentration for O26, O103 and O111 in positive field samples was 4.55 (range: 2.31-7.32). For O45, O121 and O145, it was 4.59 (range: 1.98-6.79). Model concentration results were validated against spiral plating counts on field data. Further work will estimate the full distribution of concentrations in field fecal samples accounting for PCR false negative samples.
Conclusions and Relevance
These results provide a method to estimate concentration of STEC in cattle feces along with their measures of uncertainty in PCR positive samples for use in quantitative microbial risk analysis.

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Factors affecting Escherichia coli O157:H7 hide contamination of feedlot cattle

Liesel G. Schneider[1], Galen E. Erickson[2], Rodney A. Moxley[3], David R. Smith[1], [1]Mississippi State University College of Veterinary Medicine, Mississippi State, MS, [2]University of Nebraska-Lincoln, Lincoln, NE, [3]University of Nebraska-Lincoln, Lincoln, NE, Contact: ljg103@msstate.edu

Purpose: Cattle are reservoirs of Shiga-toxin producing Escherichia coli O157:H7 (STEC O157). Hide-to-carcass transfer of STEC O157 at harvest presents a risk for beef contamination and human foodborne exposure. Our objective was to determine factors that increase prevalence of hide contamination in feedlot cattle.
Methods: We analyzed a dataset with culture results of feces, TRM cells, and hide swabs collected during a randomized controlled study to test the effect of vaccination on STEC O157 carriage by feedlot cattle. In that study, steers (n=504) were assigned to 63 pens (8 animals/pen) in 3 vaccination treatment regions of the feedlot. Treatments were assigned to pens within each region as follows: (1) two doses of vaccine (ALLVAC), (2) two doses of adjuvant placebo (NOVAC), or (3) commingled vaccination where four of the eight steers received two doses of vaccine and the others were given placebo (HALFVAC). Fecal shedding of STEC O157 was measured by culture of feces collected from the rectum on the last day in the feedyard 84 days post vaccination (dpv). Hide contamination and TRM colonization was measured by culture of samples collected at the abattoir 85 dpv. Data were analyzed using a multilevel multivariable logistic regression in a generalized linear mixed model with random effects of pen and time block as appropriate for the level of analysis.
Results: Pen vaccination was significant in both individual and pen-level analyses ($p<0.05$). At the individual-level, neither fecal shedding nor TRM colonization with STEC O157 were significant in predicting whether steers had contaminated hides, (OR 1.74, p=0.107) and (OR 1.13, p=0.76) respectively. At the pen-level, each additional 10 percent of TRM colonized cattle in the pen significantly increased the odds for hide contamination (OR 1.17, 95% CI: 1.01-1.35, p= 0.043), but prevalence of fecal shedding in the pen was not associated with odds for hide contamination (p=0.75).
Conclusions: Pen-level prevalence of TRM colonization was predictive of hide contamination.
Relevance: Therefore, strategies to reduce prevalence of hide contamination with STEC O157 should focus on group-based methods that reduce prevalence of TRM colonization.

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Synchronisation of *E. coli* O157 in an extensive beef system: a longitudinal study

Geraldine A. C. Lammers[1], Craig S. McConnel[2], David Jordan[3], Stephen Morris[3], Michael P. Ward[4], Jane Heller[1], [1]Charles Sturt University, Wagga Wagga, Australia; [2]Colorado State University, Fort Collins, CO, [3]New South Wales Department of Primary Industries, Wollongbar, Australia; [4]The University of Sydney, Sydney, Australia. Contact: glammers@csu.edu.au

Purpose:
Escherichia coli O157 is a bovine gut-commensal capable of causing serious disease and death in humans. Intermittent patterns of shedding have been shown in calves, but little is known about the shedding pattern of live adult beef cattle. This study aimed to describe in detail the temporal dynamics and risk factors for shedding of *E. coli* O157 in grass-fed beef cattle.

Methods:
An observational study was performed in which the presence and concentration of *E. coli* O157 in faeces was identified on a bi-weekly basis over nine months. Trend in the proportion of animals testing positive to *E. coli* O157 on each sampling day was estimated by a cubic spline model. Visual assessment of this curve revealed that three discrete peaks in shedding occurred over the study period. The three peaks with an estimated proportion of herd shedding at greater than 20% were described as a "herd shedding event". Reassessing the data in light of herd shedding events allowed all sampling points to be classified as occurring within six discrete events comprised of three shedding events alternating with three non-shedding events. Generalised linear mixed models were used to assess whether variation in animal, environmental and management variables at each sampling point could be associated with a "herd shedding event".

Results:
This study demonstrated that there was synchronisation of shedding amongst cows accompanied by a marked elevation in the concentration of the pathogen in faeces. The occurrence of rainfall ($P<0.01$) was found to be a predictor of shedding.

Conclusion:
This approach, based on short-interval sampling, confirms the known variability of shedding within a herd and highlights that high shedding events are rare. The extent of individual animal variability revealed in this work and previous studies casts doubt on findings of risk factor studies where outcomes are based on single assessment of dichotomous shedding status.

Relevance:
The major findings suggest that animals within a herd can be synchronised in their shedding (and non-shedding) which may have practical implications for the risk of human exposure to *E. coli* O157 and implementation of control measures at the level of the abattoir.

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Stress and E. coli O157 shedding in cattle.

Clare A. Ferris, Jane Heller, Geraldine Lammers, Victoria Brookes, Glenys Noble, Charles Sturt University, Wagga Wagga, Australia. Contact: clareferris88@gmail.com

Purpose:
Cattle are a major reservoir of *E. coli* O157 and source of food-borne disease outbreaks worldwide. Individual animals exhibit significant variation in faecal shedding of *E. coli* O157 despite known environmental exposure to the bacteria. The host factors that predispose ruminants to *E. coli* O157 colonisation and the variation in individual animal shedding remain poorly understood. The aim of this study was to explore the relationship between physiological stress and the presence and concentration of *E. coli* O157 shedding in cattle.
Methods:
Faecal samples were collected from 24 beef cows daily over 14 days in summer. The concentration of faecal glucocorticoid metabolites (FGMs) was measured using the previously validated corticosterone I^{125} radioimmunoassay kit. The faecal samples were also analysed for *E. coli* O157 using standard techniques. Statistical analyses were performed using a mixed model approach to determine associations between FGMs, numerous environmental variables and a) presence and b) concentration of *E.coli* O157.
Results:
Associations were identified between FGMs and presence ($P = 0.018$) and concentration ($P = 0.012$) of *E. coli* O157 in bovine faeces. Both probability of shedding and quantity of pathogen shed increased with increasing FGMs and changes in FGMs were found to precede changes in shedding. Interactions were also identified between humidity and FGMs, for both models ($P = 0.030$ and $P = 0.028$ respectively).
Conclusions:
The findings of the present study are the first to show an association between the concentration of FGMs, as a measure of physiological stress, and the presence and concentration of *E. coli* O157 in bovine faeces.
Relevance:
Despite extensive research and increased implementation of intervention strategies to minimise shedding and carcase contamination, foodborne outbreaks of *E. coli* O157 continue to occur. This study identifies a link between a marker of physiological stress and the occurrence and quantity of pathogen shed that warrants further investigation in order to elucidate the precise nature of the link and potentially facilitate the development of targeted mitigation strategies.

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Saltelli sensitivity analysis to identify risk factors for beef carcass contamination with E. coli O157

Victoria J. Brookes[1], David Jordan[2], Stephen Davis[3], Michael P. Ward[4], Jane Heller[1], [1]Charles Sturt University, Wagga Wagga, Australia; [2]NSW Department of Primary Industries, Wollongbar, Australia; [3]RMIT, Melbourne, Australia; [4]University of Sydney, Sydney, Australia. Contact: viki.brookes@bigpond.com

Purpose:
Escherichia coli O157 (STEC O157) is an important foodborne pathogen in humans, with cattle the main reservoir. Despite much microbiological research, it is still uncertain which risk factors most influence beef carcass contamination; therefore, it is difficult to determine the most effective mitigation strategies in the beef harvest chain. We address this gap using a stochastic, individual-animal based, computational model and Saltelli sensitivity analysis, a method not previously used in animal disease modelling.
Methods:
Information from previous empirical studies was used to parameterise model inputs (18 risk factors). Saltelli global sensitivity analysis (GSA) - a variance-based method that can account for non-linearities and interactions between inputs, providing greater insight about the importance of inputs than traditional methods for sensitivity analysis - was used to identify risk factors with the greatest influence on variance of output (the prevalence of STEC O157 contaminated beef carcasses) and guided the stepwise introduction of interventions.
Results:
The sum of total effect sensitivity indices (1.38) indicated that interactions between risk factors strongly influenced output in this model. Therefore, interventions were most effective when introduced in combination, when the reduction in STEC O157 contaminated carcasses was greater than that expected due to an additive effect. Improved abattoir hygiene - reduction of transfer of STEC O157 from both hide and gut to carcass - was the most effective combination. Interventions introduced subsequently, for example, vaccination, had relatively small impact on output.
Conclusions:
This model and Saltelli GSA provided insight with practical application; improving abattoir hygiene is likely to be the most effective mitigation strategy, and targeting interventions at individual risk factors is likely to be ineffective in reducing the prevalence of STEC O157 contaminated carcasses.
Relevance:
Implementation of effective combinations of interventions might reduce the incidence of STEC O157 associated disease in humans. Saltelli GSA shows promise for analysing complex modelling data.

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Understanding antibiotic prescribing behaviours by pig veterinary surgeons: a mixed methods approach.

Gina Pinchbeck[1], Lucy Coyne[1], Nicola Williams[1], Susan Dawson[2], Robert Smith[3], Richard Pearson[4], Sophia Latham[1], [1]University of Liverpool, Liverpool, United Kingdom; [2]University of Liverpool, Liverpool, United Kingdom; [3]University of Liverpool, Liverpool, United Kingdom; [4]The George Pig Practice, Malmesbury, United Kingdom. Contact: ginap@liv.ac.uk

Background: The prudent use of antibiotics is essential to reduce selection pressure and preserve efficacy and availability for use by veterinarians. In the UK pigs contribute the largest proportion towards the sale of single species antibiotic products.
Objective: The aim of this study was to develop an understanding of the drivers and attitudes around antibiotic prescribing decisions and behaviours by vets working in pig practice in the UK.
Methods: A mixed methods approach was employed including qualitative in-depth interviews with purposively selected pig veterinarians (n=21) followed by a cross sectional questionnaire that encompassed concepts from the interviews and gathered data from veterinarians that treated pigs across the UK (n=61).
Results: 8 major and 76 minor themes emerged from thematic analyses of the interviews. Major themes included Agricultural Factors; External Pressures; Vet-Client Relationship; Drug-related Factors; Disease Epidemiology and Outcomes; Responsibility; Economic Factors; and Knowledge Base. The majority opinion was that vets considered themselves to use antibiotics responsibly but a minority felt that others, both within and outside of the pig sector, may be less responsible. Vets did not perceive resistance a major problem for the health of pigs in the UK currently, but did report treatment failures. Vets perceived pressure from clients to prescribe antibiotics or a particular antibiotic and, in some cases, to continue to prescribe in feed antibiotics perceived to be effective.
Questionnaire responses indicated that 100% of vets felt they were quite or very important in terms of responsibility for the prudent use of antibiotics, whereas lower proportions felt that famers, retailers and, government were important. 52% of vets reported that they sometimes encountered a lack of response to antibiotics and 39% felt this was due to resistance; with 31% reporting that resistance was demonstrated on culture and sensitivity.
Conclusions and relevance: This mixed methods approach described behaviours and attitudes underpinning prescribing practice, a critical step towards designing strategies to promote effective antibiotic prescribing.

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Transmission dynamics of ESBL-*E. coli* in a broiler flock without antibiotic pressure

Patricia M. C. Huijbers[1], Elisabeth A. M. Graat[1], Angela H. A. M. van Hoek[2], Christiaan Veenman[2], Mart C. M. de Jong[1], Engeline van Duijkeren[2], [1]Wageningen University, Wageningen, Netherlands; [2]National Institute for Public Health and the Environment, Bilthoven, Netherlands. Contact: patricia.huijbers@wur.nl

Purpose: The aim was to quantify transmission rates and routes of extended-spectrum β-lactamase-producing *Escherichia coli* (ESBL-EC), and specific phylogenetic groups, in an organic broiler flock where no antibiotics are used.
Methods: Eighty randomly chosen broilers were followed individually. Cloacal swabs from these, and 20 other randomly chosen broilers, and 11 environmental samples were taken from arrival till slaughter (day 1, 3, 4, 7, 10, 42, 70). ESBL-EC were isolated using standard procedures. Transmission was described using a susceptible-infectious-susceptible model. The log of transmission parameter β was estimated using a Generalised Linear Model for binomial distributed data, with complementary log-log link function, and an offset variable using ESBL-prevalence of broiler and environmental samples. Effect of direct contact was included as explanatory variable. R_0 was calculated by multiplying β with length of the infectious period, based on the observed average duration of successive positive results.
Results: ESBL-EC prevalence was 24.0% in broilers, and 45.5% in environmental samples on day 1, with A1 as dominant EC phylogenetic group. After 3 days, almost 100% of broiler and environmental samples were positive, with a shift towards more different phylogenetic groups. R_0 was 1.35 (95% CI 1.09-1.68) for total ESBL-EC, and environment seemed relatively more important in transmission compared to direct broiler contact. When looking at phylogenetic groups separately, R_0 was 0.77 (95% CI 0.62-0.95) and 0.32 (95% CI 0.24-0.41) for A1 and B1 groups respectively, and direct broiler contact appeared relatively more important.
Conclusion: This suggests that total ESBL-EC persistence, and resulting endemic situation, is determined by shifts in phylogenetic groups. Positive day old chicks and the environment both play a role in introduction into new flocks.
Relevance: ESBL-EC, found at all levels of the broiler production pyramid, might present a threat for public health, as ESBL mediated resistance complicates treatment of human bacterial infections. Insight in farm transmission dynamics could provide a basis for control, leading to fewer contaminated broilers.

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Application of a Rapid Knowledge Synthesis and Transfer Approach to Assess the Microbial Safety of Low-Moisture Foods

Lisa Waddell[1], Ian Young[2], Sarah Cahill[2], Mina Kojima[3], Renata Clarke[2], Andrijana Rajic[2], [1]Public Health Agency of Canada, Guelph, ON, Canada; [2]Food and Agricultural Organisation, Rome, Italy; [3]World Health Organisation, Rome, Italy. Contact: lisa.waddell@phac-aspc.gc.ca

Purpose:
Low-moisture foods (LMF) are increasingly implicated in outbreaks of foodborne illness resulting in a significant public health burden. The Codex Alimentarius Committee on Food Hygiene initiated work to develop a Code of Hygienic Practice to set standardized and comprehensive international guidance on the microbial safety of LMF. To inform the development of the new Codex guidelines with rigorous and transparent scientific inputs, we applied a rapid knowledge synthesis and transfer approach to review global research on the burden of illness, prevalence, and interventions to control selected microbial hazards in LMF.
Methods:
Knowledge synthesis methods included an integrated scoping review (search strategy, relevance screening and confirmation, and evidence mapping), systematic review (detailed data extraction), and meta-analysis of prevalence data. Knowledge transfer of the results was achieved through multiple reporting formats, including evidence “summary cards”.
Results:
From eight categories of LMF products and nine microbial hazards, ‘cereals and grains’ (n=142) and *Salmonella* spp. (n=278) were the most commonly investigated. *Salmonella* spp. was implicated in the most outbreaks (n=96, 45%), resulting in the most hospitalizations (n=895, 89%) and deaths (n=14, 74%) attributed to LMF. *Salmonella* spp. had a consistently low prevalence across all LMF categories (0-3%), while
other hazards (e.g. *B. cereus*) were found at highly variable levels. A variety of interventions were investigated in small challenge trials. Key knowledge gaps included under-reporting of LMF outbreaks, limited reporting of microbial concentration data from prevalence studies, and a lack of intervention-efficacy research under commercial conditions. Summary cards for each LMF category were a useful knowledge transfer format to inform complementary risk ranking activities.
Conclusion / Relevance:
This review builds upon previous work in this area by synthesizing a broad range of evidence using a structured, transparent, and integrated approach to provide timely evidence-informed inputs into the decision-making process for developing international guidelines.

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In vivo effect of ingestion of milk containing drug residues on fecal microbiota and selection of resistant Escherichia coli in preweaned dairy calves.

Richard Pereira, Svetlana Lima, Julie Siler, Carla Foditsch, Rodrigo Bicalho, Lorin Warnick, Cornell University, Ithaca, NY, Contact: rvp25@cornell.edu

Purpose: Evaluate effects of ingestion of milk containing drug residues on fecal microbiota and selection of resistant Escherichia coli in preweaned dairy calves
Methods: At birth, thirty calves were randomly assigned to a controlled feeding trial where: 15 calves were fed raw milk without the addition of antimicrobial drugs (NR), and 15 calves were fed raw milk with the addition of ceftiofur, penicillin, ampicillin and oxytetracycline at final concentrations in the milk of 0.1, 0.005, 0.01, and 0.3 μg/ml (DR).
Results: A significantly greater proportion of E. coli resistant to ampicillin, cefoxitin, ceftiofur, streptomycin and tetracycline was observed in DR calves when compared to NR calves. Additionally, isolates from DR calves had a significant decrease in susceptibility to ceftriaxone and ceftiofur when compared to isolates from NR calves. A greater proportion of E. coli isolates from calves in the DR group were resistant to 3 or more antimicrobial drugs when compared to calves in the NR group. Discriminant analysis showed that, except for pre-treatment samples, DR and NR calves' weekly microbial profile discriminated at the genus level. However, analysis comparing the abundance of taxon between NR and DR showed significant differences only at the genus levels, and not at the phylum, class, order or family levels.
Conclusions: These findings highlight the role that ingestion of sub-MICs of antimicrobials has on the selection of antimicrobial resistance E. coli and on the fecal microbial community in preweaned calves.
Relevance: Although antimicrobial drugs are central to combat disease in modern medicine, the use of these drugs can have undesired consequences for human and animal health. One consequence is the post-therapy excretion of pharmacological agents, such as the elimination of drug residues in the milk of lactating mammals. The ingestion of milk with drug residues is a concern to humans and animals. In the United States approximately one third of dairy farms feed milk containing drug residues to calves. Potential outcomes from this practice include disruption of the developing gut microbiota and selection of antimicrobial resistance.

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A quantitative risk assessment for transfer of ESBL-producing E. coli to calves via waste milk.

Robin Simons, Louise Kelly, Emma Snary, Lucy Brunton, Verity Horigan, Jeff Jones, Animal and Plant Health Agency (APHA), Addlestone, United Kingdom. Contact: robin.simons@apha.gsi.gov.uk

Purpose:
Antimicrobial resistant bacteria are an increasing problem and a major concern for both animal and human health. Antimicrobial usage is considered a major determinant for the selection and spread of resistant microorganisms which can become refractory to front line treatments in hospitals, rendering them ineffective.
Waste milk is milk unfit for human consumption, including that from treated cattle. It may contain antibiotic residues which could increase the risk of selection for resistant bacteria. In the UK it can be common practice to feed waste milk to calves.
Methods:
A stochastic simulation model was developed to assess the risk of transfer of, and selection for, E. coli with resistance to extend-spectrum β-lactam antibiotics (ESBL E. coli) to calves, via the feeding of waste milk. Scenarios were modelled to investigate the impact of practical control measures aimed to minimise the risk.
Results:
The results of the baseline model predict an average farm level prevalence (over 5,000 simulated farms) of calves with ESBL E. coli in their faeces of 75% (5th and 95th percentiles (pctl) 0% and 100%), while the average prevalence of calves with residues in their gut was 83.3% (5th and 95th pctl 0% and 100%). The baseline model predicted an average concentration of ESBL E. coli in calf faeces of 5.6 log cfu/g (5th and 95th pctl 1.3 - 8.7 log cfu/g), while the average concentration in scenarios with no residues present was only 2 log cfu/g. There was very wide variability and uncertainty in the actual dairy cow prevalence of ESBL E. coli, sensitivity analysis of the model suggests that this is very important with regards to the ESBL E. coli prevalence and microbial load in calves predicted by the model.
Conclusions/Relevance:
The scenario analyses indicated that completely stopping the practice of feeding waste milk to calves was the most effective measure, but a scenario assuming complete eradication of ESBL E. coli and residues from the waste milk was almost as effective. Thus, the model suggests that any potential intervention package targeted at the waste milk tanks must be able to deliver a large reduction of both ESBL E. coli and residues in the waste milk tank in order to be considered effective.

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Direct economic cost of bovine respiratory disease in US beef calves prior to weaning

Min Wang, Liesel G. Schneider, David R. Smith, College of Veterinary Medicine,Mississippi State University, Mississippi State, MS, Contact: mw1981@msstate.edu

Purpose: Bovine respiratory disease (BRD) is a leading cause of sickness and death in pre-weaned beef calves. The economic loss due to BRD in feedlot cattle has been reported, but similar information for beef calves prior to weaning is not available. The objective was to estimate the direct economic cost of BRD in beef calves prior to weaning.
Methods: Data were obtained from USDA reports (NAHMS 2007-2008, NASS 2014, and AMS 2014), peer-reviewed papers, and surveys to veterinary professionals. A stochastic simulation model was conducted using computer spreadsheet add-on software. The model was comprised of three parts, cost of BRD mortality, cost to treat BRD, and losses associated with decreased weaning weight from BRD based on the beef cow inventory in 2014. The input variables included percentage of beef cows that calved, percentage of calves born alive, percentage of calves born alive but died before weaning, percentage of deaths at any pre-weaning age due to BRD, weaning weight of calves, 2014 market price of calves weighing 226.8-249.5kg, BRD incidence rate, weight lost due to BRD, and cost to treat a calf for BRD, including estimates for medication and diagnostic costs. Labor costs to treat calves were not included.
Results: The results showed the estimate of the total direct economic cost of BRD in pre-weaned beef calves for 2014 was $259.4 million (90% CrI 178.4-367.1), of which the total death losses, medical treatment cost and weight loss cost were $179.0 million (90% CrI 123.4-241.7), $26.6 million (90% CrI 11.6-56.0), and $53.8 million (90% CrI 27.2-110.3), respectively. Costs associated with death due to BRD in calves <3 weeks and ≥3 weeks of age were $60.7 million (90% CrI 38.3-86.5) and $118.3 million (90% CrI 78.2-164.1), respectively.
Conclusions: We estimate that BRD in pre-weaned beef calves most likely cost US cattle farmers $259.4 million in 2014, of which the largest component (45.6%) was death in calves ≥3 weeks.
Relevance: Strategies to decrease BRD deaths in calves ≥3 weeks of age might best minimize the cost of BRD in pre-weaned beef calves.

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National screening of Antibodies against Bovine Respiratory Syncytial Virus and Bovine Coronavirus and the association to Herd Health

Anna Ohlson[1], Nils Fall[2], Håkan Landin[1], Jonas Carlsson[1], [1]Växa Sweden, Stockholm, Sweden; [2]Swedish University of Agricultural Sciences, Uppsala, Sweden. Contact: anna.ohlson@vxa.se

Purpose:
Bovine respiratory syncytial virus (BRSV) and bovine corona virus (BCV) affects cattle worldwide. In order to investigate the possibility of a future control program for these infections, the national and regional prevalences need to be mapped out. Our objective was to examine the prevalence of antibodies against BRSV and BCV in Swedish dairy herds and to evaluate possible association between herd health and antibody status. **Methods:**
We included bulk tank milk (BTM) from 4661 dairy herds, corresponding to 95% of all existing dairy herds in Sweden. Herd health data was available from 3541 herds. Logistic and linear regression models were used to evaluate the association regarding herd health parameters between the 177 herds that were antibody negative to both BRSV and BCV and 3364 herds positive to BRSV and/or BCV.
Results: The prevalence was 84% for BSRV and 90% for BCV. There were large regional differences; 21-99% and 60-100 % for BRSV and BCV respectively, with the lowest prevalence in the northern counties. Herds that were antibody-positive to BCV and/or BRSV had higher BTM somatic cell count, higher calf mortality as well as cow culling rate compared to herds negative to both BCV and BRSV.
Conclusions:
The BTM status reflects the long term history of the herds which implies that negative herds have been free from the infections for many years. The current situation for BRSV in the northern parts of Sweden is appropriate for the initiation of a voluntary control program based on increased awareness and biosecurity measures targeting indirect contacts and purchase of animals.
Relevance:
Given that Sweden and the other Scandinavian countries have successfully eradicated bovine viral diarrhea virus, a possible challenge would be to establish areas with freedom from BRSV and perhaps BCV. A reduced incidence would benefit the farmer economically, enhance animal welfare, and reduce the use of antibiotics.

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Preliminary control and eradication measures for Lumpy Skin Disease in northern part of Cyprus

Mehmet Demirpence[1], Vittorio Cagnolati[2], Huda Hudaoglu[1], Ramadan Goksan[1], [1]Veterinary department, Nicosia, Cyprus; [2]European Commission, Brussels, Belgium. Contact: vittorio.cagnolati@ec.europa.eu

Purpose:
The objective is to describe the first outbreak of Lumpy Skin Disease in the northern part of Cyprus and measures enforced to control and eradicate the disease from the island

Methods:
Cyprus is the third largest island (9,251km^2) in the Mediterranean Sea with the Northern Part (3,355km^2) hosting 66,000 cattle, 240,000 sheep and 90,000 goats. Cattle are mainly Friesians housed in small to large holdings for milk production. The first outbreak of LSD was discovered in two farms on 27.11.2014 in the Karpaz peninsula, an area with the lowest cattle density. Measures were immediately enforced to contain the infection, such as stamping out of clinically infected or suspected animals, quarantine, disinfection and insecticide spraying of farms, surveillance, and notification to farmers.

Results:
During the first outbreak, investigations were carried out in three villages in which 8 farms, with 156 cattle, were investigated and 27 clinically positive cases detected, with all animals killed by the 24th of December 2014. Laboratory confirmation was obtained by Istanbul Pendik Veterinary Control Institute, using PCR method. In January and February 2015 new outbreaks were reported in two farms more than 60 km from the first outbreak, in a high-density cattle population area. The two farms, with 194 heads of cattle, reported 36 new cases, all of which were killed and destroyed, while the others animals were vaccinated.

Conclusions:
In light of the evolution of the infection and recommendations of the EU Veterinary Emergency Team (CVET) the initial stumping out policy, with compensation for the market value of animals and milk yield losses, was replaced by a mass vaccination campaign with homologous vaccine, to cover the whole cattle population in northern part of Cyprus. Clinical surveillance, movement restriction and insecticide spraying continued in the protection and the surveillance zone. In the first month of vaccination, half cattle population was successfully immunized and no suspected cases were reported. During the vaccination campaign some side effects, extended edema, mild infection and limited milk yield drop, were noted in a limited number of animals.

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Eradication of Bovine Leukaemia Virus infection at a regional level in Miyazaki, Japan: Scenario-tree modelling of the surveillance system

Yumi Kirino[1], Takeshi Taniguchi[2], Sayaka Ueno[2], Hiroshi Kudoh[2], Hirohisa Mekata[3], Nariaki Nonaka[4], Yoichiro Horii[4], Junzo Norimine[5], Satoshi Sekiguchi[6], [1]University of Miyazaki, Miyazaki, Japan; [2]Nobeoka Prefectural Livestock Hygiene Centre, Miyazaki, Japan; [3]University of Miyazaki, Miyazaki, Japan; [4]University of Miyazaki, Miyazaki, Japan; [5]University of Miyazaki, Miyazaki, Japan; [6]University of Miyazaki, Miyazaki, Japan. Contact: kirinoyumi@cc.miyazaki-u.ac.jp

Purpose:
Despite the high seroprevalence of bovine leukemia virus (BLV) infection in both dairy and beef cattle and the continuous increase in enzootic bovine leukosis cases in Japan, the control of the disease is still in voluntary phase and no eradication programme at national level has been implemented yet in the country. This study aimed at evaluation of surveillance system components during and after a BLV eradication programme conducted at a regional level in Kyushu, Japan.

Methods:
BLV eradication programme was implemented by local governments and relevant local branch of Japan Agricultural Cooperatives in cooperation with University of Miyazaki between April 2013 and March 2015 in a district consisting of adjacent three towns. Following an initial survey on voluntarily participating farms, all 870 calf-rearing farms participated in active surveillance. 4823 blood samples were collected from all animals serving as breeding cattle and all replacement heifers in the district and underwent serological testing for BLV infection. BLV gp51 *env* gene sequences taken from infected animals were analysed to provide information on the history of transmission events within the population. To establish a surveillance system to detect potential subsequent introduction of BLV into the district, passive and active surveillance system components were quantified by using scenario tree modelling.

Results:
ELISA test results showed that a total of 42 (0.87 per cent) animals and 17 (1.95 per cent) farms in the district were infected with BLV. Test-positive animals were isolated within the farms or purchased by the local governments and moved to public fattening centres. Compensation for those farmers who replaced their test-positive animals was offered. An optimal and cost-effective surveillance system was developed.

Conclusions:
The completion of the programme led to the first scientific claim of freedom from BLV infection at a regional level in Japan. The post-eradication surveillance system suggested in this study can be used when initiating compulsory eradication programme of BLV infection at regional and national levels.

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Schmallenberg virus: The impact of clinical and subclinical disease on milk yield and reproduction parameters in dairy cattle in Switzerland

Isabel Lechner[1], Marianne Wuethrich[2], Mireille Meylan[2], Bart H. P. van den Borne[1], Gertraud Schuepbach-Regula[1], [1]Veterinary Public Health Institute, Liebefeld, Switzerland; [2]Clinic for Ruminants, Bern, Switzerland. Contact: isabel.lechner@vetsuisse.unibe.ch

Purpose: Schmallenberg virus (SBV) is an emerging Orthobunyavirus that was first detected in Germany in November 2011 before rapidly spreading throughout Europe. In Switzerland, the virus was first detected in July 2012 and a high rate of seroconversion was observed. So far, very little is known on how clinical disease affects milk production and fertility. The aim of this study was to compare milk yield, somatic cell counts (SCC), reproductive performance and incidence of abortions between farms with clinically affected cows, and control farms where cows remained clinically healthy despite seroconversion.Methods: A matched case control study was performed, where cases were defined as farms diagnosed with SBV and reporting acute clinical signs (drop in milk yield, fever, diarrhea or several abortions). Farms that tested serologically positive but without clinical disease were taken as controls and matched to case farms. Individual cow data on clinical signs, milk yield, calving interval and abortions were collected for the period from July 2011-June 2013 to allow for a comparison of production and fertility parameters before and after the infection period. Herd-level analysis was performed and subsequent analysis using cow-level data will be conducted by building hierarchical multivariable regression models for the separate outcomes.Results: Herd-level results revealed that case and control farms had a significant drop in milk yield during the SBV epidemic period compared to the previous year. In case farms, the calving interval was longer after the spread of SBV compared to control farms and the SCC was significantly higher in case farms compared to controls. Preliminary results on cow-level were consistent with herd-level findings and animals with clinical signs showed a trend for higher abortion rates compared to animals without clinical signs. Conclusions: Results of this study will provide an estimate of the effect of clinical and subclinical SBV infection on the productivity of both individually affected cows and the herd.Relevance: As SBV might not induce livelong immunity, these results will provide important information for decisions on sanitary measures or vaccination.

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Predicting within-herd prevalence of infection with bovine leukemia virus using bulk-tank milk ELISA titer

Omid Nekouei[1], Henrik Stryhn[1], John VanLeeuwen[1], Paul Hanna[2], David Kelton[3], Greg Keefe[1], [1]University of Prince Edward Island, Charlottetown, PE, Canada; [2]University of Prince Edward Island, Charlottetown, PE, Canada; [3]University of Guelph, Guelph, ON, Canada. Contact: onekouei@upei.ca

Purpose: Estimating prevalence of infection with bovine leukemia virus (BLV) in dairy herds is a fundamental step towards pursuing efficient control programs. Objectives of this study were 1) to determine the prevalence of BLV at herd-level using bulk-tank milk (BTM) ELISA in the Maritime region of Canada (Prince Edward Island, New Brunswick, and Nova Scotia), and 2) to develop appropriate statistical models for predicting within-herd prevalence of BLV using BTM ELISA results.
Methods: during 2013, three monthly BTM samples were collected from all dairy farms in the Maritime region of Canada (n = 623; a census) and tested for BLV milk antibodies using a commercial indirect ELISA. Based on the average value of the BTM titers, 15 strata of herds (5 per province) were defined. From each stratum, 6 herds were randomly selected (n = 90). Within every selected herd, another round of BTM sample was taken (round 4); simultaneously, all cows that contributed milk to the BTM were individually tested for BLV milk antibodies (n = 6111) to establish the within-herd prevalence. This reference within-herd prevalence of BLV was modeled (linear regression), using various combinations of the repeated BTM titers as the predictor of interest. Lactating herd size and stratified design of the study were taken into account in the analyses.
Results: herd-level prevalence of BLV in the region was 90.8%. In the individual testing, 30.4% of cows were positive. All models were reasonably able to predict the within-herd prevalence of BLV ($R^2 > 0.7$); more precisely, over low-to-medium spectrum of BTM titers. As a greater number of the four repeated BTM titers were incorporated in the final models (using mean value of the BTM rounds as the predictor), narrower uncertainties around the prediction lines were achieved (i.e. more precise estimates).
Conclusions: as a part of a control program, farmers were advised to submit two BTM samples taken two months apart, or three monthly samples, to be provided with reliable estimates for BLV prevalence within their herds.
Relevance: the developed models could effectively and economically be applied to control and eradication programs for BLV.

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Associations between animal characteristics and environmental risk factors and the occurrence of bovine respiratory disease in Australian beef feedlot cattle.

K. E. Hay[1], J. M. Morton[2], A. C. A. Clements[3], T. J. Mahony[1], T. S. Barnes[4], [1]University of Queensland, St Lucia, Australia; [2]Jemora Pty Ltd, Geelong, Australia; [3]The Australian National University, Canberra, Australia; [4]University of Queensland, Gatton, Australia. Contact: k.hay1@uq.edu.au

Purpose:
Bovine respiratory disease (BRD) is the major cause of clinical disease and death in feedlot cattle populations worldwide. This study was part of the National Bovine Respiratory Disease Initiative, a nationwide prospective longitudinal study investigating numerous putative risk factors for BRD in Australian beef feedlot cattle. The study population comprised 35,131 cattle sourced from a wide geographical area throughout the year over a three year period. These cattle entered 170 cohorts (feedlot pens) at 14 feedlots.
This study aimed to quantify associations between animal characteristics and environmental risk factors measured at induction (i.e. when animals were identified and data were recorded before being placed in pens) and occurrence of BRD.
Methods:
Causal diagrams were used to identify appropriate sets of covariates to include in Bayesian multilevel logistic regression models to estimate total and direct effects of risk factors of interest on the occurrence of BRD during the first 50 days at risk.
Results:
Herefords, Angus and British breed crosses were at markedly increased risk compared to Bos indicus breeds (either purebred or crosses) and steers were at increased risk compared to heifers. There was a negative, approximately linear association between animal weight at induction and subsequent risk of BRD. Animals inducted into southern feedlots were at increased risk compared to northern feedlots. Animals inducted during summer or autumn were at markedly increased risk compared to animals inducted during spring.
Conclusions:
BRD risk varies markedly with animal characteristics and environmental factors.
Relevance:
Evaluation of the effects of animal characteristics and the timing of induction in a population with a broad range of characteristics and a balanced temporal distribution of feedlot entry throughout the year has facilitated a more informed assessment of the role of these factors than has been possible in more restricted populations.
Knowledge of these risk factors would be useful in predicting BRD risk for incoming groups of feedlot cattle.

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Associations between serological risk factors and bovine respiratory disease in Australian beef feedlot cattle.

K. E. Hay[1], T. S. Barnes[2], J. M. Morton[3], J. L. Gravel[4], M. A. Commins[4], P. F. Horwood[4], R. A. Ambrose[4], A. C. A. Clements[5], T. J. Mahony[1], [1]University of Queensland, St Lucia, Australia; [2]University of Queensland, Gatton, Australia; [3]Jemora Pty Ltd, Geelong, Australia; [4]Department of Primary Industries and Fisheries, St Lucia, Australia; [5]The Australian National University, Canberra, Australia. Contact: k.hay1@uq.edu.au

Purpose:
Respiratory viral infections are key components in predisposing cattle to the development of bovine respiratory disease (BRD), but the relative importance of some viruses in causing BRD remains unclear. The study aimed to describe serostatuses at initial sampling, and to investigate the effects of four viruses on risk of BRD.

Methods:
A large nested case-control study was conducted on a subset of cases and controls randomly selected from eligible animals enrolled in a nationwide prospective longitudinal study in Australian beef feedlot cattle. Paired blood samples were collected from all animals at induction (when animal characteristics and identifiers were recorded before being placed in pens), and at follow-up (after 35 to 60 days). Sera were tested using an indirect multiplex ELISA. The total effects of each of the serological variables describing serostatus at initial sampling, and serochange between initial and follow-up sampling to each of the viruses, Bovine viral diarrhoea virus 1 (BVDV-1), Bovine herpesvirus type 1 (BoHV-1), Bovine respiratory syncytial virus (BRSV) and Bovine parainfluenza virus 3 (BPIV-3) and combinations of these viruses, on risk of BRD were determined using Bayesian three-level logistic regression models.

Results:
At induction, weighted seroprevalences to BoHV-1, BVDV-1, BRSV and BPIV-3 were 24%, 69%, 89% and 91%, respectively. For each virus, animals that were initially seropositive were at modestly reduced risk of subsequently acquiring BRD. Risk decreased approximately linearly with each extra virus to which the animal was seropositive. Seroincrease to any of the four viruses was associated with modestly increased risk of BRD, with animals that seroincreased to more than one virus at markedly increased risk.

Conclusions:
Each of the four viruses contributes to occurrence of BRD. Because more animals were initially seronegative, BoHV-1 and BVDV were of greater importance at the population level. However, interventions focussed directly on just one of these four viruses are unlikely to markedly reduce BRD incidence.

Relevance:
This study has informed the relative importance of these viruses in causing BRD in Australian feedlots.

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Mapping the global trends in antimicrobial use in food animals

Thomas P. Van Boeckel[1], Charles Brower[2], Marius Gilbert[3], Bryan Grenfell[1], Simon Levin[1], Tim Robinson[4], Aude Teillant[1], Ramanan Laxminarayan[5], [1]Princeton University, Princeton, NJ, [2]Center for Disease Dynamics Economics & Policy, New Delhi, India; [3]Universite Libre de Bruxelles, Brussels, Belgium; [4]International Livestock Research Institute, Nairobi, Kenya; [5]Center for Disease Dynamics Economics & Policy, Washington DC, WA, Contact: tboeckel@princeton.edu

Purpose: Demand for animal protein for human consumption is rising globally at an unprecedented rate. Modern animal production practices are associated with regular use of antimicrobials, potentially increasing selection pressure on bacteria to become resistant. Despite the significant potential consequences for antimicrobial resistance, there has been no quantitative measurement of global antimicrobial consumption by livestock.
Method: We address this gap by employing Bayesian statistical models combining maps of livestock densities, economic projections of demand for meat products and current estimates of antimicrobial consumption in high-income countries to map antimicrobial use in food animals for 2010 and 2030.
Results: We estimate that the global average annual consumption of antimicrobials per kilogram of animal produced was 45, 148 and 172 milligrams per kilogram for cattle, chicken and pigs, respectively. Starting from this baseline, we estimate that between 2010 and 2030, the global consumption of antimicrobials will increase by 67%, from 63,151 ±1,560 tons to 105,596 ±3,605 tons. Up to a third of the increase in consumption in livestock between 2010 and 2030 will be imputable to shifting production practices in middle-income countries where extensive farming systems currently dominates. For Brazil, Russia, India, China and South Africa, the increase in antimicrobial consumption will be 99%, up to seven times the projected population growth in this group of countries.
Conclusion: The rise in antimicrobial consumption in food animals is likely to be driven by the growth in consumer demand for livestock products in middle-income countries and a shift to large-scale farms where antimicrobials are used routinely. Better understanding of the consequences of the uninhibited growth in veterinary antimicrobial consumption is needed to assess its potential effects on animal and human health
Relevance: Our findings call for initiatives to preserve antibiotic effectiveness while simultaneously ensuring food security in low- and lower-middle income countries.

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Data collection, analysis and reporting of antimicrobials used in animals by the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS)

Carolee A. Carson[1], David Leger[1], Anne Deckert[1], Agnes Agunos[1], Sheryl Gow[2], Richard Reid-Smith[1], Jane Parmley[1], Brent Avery[1], Rebecca Irwin[1], [1]Public Health Agency of Canada, Guelph, ON, Canada; [2]Public Health Agency of Canada, Saskatoon, SK, Canada. Contact: carolee.carson@phac-aspc.gc.ca

Purpose: Antimicrobial resistance (AMR) is a growing global health concern in human and veterinary medicine. Antimicrobial use (AMU) is a major selection pressure for AMR. This paper describes the evolution of analysis and reporting of animal AMU data by the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS).
Methods: CIPARS reports the quantities of antimicrobials distributed for sale for use in animals; data provided by the Canadian Animal Health Institute. CIPARS has explored various contextual denominators, including an approach similar to that of the European Surveillance of Veterinary Antimicrobial Consumption, in order to best reflect changes in these data over time. CIPARS also collects AMU data from sentinel grower-finisher pig farms and broiler chicken farms. The farm AMU data provide information on reasons and duration of use, the proportion and weight of animals exposed, and route of administration.
Results: Between 2006 and 2013, there was a decrease in the quantity of antimicrobials distributed for sale nationally; the magnitude of this decrease differed depending on the AMU metric. For the farm data, both qualitative and quantitative use metrics have been useful for temporal comparisons and for comparing between animal species. By kg active ingredient, the most common antimicrobial classes (AC) sold nationally (across all species) were tetracyclines, ionophores/chemical coccidiostats (ICCs) and 'other antimicrobials'. The most common AC used on grower-finisher pig farms were tetracyclines, macrolides and lincosamides, while the most common AC used on broiler chicken farms were ICCs, bacitracins and streptogramins. The majority of antimicrobials administered to grower-finisher pigs and broiler chickens were for disease prevention purposes.
Conclusions: Reporting of both national distribution and farm data provides a substantially greater ability to understand the AMU needed to inform AMR mitigation policies.
Relevance: It is important to understand and choose the AMU metric best suited for the purpose: descriptive communication, policy evaluation, international comparisons, or understanding associations with AMR.

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Establishing dose-response relationships and antimicrobial use thresholds for an active policy against antimicrobial resistance in food producing animals

Alejandro Dorado Garcia[1], José J.H. Jacobs[1], Inge I.M. van Geijlswijk[2], Dik Mevius[3], Jaap A. Wagenaar[4], Dick J.J. Heederik[1], [1]Utrecht University, Utrecht, Netherlands; [2]Utrecht University, Utrecht, Netherlands; [3]Wageningen University, Lelystad, Netherlands; [4]Utrecht University, Utrecht, Netherlands. Contact: a.doradogarcia@uu.nl

Purpose: currently, the Netherlands has one of the most active policies to contain the antimicrobial resistance (AMR) threat in livestock. Since 2009 more than a 50% reduction in animal antimicrobial use (AMU) has been achieved. Benchmark indicators (as Defined Daily Dosages per Animal per Year (DDDA)) are established by the Netherlands Medicines Authority (SDa); this way individual farms are classified in target, signaling or action categories according to their antimicrobial consumption and corrective actions are implemented. The current benchmarking is based on the AMU distribution but does not consider associated resistance levels. This project aims at establishing evidence-based benchmark indicators.
Methods: the Dutch report on Monitoring Antimicrobial Resistance and Antibiotic Usage in Animals is issued annually. Additionally the SDa, publishes a detailed description of AMU in livestock at the national level. Using data from these reports between the years 2004 to 2014, the ecological relationship between AMU and AMR in *E.coli* was evaluated with logistic regression. Moreover, a Benchmark Dose (BMD) analysis was done fitting a battery of dichotomous models. Both analyses related *E.coli* resistance to penicillins (AMPr), tetracyclines (TETr), 3rd generation cephalosporins (FOTr) and fluoroquinolones (CIPr) with total AMU.
Results: positive AMU-AMR associations were shown in all animal sectors; ORs per 1 DDDA increase ranged between 1.01 to 1.17 and were statistically significant in all selected resistances for poultry and in AMPr, TETr and CIPr in fattening pigs and veal calves. BMDs for a 10% increase in baseline resistance ranged from 1.8 DDDA (TETr) to 17.1 (FOTr) in fattening pigs and from 18.8 (AMPr) to 55.7 (FOTr) in veal calves; in poultry, only the FOTr model could be fitted (BMD=16.2).
Conclusions: this work shows a positive ecological association between AMU and resistance levels within livestock sectors; as a proof of concept, it demonstrates that AMU thresholds can be derived with a more science based approach.
Relevance: this pioneering experience could serve as a framework for addressing the emergence of AMR in animals in other countries.

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Impact of management practices on antimicrobial resistance in coagulase-negative staphylococci isolated from bovine mastitis

Diego B. Nóbrega, Jeroen De Buck, Vineet Saini, Larissa A. Z. Condas, Domonique Carson, **Herman W. Barkema**, University of Calgary, Calgary, AB, Canada. Contact: barkema@ucalgary.ca

Purpose: Antimicrobial therapy is commonly used for mastitis prevention and control. However, failure of antimicrobial cure is common, attributed, in part, to antimicrobial resistance (AMR). In this study, we are determining risk factors influencing AMR in coagulase-negative staphylococci (CNS) isolated from the milk of Canadian dairy cattle (91 herds). The objectives are to: 1) determine occurrence of drug-specific AMR in CNS isolated from milk; and 2) assess and evaluate relationships among on-farm antimicrobial use, management practices and AMR.
Methods: The AMR profile will be determined for 2,000 well-characterized CNS isolates using minimum inhibitory concentrations (MIC) for antimicrobials commonly given to dairy cattle. For all herds, we have the following data: housing, bedding types and management, antimicrobial use in heifers, dry and lactating cows (for mastitis and non-mastitis conditions), milking technique and hygiene, and owner/farm worker/veterinarian involvement in mastitis prevention, control and treatment. For statistical analyses, mixed effects logistic regression models will be used to estimate animal-level risk factors, considering observations clustered within herds and cows, and also to estimate AMR prevalence (herd and animal levels). To determine herd-level risk factors, negative binomial regression models will be used.
Results: At abstract submission, the MIC profile has been determined for 370 CNS isolates. Eighteen isolates (4.9%) were resistant to ampicillin, 34 (9.2%) to penicillin, 13 (3.5%) to erythromycin, 12 (3.2%) to pirlamycin, 1 (0.3%) to the penicillin/novobiocin combination and ceftiofur, 33 (8.9%) to tetracycline, and 66 (18%) to sulphadimethoxine. However, no isolates were resistant to oxacillin or cephalotin.
Conclusions:AMR is prevalent in bovine CNS species and was species-specific in the preliminary analysis. The association between management and prevalence of AMR will be presented at the conference.
Relevance: This information will be valuable for interpreting AMR patterns and trends, providing risk assessment of AMR, implementing control measures, and evaluating effects of interventions for reducing AMR.

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An integrated method to evaluate the risk attribution of livestock for the antibiotic resistance problem in public health

Aline De Koeijer[1], Engeline van Duijkeren[2], Eric Evers[2], Egil Fischer[1], Joost Smid[3], [1]Central Veterinary Institute (CVI), Lelystad, Netherlands; [2]RIVM (National Institute for Public Health and Environment), Bilthoven, Netherlands; [3]IRAS, Utrecht, Netherlands. Contact: aline.dekoeijer@wur.nl

Purpose:
Develop a method to evaluate the risk attribution of antibiotic resistance in bacteria in livestock for public health.
Methods:
Although a link is assumed between antibiotic resistance in different species, including man, the impact is difficult to assess, because the resistance genes can spread both ways, and pass through the environment. Sequencing data has been used to prove a link between occurrence of certain strains in livestock and in man. However, such data only prove a correlation, and no causal connection. Therefore, we developed a Next Generation Matrix (NGM) that incorporates the relevant risk groups, and the transmission between those groups, to evaluate the relative impact of each group in the overall growing prevalence of antibiotic resistance genes. We evaluated hospital patients, general population, pet animals and broilers.
Results:
The various elements of the NGM are very hard to quantify. Especially for quantifying transmission between the different risk groups, data are lacking, although some information is available to quantify transmission within groups. Furthermore, the lack of quantitative data on how many bacteria with a specific gene are found in an “infected” individual makes quantitative analysis hard. Furthermore, such an analysis is specifically valuable if detailed data on a specific strain are available from all kinds of species.
Conclusions:
The NGM can be a valuable tool in risk assessment and risk attribution questions, if more quantitative data on “contamination” levels become available. At this stage is can rather be used indicatively, in evaluating the relative importance of transmission routes and control measures.
Relevance:
The increasing occurrence of antibiotic resistance leads to a more and more limited panel of treatment options for potentially harmful or lethal bacterial infections, both in veterinary and human medicine. More knowledge on the transmission of these resistance genes can help limit their spread, and thus keep the treatment options wider.

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Antimicrobial consumption and vaccination against PCV2 in Danish pig herds.

Amanda Brinch Kruse[1], Liza Rosenbaum Nielsen[1], Lis Alban[2], [1]University of Copenhagen, Frederiksberg C, Denmark; [2]Danish Agriculture & Food Council, Aarhus N, Denmark. Contact: amanda@sund.ku.dk

There is focus on antimicrobial use because of the risk related to antimicrobial resistance. In Denmark, several initiatives have been put in place to reduce the antimicrobial use in pig production. Vaccination has been identified as a potential alternative to antimicrobial use. In Denmark, purchase of vaccines against porcine circovirus type 2 (PCV2) increased substantially along with a decrease in antimicrobial consumption between 2009 and 2011 related to official restrictions. PCV2 is a virus associated with development of Postweaning Multisystemic Wasting Syndrome (PMWS) leading to increased mortality in weaner and finisher pigs worldwide.
The aim of this study was to determine whether use of PCV2 vaccination had an effect on the antimicrobial consumption in weaner and finisher pigs.
Data on purchase of vaccines and antimicrobial use between 2005 and 2012 were extracted from the Danish VetStat database. Initiation of vaccination was represented by the first registration of purchase of vaccines against PCV2 for the sow unit (N=146 herds). Antimicrobial use was extracted for the weaner and finishers units receiving piglets from the vaccinated sow unit. Data was extracted from 12 months before until 12 month after vaccination was initiated. Data on weaner and finisher pigs was analysed separately using a multivariable linear regression model including several risk factors. The outcome was change in antimicrobial use, represented by antimicrobial use before vs. after vaccination was initiated. The same model was tested with data from all herds with weaner and finisher pigs regardless of vaccination status (N=463) and by including a random selected period.
There was a significant effect of baseline antimicrobial use; the higher the baseline, the larger the decrease in antimicrobial use was seen after vaccination. The effect was confounded by the year in which vaccination was initiated. In finisher pigs there were no effect of vaccination on the antimicrobial use when compared to all finisher herds. For weaner pigs the effect of baseline was more pronounced in vaccinated herds, indicating an effect of vaccination against PCV2 in herds with high antimicrobial use for weaner pigs.

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Salmonella population dynamics in response to the use of antibiotics in Texas feedlot cattle

Naomi Ohta[1], Keri N. Norman[1], Sara Lawhon[1], Javier Vinasco-Torres[1], Bo Norby[2], Guy H. Loneragan[3], Harvey M. Scott[1], [1]Texas A&M University, College Station, TX, [2]Michigan State University, East Lansing, MI, [3]Texas Tech University, Lubbock, TX, Contact: NOhta@cvm.tamu.edu

Salmonellosis is a serious public health concern worldwide. Although controversial, intensive use of antibiotics in livestock has been blamed for the transmission of multidrug-resistant (MDR) *Salmonella* to humans. Meanwhile, defining prudent use of antibiotics in the context of treatment, control and prevention remains difficult. We conducted an experimental study to assess the metaphylactic use of injectable ceftiofur (Excede®; EXE) and in-feed chlortetracycline (CTC) on the dynamics of antibiotic-resistant *Salmonella enterica* in feedlot cattle. Sixteen pens (11 steers/pen) were subjected to 4 regimens; 1) all steers in 8 pens were treated with EXE on Day 0; 2) 4 of these pens followed with intermittent CTC from Day 4 through Day 20; 3) 1 out of 11 steers in the remaining 8 pens were treated with EXE on Day 0; 4) 4 of these pens received CTC as above. We isolated *Salmonella* from feces collected from individual steers on Days 0, 4, 14, and 26. *Salmonella* in the feces were quantified by spiral-plating and by metagenomic qPCR for enterotoxin gene, stn. Resistance phenotypes were analyzed via the TREK Sensititre® system. Serotypes were determined for a randomly selected subset of *Salmonella* isolates using whole genome sequencing. Results were compared with multiplex-PCR serotyping and serological agglutination test. The mean *Salmonella* prevalence in the samples before treatments was approximately 70%. Most of the *Salmonella* isolated on Day 0 were pan-susceptible to the panel of 14 antibiotics. Treatments with both EXE and CTC initially reduced both the prevalence and the total quantity of *Salmonella* in feces ($P < 0.05$); however, the proportion of MDR-*Salmonella* increased on Day 14 and 26 in those steers treated with both EXE and CTC or CTC alone, suggesting a shift in population that remained well after the regimens ceased. *Salmonella* isolated from the pens with the least antibiotic selection pressure did not show a significant phenotypic change throughout the study period; in addition, the quantity of *Salmonella* remained stable ($P > 0.05$). Our study suggests that the use of antibiotics during the feeding period contributes to population changes among *Salmonella* in the cattle intestinal tract.

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Impact of a decreased antimicrobial therapy at early stage of spontaneous bovine pneumonia cases on antimicrobial consumption and therapeutic efficacy

Guillaume Lhermie[1], Alain Bousquet-Melou[2], Farid El Garch[3], Henri Seegers[4], Sébastien Assié[4], [1]Vetoquinol, Paris, France; [2]National Veterinary School of Toulouse, Toulouse, France; [3]Vetoquinol, Lure, France; [4]National Veterinary School of Nantes, Nantes, France. Contact: guillaume.lhermie@vetoquinol.com

Purpose
Antimicrobial resistance associated with veterinary use of antimicrobials is a potential hazard for human health. In this context, it is crucial to decrease number of animals unnecessarily treated and to optimize treatments when needed. As shown in experimental models, efficacious antibiotic dosage regimen could be decreased when given at early stage of disease. We conducted a field study to evaluate at the group level antimicrobial consumption and therapeutic efficacy of such protocol to treat bovine respiratory disease (BRD).
Methods
In 20 barns, 217 young bulls (YBs) were randomly assigned to one of two experiment groups E2 and L10, based on detection time of BRD (Early or Late) and on dosage regimen (2 or 10 mg/kg), and follow up during the first month on feed. In the E2 group, YB temperature was continuously monitored using a ruminal temperature bolus. YBs with a ruminal temperature ≥40.2°C for more than 12h and presenting no or only slight signs of BRD were considered as Early detected and treated with 2 mg/kg of marbofloxacin, a fluoroquinolone used in Europe to treat BRD. In the L10 group, YBs with moderate or severe signs of BRD were considered as Late detected and treated with 10 mg/kg of marbofloxacin. Relapses were treated according to farmers' habits. The treatments units [amount (mg)/ Used Daily Dose (mg/kg)] for a standard YB of 300 kg at risk were calculated and summed to determine total amount of antibiotics (TA). First line treatment and relapse rates were recorded.
Results
TA was decreased by 33% and marbofloxacin amount by 63% in E2 vs L10 group. A standard YB received 173 and 471 marbofloxacin units and 54 and 9 relapse treatment units in E2 and L10 groups respectively. First line treatment and relapse rates were higher in E2 (50 and 35%) vs L10 (30 and 13%). 97% and 100% of YBs treated in E2 and in L10 group were cured at the end of the study.
Conclusions
Our results suggest that the combination of an early detection of disease with lower antibiotic doses could be used to optimize drug consumption at the herd level without affecting treatment efficacy.
Relevance
Such findings evidence the possible rationalization of antimicrobial use under field conditions, to limit its impact on public health.

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Towards sensible risk analysis and disease simulation models in animal health and food safety: a concept paper

Francisco J. Zagmutt, EpiX Analytics, Boulder, CO, Contact: fzagmutt@epixanalytics.com

Purpose: Quantitative risk analysis and disease simulation models (QRADSMs) have become key tools to support animal health and food safety decisions. The design of robust QRADSMs requires significant quantitative skills, as both statistical inference (to estimate model parameters from data and expert opinion) and predictions (to assess intervention strategies) need to be considered simultaneously, while also providing results that are informative to decision makers. Modeling mistakes are easy to make, and can significantly affect the results relied upon by decision makers.
The objective of this talk is to present key indicators of decision-impacting modeling mistakes, and propose novel methods to prevent them.

Methods and results: Modeling mistake indicators reviewed will include abnormally broad or narrow confidence intervals, unrealistic results from individual model iterations, and normally distributed results from models with skewed inputs. Their common causes will be grouped in broad categories, such as the incorrect modeling of variability and uncertainty, the incorrect use of products to sum random variables, mistakes in fitting distributions to data, ignoring joint uncertainties, and the improper marginalization of nuisance parameters. Examples from real QRADSMs will be used to illustrate each mistake and solution. The methods to prevent them will include bayesian and frequentist options.

Conclusions and relevance: QRADSMs are increasingly used for epidemiological decision support. The common mistakes addressed during this talk can significantly affect model usability. This talk provides a structured summary of key indicators of these mistakes, and proposes methods to avoid them. This information should be relevant to model practitioners, reviewers, and decision makers.

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A generic quantitative risk assessment framework for the introduction of bat-borne viruses into the European Union

Robin R. L. Simons, Verity Horigan, Paul Gale, Rowena Kosmider, Andrew Breed, Emma Snary, Animal and Plant Health Agency (APHA), Addlestone, United Kingdom. Contact: robin.simons@apha.gsi.gov.uk

Purpose:
Bats have been linked to a number of zoonotic diseases such as Nipah Virus (NiV), Ebola Virus (EBOV) and MERS-CoV. In 2014 there have been human cases of NiV in Bangladesh, EBOV in Africa and MERS-CoV in the Arabian Peninsula, with sporadic cases of EBOV and MERS-CoV further afield. Given current anthropogenic activities and an intricately connected global world through trade and travel, it is likely there will be further spill-over of viruses from mammalian reservoirs, with global spread among humans a serious concern.
In order to assess the risk of entry of bat-borne zoonotic viruses to European Union (EU) Member States, a generic risk assessment framework has been developed.
Methods:
The model framework combines multiple routes by which bat-borne viruses are most likely to be introduced: human travel, legal importation of both foodstuffs and live animals, and illegal importation of bushmeat. The model does not consider further potential exposure of the virus to humans, livestock or wildlife and the subsequent consequences.
The model was parameterised for NiV and uncertainty in parameter estimates assessed through a series of scenarios.
Results:
While the baseline model expected number of years to an introduction event into the EU was 10 years, this decreased considerably if the bat infection prevalence (a highly uncertain parameter) was reduced. Legal trade was consistently the most likely route of entry for all scenarios considered. At a MS level, the Netherlands was the most likely point of entry via legal trade, while the UK was the most likely entry point for human travel, bushmeat and live animals.
Conclusions/Relevance:
The model framework described here is a useful tool for initial quantitative prediction of potential risk of introduction to the EU of bat-borne viruses. While the absolute risks should be treated with caution due to the inevitable high uncertainty of parameter estimates, the strength of this model lies in the provision of relative comparisons of routes and overall risk among MSs, as well as analysis of the uncertainty through scenarios. The modular design of the framework allows for future inclusion of additional routes as well as adaptation to other pathogens.

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Quantitative risk assessment for African horse sickness in live horses exported from South Africa

Evan Sergeant[1], John Grewar[2], Camilla Weyer[3], Grietjie de Klerk[4], Alan Guthrie[5], [1]AusVet Animal Health Services, Orange, Australia; [2]Western Cape Government, Elsenburg, South Africa; [3]Equine Health Fund, Johannesburg, South Africa; [4]Department of Agriculture, Forestry and Fisheries, Pretoria, South Africa; [5]University of Pretoria, Pretoria, South Africa. Contact: evan@ausvet.com.au

Purpose

African horse sickness (AHS) is a severe arboviral infection of equids, spread by *Culicoides* spp. vectors and causing up to 95% case fatality rates in susceptible horses. AHS is endemic in South Africa. Since 1997, live horses have been exported through a vector-protected quarantine facility in a small free zone in Cape Town. Periodic AHS outbreaks have disrupted trade, so that exports were only possible about 50% of the time between 1997 and 2014. This study was undertaken to evaluate risk management options to allow safe export of horses from South Africa on a regular and ongoing basis.

Methods

A stochastic simulation model was developed to estimate the probability of an undetected AHS-infected horse being exported from South Africa, under a variety of scenarios. Six scenarios were simulated for horses exported from a biosecure, vector-protected facility in either a low-risk area, with additional risk management, or from an endemically infected area, with varying numbers of PCR tests during pre-export or post-arrival quarantine. Inputs to the model included estimated incidence in the source area, probabilities of breakdown of vector protection during quarantine and loading and the probability of detecting midges if a breakdown of vector protection occurs. Results are presented as probability distributions of the expected number of horses and shipments per undetected infected horse being exported.

Results

The median probability of an exported horse being infected and undetected from the low risk area was 9.1 x 10^-6 (0.00091%) and 97.5 percentile of 7.8 x 10^-5 (0.0078%), assuming a single PCR test in pre-export quarantine. The expected number of shipments per undetected, infected horse exported was 3 434 (2.5 percentile: 398 shipments), increasing more than 10-fold for each additional PCR test applied. The probability of exporting an undetected infected horse from the endemic area was between 10 and 20-fold that of exports from the low-risk area for otherwise similar scenarios.

Conclusions

These results show that, with appropriate risk mitigation measures, the export of horses from South Africa is possible with negligible risk of exporting an undetected infected animal.

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Veterinary services and territorial risk analysis for disaster reduction in animal health

María-Irian Percedo-Abreu[1], Miguel Lorenzo[2], Paulino Santos-Montero[3], Aramís Fernández-Luciano[4], Osvaldo Fonseca[1], Isel González-Hernández[5], Herminia Serrano[2], [1]Centro Nacional de Sanidad Agropecuaria, Mayabeque, Cuba; [2]Agencia de Medio Ambiente, La Habana, Cuba; [3]Instituto de Medicina Veterinaria, La Habana, Cuba; [4]Sociedad Cubana de Medicina Veterinaria de Desastres, La Habana, Cuba; [5]Centro Nacional de Sanidad Agropecuaria, Mayabeque, Cuba. Contact: percedo@censa.edu.cu

Transboundary emerging and reemerging diseases, climate change and other disaster situations are among the threats for animal health and welfare, as well as veterinary public health. The World Organization for Animal Health (OIE), by the warning of the increasing frequency of such situations, has highlighted the need of a rapid and opportune intervention of the Veterinary Services (VS) in effective disaster risk reduction and management. Actions, materials and human resources should be based on risk analysis (RA) in the occurrence of disaster situations in each territory. Cuba has an increasing and effective experience on disaster situations since many years ago. So, the territorial risk analysis methodology applied in Cuba for animal epizootic diseases since the 90s was updated, following the international statements of the United Nations International Strategy for Disaster Reduction (UNISDR), taking into account the current guidelines developed by the Cuban Environmental Agency (AMA), which coordinates the multisectoral and multidisciplinary expertise. This work shows methodological base of the new territorial risk analysis for the productive animal species and wildlife and its strategic application in Cuba. Peril characterization has been considered due to the probability affectation by the pathogens identified as potential biological threats, its sceneries in each territory and many factors which determine the vulnerability (physical, functional, ecological and social) of animal population to face epizootic disease threats. RA is developed at municipality and provincial level by a group of specialists from different sectors belonging to each territory. There are results included in the territorial disaster reduction plan and there is an adequate communication with the respective Government for the economic support through the budget of each sector engaged. The methodology developed, together with its application strategy; contribute to the effective participation of the VS and the stakeholder's engagement in the risk reduction of animal diseases and other risks disaster, as a paramount goal for facing the future challenges.

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Risk assessment of seven emerging vector-borne animal diseases for the Netherlands: a structured approach

Herman J. W. van Roermund, Egil A. J. Fischer, Aline A. de Koeijer, **Clazien J. de Vos**, Central Veterinary Institute, part of Wageningen UR, Lelystad, Netherlands. Contact: clazien.devos@wur.nl

Purpose
The risk of seven vector-borne animal diseases (VBADs) for the Netherlands was assessed with the aim to prioritize diseases for preparedness and to identify common parameters that contribute most to the risk.
Methods
The risk assessment was performed for tularaemia, bovine babesiosis, epizootic haemorrhagic disease (EHD), Crimean-Congo haemorrhagic fever (CCHF), Rift Valley fever (RVF), West Nile (WN), and African horse sickness (AHS). These include protozoan, bacterial and viral diseases that are either transmitted by ticks, biting midges or mosquitoes, five of which are zoonotic.
The MINTRISK calculation methodology[1] was used. This method provides a questionnaire in which semi-quantitative answers need to be given and the uncertainty in the answers is to be made explicit. Using Monte Carlo simulation a semi-quantitative estimate of the risk is given, along with the risk contribution of the different answers and uncertainty intervals.
Results
The risk of CCHF is negligible because no competent tick vector is present in the Netherlands. The risk of all other VBADs was estimated to be moderate to high. WN has the highest risk with a high probability of introduction and moderate impact. Tularaemia and bovine babesiosis both have a high probability of introduction but low impact, whereas RVF, EHD and AHS all have a low probability of introduction but high impact. Common parameters contributing most to the risk include trade volumes and vectorial capacity.
Conclusions
The risk of most VBADs that we evaluated is moderate to high for the Netherlands, although clear differences were observed when comparing the VBADs for their probability of introduction and impact. MINTRISK provided insight into the main elements contributing to the risk of each VBAD, thus indicating which parameters can be targeted for risk management and which require further study.
Relevance
Preparedness for VBADs is an important issue in North-Western Europe after recent incursions of VBADs. Assessing the risk of VBADs with MINTRISK allows for comparison and indicates those parameters that contribute most to the risk.
[1] De Koeijer et al., 8th Annual Meeting EPIZONE, September 2014, Copenhagen, Denmark.

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Southern Africa, an at-risk region for the peste des petits ruminants (PPR): the need of integrated modelling

Francois L. Roger[1], **Veronique Chevalier**[1], AGIRs Rp-pcp Groups[2], [1]CIRAD, Montpellier, France; [2]CIRAD - UP - UEM - BCA, Harare, Zimbabwe. Contact: veronique.chevalier@cirad.fr

Peste des petits ruminants (PPR) is an acute and highly contagious viral disease that predominantly affects small ruminants (sheep and goats). PPR has a widespread distribution spanning West, Central and East Africa, the Arabic peninsula, the Middle East and southern Asia. The potential and real economic impacts of PPR outbreaks are high and often disproportionately affect the poorer sections of the society. This is especially evident in developing countries where sheep and goats play an integral role in subsistence farming to supply food or goods for trade.
Since rinderpest has been eradicated, PPR has become one of the principal infectious diseases of livestock in Africa. FAO and the World Organisation for Animal Health (OIE) are currently activating the international community targeting the eradication of PPR by 2030.
PPR poses a risk to about 50 million sheep and goats in the entire Southern Africa region particularly because Tanzania and DRC have declared outbreaks in the recent years. The official services of the region need to develop strategies on how to limit the spread of the disease in the event of introduction in PPR free countries. Indeed, most of the countries are not well prepared for the diagnostic, disease containment, and legislation issues.
Based on collection of available data and estimation of parameters regarding the small ruminants demography, the type of husbandry, the legal and illegal movements and trade, and role of other potential hosts including wildlife, modelling approaches -i.e. quantitative risk assessment (QRA) and multicriteria decision analysis (MCDA) - are undertaken at the regional level in order to quantify the risk of introduction and to map the suitable areas for PPR spreading and maintenance.
The pathways of introduction are described and several at-risk areas are characterized. A zoning process is proposed at the regional level. The outputs of the models could support the prevention of disease incursion in PPR free areas and the definition of management options: risk-based surveillance and control strategies, capacity building of stakeholders and adaptation of sanitary policy.

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Effect of preslaughter transportation on the welfare of turkeys and spent hens

Guido Di Martino[1], Katia Capello[1], Silvia Zamprogna[1], Elisa Russo[2], Anna Lisa Stefani[1], Paolo Mulatti[1], Claudia Casarotto[1], Marina Speri[3], Stefania Sparesato[4], Stefano Marangon[1], Lebana Bonfanti[1], [1]IZSVe, Legnaro (PD), Italy; [2]private veterinarian, Legnaro (PD), Italy; [3]ULSS 20, Verona, Italy; [4]ULSS 19, Adria (RO), Italy. Contact: gdimartino@izsvenezie.it

Purpose: During preslaughter transportation, several factors can impair welfare in poultry. Heat stress was identified as a major cause of dead-on-arrival (DOA) incidence in broilers, while few data are available for turkeys and spent hens, with particular regard to their distribution inside the transport vehicles. Task 1 of this study was a retrospective analysis of DOA of turkeys and spent hens transported to slaughter during a 3 years period, considering the effect of all factors involved. Task 2 investigated the stress response of turkeys settled in different parts of a transport vehicle.
Methods: For Task 2 temperature (t°) and relative humidity (RH) were recorded during transport by 6 data loggers inside the cages. 30 blood samples were taken before (T0) and after transport (T1) for the quantification of major biochemical markers.
Results: Results of Task 1 indicated a DOA of 0.31±0.83% in turkeys and 0.50±0.38% in spent hens. In turkeys, travel duration and stocking density positively correlated with DOA. Male gender and specific breeds were also associated to a higher DOA. In hens, travel duration longer than 2h and brown feather breed were associated to a higher DOA (compared to white feather breed). Results of task 2 showed at T1 vs T0 a significant increase in PCV, corticosterone and H/L and a significant decrease in triglycerides and ALT. No significant differences related to cage distribution in the lorry was found. However, animals in bottom-cages showed a higher level of LDH compared to T0 and to those in top-cages. Average t° and RH were respectively 24.6±0.6°C and 73.4±3.9% on the top; 24.2±0.4°C and 75.8±3.3% on the bottom.
Conclusions:
Genotype and travel duration are major stress factors for both turkeys and hens. At mild transport t°, turkeys settled in different part of the transport vehicle did not show significant differences in term of stress, dehydration, hypoxia and thermal discomfort. However, animals in the bottom cages may present a higher level of muscle fatigue.
Relevance: These results are relevant to outline feasible changes in management for minimizing animal stress and reduce DOA. Project RC IZSVe 08/12.

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Evaluation of register data for assessment of animal welfare in cattle and pig herds using a combination of qualitative and quantitative methods

Hans Houe[1], Søren S. Nielsen[1], Matthew J. Denwood[1], Nina D. Otten[1], Tine Rousing[2], Jan T. Sørensen[2], Bjørn Forkman[1], [1]University of Copenhagen, Frederiksberg, Denmark; [2]Aarhus University, Tjele, Denmark. Contact: houe@sund.ku.dk

Purpose:
On farm welfare assessment using primary data is expensive. There is therefore a need to investigate the extent to which register or secondary data can replace or augment primary data. The objective of this study is to establish a framework for evaluating animal welfare indicator candidates, and to use this framework to determine the potential for using register data to assess animal welfare in Danish cattle and pig herds.
Methods:
Approaches for evaluating animal welfare indicator candidates based on secondary data are compiled from the literature and organised into distinct quality criteria according to methodology. Current register data are then evaluated according to the list of quality criteria in the framework.
Results:
The study identified seven quality criteria that can be logically grouped as: 1) relevance, 2) sensitivity, specificity, 3) robustness, 4) feasibility, 5) significant prevalence, 6) completeness and 7) validation if data are aggregated e.g. into an index. Qualitative methods based on judgements are in particular used for assessment criteria nos. 1, 4, 5, and 7, whereas quantitative methods are used for assessment criteria nos. 2, 3, 6 and 7. Importantly, the overall assessment includes all seven criteria.
The available central register data in Denmark that after preliminary assessment meet the quality criteria 1, 4 and 5 include geographical location, herd size, animal movements, mortality, meat inspection recordings, medicine consumption and infringement of animal welfare legislation. In addition, industry owned databases contain relevant information on disease treatments and several variables related to production. The list of useful indicators is further adjusted when applying the quantitative criteria.
Conclusions:
The currently available register data do not contain sufficient information to perform a full welfare assessment such as an animal welfare index. But some register data have potential for predicting certain welfare problems, and provide a useful and cost effective mechanism to augment a limited amount of primary data.
Relevance:
Register data can be used to increase the utility of animal welfare assessments.

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Risk factors for poor equine welfare in Sweden

Peta L. Hitchens[1], Jan Hultgren[2], Jenny Frössling[3], Ulf Emanuelson[4], Linda J. Keeling[1], [1]Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]Swedish University of Agricultural Sciences, Skara, Sweden; [3]National Veterinary Institute, Uppsala, Sweden; [4]Swedish University of Agricultural Sciences, Uppsala, Sweden. Contact: peta.hitchens@slu.se

Purpose: To estimate the prevalence of, and identify risk factors for, poor equine welfare in Sweden using information collected through official animal welfare control.
Methods: The 45 checkpoints (CP) from the horse checklist in official animal welfare control were reviewed for 2010 to 2013. Non-compliance with one or more of the four animal-level CPs (social contact, body condition, hoof condition, cleanliness) was used as a binary outcome indicator of poor equine welfare. Study factors included premises and inspection characteristics, as well as housing and management CPs which were reduced by principal component analysis. Associations with risk factors were determined using multivariable logistic regression, adjusting for clustering on premises, and expressed as odds ratios (OR) with 95% confidence intervals.
Results: Of 8,532 premises inspected, 1,954 (22.9%) were found to have poor equine welfare. Among visits based on random inspection, this proportion was 9.5%. The odds of poor welfare were higher at premises that did not comply with requirements for passports or veterinary records (OR 2.3; 1.8, 2.9), stabling access and quality (OR 2.4; 1.8, 3.2), design of facilities (OR 1.6; 1.3, 2.0), or supervision, care or feeding of horses (OR 10.9; 7.8, 15.1); and at premises with hobby horses (OR 1.6; 1.2, 2.2), or that keep poultry (OR 1.6; 1.0, 2.4). The odds of poor welfare were also higher in spring (OR 1.8; 1.3, 2.4) and summer (OR 1.5; 1.0, 2.2) compared to autumn; if there was a complaint by the public, a veterinarian or others (OR 3.5; 2.7, 4.7), or if the inspection was motivated by follow-up on previously identified deficiencies (OR 2.4; 1.7, 3.5) when compared to normal inspections; and at subsequent inspections (OR 1.3; 1.0, 1.8) compared to initial inspections.
Conclusions: Strategies to reduce the prevalence should consider that non-compliance with requirements for supervision, care or feeding of horses was the strongest risk factor.
Relevance: Epidemiological analysis of official animal welfare control data can be used to identify risk factors for poor equine welfare, in that way making official control more efficient.

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Use of decision tree analysis to inform future case definitions for epidemiological investigations of equine laminitis.

CLAIRE E. WYLIE[1], Darren J. Shaw[2], Kristien L. P. Verheyen[3], J. Richard Newton[4], [1]ROSSDALES EQUINE HOSPITAL, EXNING, United Kingdom; [2]Royal (Dick) School of Veterinary Studies and The Roslin Institute, Edinburgh, United Kingdom; [3]Royal Veterinary College, London, United Kingdom; [4]Animal Health Trust, Newmarket, United Kingdom. Contact: claire.wylie@rossdales.com

Purpose: Epidemiological studies of equine laminitis lack a standard case definition. A systematic review found nearly 70% of publications assessing laminitis frequency failed to provide any definition beyond the word 'laminitis'. The aim of this study was to compare the prevalence of lameness clinical signs in laminitis cases and non-laminitis controls to evaluate the differential capabilities of clinical diagnosis.
Methods: Veterinarians completed a checklist of laminitis-associated clinical signs identified by literature review, for lameness of any origin. A case was defined as a horse/pony with veterinary-diagnosed, clinically apparent (active) laminitis. Associations between 23 clinical signs and case/control status were tested by logistic regression with adjusted odds ratios (veterinary practice as a fixed effect), 95% confidence intervals (CI) and Wald *P*-values. Multivariable analysis using tree-based models linked laminitis prevalence to clusters of clinical signs. Two models were built, including cases with (chronic) and without (acute) evidence of previous laminitis.
Results: Data were collected for 588 laminitis cases and 201 non-laminitis lameness controls. Overall prevalence of clinical signs ranged from 2.7 to 85.0% and difference in prevalence ranged from -14.1% (more common in controls) to +71.9% (more common in cases). Two clinical signs were pathognomonic for laminitis ('coronary band depression' and 'sole prolapse'), but were found in only 13.6% and 3.7% of cases respectively. In both models, bilateral forelimb lameness was the best discriminator of chronic and acute cases – if present 92.0% [CI 89.3, 94.7] and 93.1% [CI 90.7, 95.5] had laminitis, if absent19.0% [CI 12.7, 25.2] and 19.9% [13.5, 26.2] had laminitis respectively. If horses/ponies also had increased digital pulses, 99% were laminitis cases, in both models.
Conclusions: No specific set of clinical criteria could identify all cases of active laminitis. Case definitions should feature bilateral forelimb lameness and increased digital pulses as minimum criteria.
Relevance: Standardising laminitis case definitions will permit future meta-analysis of epidemiological studies.

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Assessment of donkey body lesions and work types using the Brooke's Standardised Equine Based Welfare Assessment Tool (SEBWAT) in Kenya

JAMES M. KITHUKA, Vincent O. Oloo, THE BROOKE HOSPITAL FOR ANIMALS, NAIROBI, Kenya. Contact: james.kithuka@thebrooke.org

There are over 1.8 million donkeys in Kenya, with 75% of this population used as working animals and support livelihoods for over 3 million people. Body lesions impair welfare and their capacity to support work. A cross-sectional study of 1,924 working donkeys in Kenya was conducted using The Brooke's standardised equine based welfare assessment tool (SEBWAT) to establish welfare status using Animal Based Indicators (ABI). The ABIs are important in monitoring welfare and demonstrating effectiveness of the Brooke's approach and intervention. The aim of the study was to assess prevalence and severity of body lesions to help inform donkey welfare improvement interventions.

Donkeys were randomly selected within 13 sub counties where the Brooke operates. Lesion site (head, neck, breast/shoulders, withers/spine, hindquarters and tail base), lesion severity (not present (score 0); hairless scar (score 1); broken skin (score 2); deep enough to show muscle, tendon or bone (score 3)) and donkeys' main work type (Transport by Pack and Transport by Cart) were recorded.

As reflected across all sub counties, 44% of working donkeys sampled had severe lesions (score 2 or 3). Fisher's exact test indicated an association between donkeys transporting goods by pack and severe tail base ($p<0.001$) and breast/shoulder ($p<0.001$) lesions, and donkeys transporting goods by cart and severe neck lesions ($p<0.001$). In Kitui and Tharaka sub counties, where the majority of working donkeys were used to transport goods by pack severe lesions were predominately found on the tail base. Similarly, in Naivasha sub county where the majority of working donkeys were used to transport goods by cart, severe lesions were predominately found on the neck.

The study indicates lesions are a welfare problem of working donkeys in Kenya. Work type and owner/user practices related to donkeys' work may be a risk factor for lesion site. The findings of this study provide baseline information which will help to inform The Brooke's targeted sub counties' programmatic work and monitoring effectiveness.

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A pilot study investigating welfare for dairy cattle in Trinidad, Antigua and Barbados

Karla Georges, Meera Koongebeharry, Nirvana Dodo, **Nneka Hull James**, Tracy Sealy, Jenelle Johnson, The University of the West Indies, Mt. Hope, Trinidad and Tobago. Contact: nhulljames@gmail.com

Purpose:
Codes for farm animal practice are being developed for many types of animal husbandry systems. Best practices are evolving to promote good management and welfare through recommendations for housing, nutrition transport and handing of animals. Such best practices are not formally encoded for animals in the Caribbean region.

Methods:
Using dairy cattle as a model, the main focus was to investigate welfare in practice in three islands in the Caribbean, and to establish a precedent for welfare where there is none. Data were collected via questionnaires from 43 farms total; 32 for Trinidad, five for Tobago, five for Barbados and one for Antigua. Landless farmers were classified as “open” and those farms which contained the herd in a well-defined pen were classified as “closed”.

The basis of the questionnaire were the five freedoms of animal welfare, which were expressed as an animal’s freedom from thirst and hunger, pain, discomfort, fear and distress, and to express normal behaviour. The questionnaire was designed according to OIE recommendations for farm animal welfare. Questions and their maximum scores in parentheses were based on , biosecurity (3), health (17), environment (8), food and water (17) , milking management (8) and calving environmental management (11) were given a maximum of 64 points

Results:
Scores for food and water and health were significantly ($p < 0.05$) correlated with all the other components. Barbados scored highest overall (mean of 47.6) and closed farms had significantly higher welfare scores that open farms (t-test, 41 df $p = 0.007$)

Conclusions:
This study revealed that most concerns seemed to lie in the categories of “food and water availability” and “general health”

Relevance:
We recommend that interventions should therefore focus on improving nutrition and availability of health services to dairy farmers to improve welfare in these countries.

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Presence of back arch in headlocks: An indicator of lameness and hoof lesions in dairy cattle?

Carlie Gordon, John R. Wenz, **Dale A. Moore**, Washington State University, Pullman, WA, Contact: damoore@vetmed.wsu.edu

Purpose: Many dairy welfare assessment programs require estimation of lameness prevalence and many utilize a 5-point locomotion scoring system. Observation of an arched back while standing and walking is one criterion to distinguish a score of 2 (not lame) from a 3 (mildly lame). Objectives of these projects were to evaluate back arch and association with locomotion score (LS) and hoof lesions. Methods: (1) On one 200-cow farm, digital photographs of cows were taken while stanchioned and walking and analyzed for degree of back arch. (2) One pen of cows was observed 5 times while stanchioned to evaluate "time in headlock" effect on presence of back arch. (3) In a second herd, back arch data were collected on 233 cows while stanchioned and hoof lesion data collected on 141. Results: (1) Angle of deviation from flat back was not significantly associated with LS, however, there was a trend for cows with a score of ≥ 3 to have back angles deviating from flat. (2) The proportion of time a cow was observed with a back arch was greater for lame cows vs. non-lame cows. (3) Cows identified with a back arch were 7.45 times more likely to be lame (LS > 2) ($P < 0.001$; 95% CI 3.57-15.5). As a test to predict lameness, observation of a back arch had a sensitivity and specificity of 0.55 and 0.89, respectively. Cows with a back arch were 2.1 times more likely to have a hoof lesion ($P = 0.04$) and there was a trend for more cows with hoof lesions with increasing LS ($P < 0.0001$). As a test for detecting cows with hoof lesions, back arch had a sensitivity and specificity of 0.36 and 0.78, respectively. Conclusions: Back arch observations could be used as a method to find some lame cows but lacks sensitivity. Relevance: Early detection of lameness can lead to earlier remediation and improve welfare.

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A participatory method for assessment of passive animal health surveillance systems from the viewpoint of their local actors

Alexis Delabouglise[1], Nicolas Antoine-Moussiaux[2], Thang Dang Phan[3], Duan Cong Dao[4], Thanh Tien Nguyen[5], Bao Dinh Truong[6], Xuan Ngoc Thanh Nguyen[6], Ton Dinh Vu[3], Khong Viet Nguyen[5], Hien Thanh Le[6], Gerard Salem[7], Marisa Peyre[8], [1]RVC, Hertfordshire, United Kingdom; [2]Liège University, Liège, Belgium; [3]Vietnam National University of Agriculture, Hanoi, Viet Nam; [4]Vietnam National University of Agriculture, Hanoi, Viet Nam; [5]National Institute of Veterinary Research, Hanoi, Viet Nam; [6]Nong Lam University, Ho Chi Minh City, Viet Nam; [7]Paris Ouest University, Nanterre, France; [8]CIRAD, Montpellier, France. Contact: alexis.delabouglise@gmail.com

Purpose:
New methods are needed for the economic evaluation of animal health surveillance systems. Little research has been conducted on non-monetary costs and benefits incurred by public and private actors related to their participation in such systems. Nonetheless, these factors may have a critical influence on passive surveillance, which precisely relies on a chain of decentralized information reporting decisions.
Methods:
A new methodology was tested, using the case of Highly Pathogenic Avian Influenza (HPAI) surveillance, in three poultry production areas of Vietnam. Poultry farmers were gathered in focus groups to rank their concerns and prioritize their options of disease management. Semi-structured interviews in combination with impact flowcharts were used for qualitative identification of non-monetary constraints. A participatory tool based on conjoint analysis was built to reach a quantification of these non-monetary attributes.
Results:
Different alternative responses to HPAI suspicion occurrence ranked first in farmers' priorities, including treatment and rapid sale of the birds. Five types of non-monetary constraints on disease reporting were identified in semi-structured interviews, including uncertainties about outcomes of reporting, transaction costs and impact of disease notification on poultry market prices. On the other hand, help of authorities in disease management was considered a benefit. The adapted conjoint analysis was tested on 23 broiler producers. The estimated values ranged from 0 to 2979 USD (cost related to the responsibility in market impacts), from 0 to 1081 USD (transaction costs) and from 0 to 829 USD (benefits of support in disease management).
Conclusions:
There are non-monetary costs and benefits associated by actors with HPAI suspicions reporting in Vietnam. These components of decision making are complex but can be quantified using a combination of conjoint analysis with participatory tools.
Relevance:
The developed methodology can successfully contribute to passive surveillance evaluation. The quantification tool needs to be further implemented in a wider range of sanitary and production contexts.

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Modeling immunity distribution profiles through animal value chain network: a decision tool for disease management

Marisa Peyre[1], Marc Choisy[2,3], Walid Hassan Kilany[4,5], Julie Pecqueur[6], Hiep Dao Thi[7], I. Monuyl[8], **Alexis Delabouglise**[1], Pierre-Marie Borne[6], Gwenaelle Dauphin[9], Yilma Jobre[10], Dinh Ton Vu[11], F. H. Ansarey[8], François Roger[1], [1]CIRAD, Montpellier, France; [2]IRD, Montpellier, France; [3]OUCRU, Hanoi, Viet Nam; [4]Reference Laboratory for Veterinary Quality control on Poultry Production, Cairo, Egypt; [5]FAO, Cairo, Egypt; [6]CEVA santé animale, Libourne, France; [7]CIRAD, Vietnam National University of Agriculture, Viet Nam; [8]ACI, Dhaka, Bangladesh; [9]8Food and Agriculture Organization of the United Nations, Rome, Italy; [10]Food and Agriculture Organization of the United Nations, Cairo, Egypt; [11]Vietnam National University of Agriculture, Hanoi, Viet Nam. Contact: alexis.delabouglise@gmail.com

Purpose: Vaccination against avian influenza (AI) is currently applied worldwide with inactivated vaccines. Since November 2012, a novel recombinant HVT-AIH5 (Herpes virus of turkeys vector) vaccine has been commercialized and applied to day-old chicks (DOC) in Egypt and in Bangladesh. The objectives of this study were to assess the cost-effectiveness of AI DOC vaccination in hatcheries and the feasibility of implementing AI DOC vaccination in the different production sectors in HPAI H5N1 endemic countries.
Methods: For each country, a model of the poultry production network was combined with a model of flock immunity to simulate the distribution profile of AI immunity according to different vaccination scenarios (including DOC vaccination or not). The model estimates the vaccine coverage rate, positive sero-conversion levels and the duration of sero-protection for each network node. Economic evaluation of the different strategies was performed using cost-effectiveness analysis. spatial analysis was performed to account for spatial clustering of the different poultry production types.
Results: In all study areas the model predicted that targeting DOC AI vaccination in industrial and large size hatcheries would increase immunity levels in the overall poultry population and especially in small commercial poultry farms. The level of improvement and best scenario was variable according to the specificity of each production networks. DOC vaccination strategy was shown to be more efficient than the current strategy using inactivated vaccines.
Conclusion: This study demonstrated the interest of combining network analysis and immunity modelling to assess the efficacy of AI vaccination scenarios. The model predicted that targeting DOC AI vaccination would increase immunity levels in the overall poultry population up to sufficient levels to improve HPAI disease control.
Relevance: Improving HPAI control in commercial poultry sector could have positive spill over effect on the epidemiological situation of the disease in backyard poultry. This model could be applied for strategic management of other contagious diseases such as Newcastle Diseases.

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Using operations research concepts to identify the optimal levels and locations of laboratories within the National Animal Health Laboratory Network (NAHLN)

Amy Delgado[1], Amy Hagerman[1], Sarah Tomlinson[2], [1]USDA-APHIS-VS-STAS, Fort Collins, CO, [2]USDA-APHIS-VS-STAS, Fort Collins, CO, Contact: amy.h.delgado@aphis.usda.gov

Purpose

The National Animal Health Laboratory Network (NAHLN) in the US began a restructuring process in 2013. A concept paper published in the Federal Register defined the new structure and described criteria for each of 5 levels. The number of labs at each level will be defined through a series of stages including a laboratory self-assessment, an external review by stakeholders, and a needs evaluation. The objective of this work was to provide scientific support for the needs evaluation step.

Methods

Using accepted operations research concepts, number and geographic distribution of laboratories was optimized for each of five levels, accounting for factors including: geographic distribution of animals/ farms; animal population density; lab capacity for foot-and-mouth disease (FMD) and highly pathogenic avian influenza (HPAI), and previous and anticipated demand for diagnostic testing. The model was programmed in the General Algebraic Modeling System (GAMS). Population files were built for 7 commodity groups (beef cattle, dairy cattle, poultry, game birds, swine, sheep, goats) with 39 farm types based on the 2012 Census of Agriculture. Laboratory profiles included: self-assessed level, BSL2 and BSL3 space, approved assays and diseases, historical data on testing diseases of regulatory concern, and reported surge capacity for FMD and HPAI. Anticipated surge capacity was estimated from disease spread modeling studies.

Results & Conclusions

Preliminary results indicate that BSL3 space is the primary limiting factor for level-1 eligibility; 30% of labs met this mandatory requirement. All of the labs that met level-1 requirements have staff trained and proficiency tested for multiple diseases. Due to high throughput capacities, these labs absorb the largest proportion of diagnostic demand during an outbreak. However, diagnostic demand generated from surveillance within zones during an FMD outbreak could only be met with local capacity in 33% of the outbreaks simulated, highlighting the need for surge capacity across the NAHLN.

Relevance

Presentation of this research at ISVEE offers exposure to a well-accepted methodology to support decision making which may be new to participants.

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Bovine brucellosis surveillance in Canada: How combining surveillance activities has contributed to an efficient surveillance system

Julie Paré[1], Krista J. Howden[2], [1]Canadian Food Inspection Agency, Saint-Hyacinthe, QC, Canada; [2]Canadian Food Inspection Agency, Edmonton, AB, Canada. Contact: julie.pare@inspection.gc.ca

Since Canada has successfully eradicated bovine brucellosis from its domestic herd in 1985, many sources of information have contributed to supporting freedom. Various programs of the Canadian Food Inspection Agency (CFIA) included serological testing for *Brucella abortus* but these were not accounted for when planning the periodical bovine serological surveys. In 2013, the CFIA implemented a bovine serological surveillance system which combines the various sources of surveillance information, to a structured population based active ongoing surveillance. This abstract presents the efficiencies gained by using this system in maintaining a high probability of freedom of bovine brucellosis in the domestic Canadian herd.

The objective of the surveillance system is to estimate the probability of freedom from bovine brucellosis in the national domestic cattle population on an annual and ongoing basis at a prevalence level of 0.0002. A scenario tree model was built using the following stochastic input variables: initial probability of freedom; probability of introduction; relative risks associated with the surveillance streams and diagnostic test performances. Surveillance data from 2008 to 2014 were included in a scenario tree model built in an Excel® spreadsheet using the Poptools® add-in for stochastic simulation. The outputs estimated were yearly surveillance system sensitivity (SSSe) and cumulative probability of freedom (Pfree).

The total yearly sample size in the system decreased from 56,709 in 2008 to 7,647 in 2014. SSSe was estimated to be 1.0 in 2008, and remained above 0.90 up to 2014. For the whole period, Pfree was maintained above 0.99 (2.5^{th} percentile 0.97).

The historical surveillance, ongoing active slaughter surveillance, inclusion of weighted test data from other programs, and low probability of introduction have contributed to the significant decrease in samples needed for bovine brucellosis surveillance in Canada.

The use of scenario tree modeling has allowed the CFIA to decrease the amount of active sampling for brucellosis, while maintaining a high probability of freedom.

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The enhanced passive surveillance system: a solution supporting data collection, integration and analysis for disease surveillance

Lindsey Holmstrom[1], Keith Biggers[2], Austin Riddle[2], Lina Mur[1], Jim Wall[2], Tammy Beckham[1], [1]Institute for Infectious Animal Diseases, College Station, TX, [2]Texas Center for Applied Technology, College Station, TX, Contact: lindsey.holmstrom@ag.tamu.edu

Purpose:
The future of disease surveillance requires systems for real-time collection of multiple data streams to detect disease events and trends. The Enhanced Passive Surveillance (EPS) system provides a platform to rapidly collect and integrate animal health data in real-time for early detection of disease outbreaks or changes in endemic disease.

Methods:
Working with U.S. agricultural industries, veterinarians, diagnostic laboratories, and state/federal animal health officials, mobile applications were developed that allow participants to enter data on healthy and sick animals into the EPS system using mobile devices and web-based reporting tools. Submitted data are assimilated into an online EPS Analyst Workstation (AWS) and combined with veterinary diagnostic laboratory and climate/environmental data sources for monitoring and analysis.

Results:
The EPS system is being piloted in the U.S. by 61 mixed animal and equine veterinary practitioners and two diagnostic laboratories reporting on cattle, cervids, equine, poultry, small ruminants, and swine species. Since July 2012, over 24,077 healthy and syndromic reports have been submitted, representing the animal health status of over 1.3 million animals in four States. Eleven state/federal animal health officials have been trained on the EPS AWS and its use for determining baselines and trends. Using automated temporal algorithms (control charts), the system successfully identified two separate events in cattle: a widespread reproductive loss and a localized environmental toxic event in two states.

Conclusions:
Piloting the EPS system has had many successes, including obtaining industry buy-in, demonstrating security of information, integrating data streams, and customizing the mobile apps to meet daily industry requirements and encourage participation. The system is being expanded to all U.S. livestock/poultry industries and wildlife.

Relevance:
The EPS system is adaptable with broad applications in the international community for early disease detection and animal health monitoring. The system provides a low-cost, low-maintenance solution supporting real-time situational awareness and surveillance.

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Viral infection triggers calving: perspectives for surveillance of emerging diseases

Christine Fourichon, Simon Nusinovici, Aurelien Madouasse, Oniris - INRA, Nantes, France. Contact: christine.fourichon@oniris-nantes.fr

Purpose:
Reproduction data are good candidates to develop syndromic surveillance: insemination and calving events are often monitored for management purposes and many infectious diseases can be assumed to affect the course of pregnancy. The objectives were to describe the effect on pregnancy length of exposure of dairy cows to bluetongue virus (BTV) and to evaluate the potential for syndromic surveillance of an indicator on early calvings.
Methods:
A calving was considered as early when occurring after a pregnancy with a duration within a normal range but in the first quartile. The emergence of BTV serotype 8 in Europe in 2006-08 was used as a case study for the proof of concept.
Statistical analysis was conducted in three steps. Change in occurrence of early calvings was quantified by multivariable logistic regression in cows from herds with clinical signs of BTV. Kriging was used to estimate likely date of infection in herds from exposed areas but with no clinical signs, before doing a similar logistic regression. Time series and cumulative sum models were used to detect an increase of early calvings in infected areas.
Results:
Early calving occurred twice more often in cows that were in late gestation when clinical signs of BTV were first detected in their herd. It was also more frequent for cows in non-clinical herds in exposed areas around their estimated date of infection. Time series analysis triggered an alarm in 96% of the districts infected. The increase in frequency of early calvings was detected within a few weeks (median 5) after the first reporting of clinical signs in the district.
Conclusions:
Exposure of herds to BTV is associated with triggering of early calving in cows in late gestation, even in the absence of clinical signs. The increase in occurrence is high enough to make possible the early detection of virus introduction in a free area.
Relevance: This is the first study evidencing an effect of a viral infection on the length of pregnancies without an abortion. The frequency of early calvings is a sensitive and timely indicator for the detection of emerging viral diseases. Coverage can be excellent when density of cattle is high enough and use of artificial insemination extended.

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Disease outbreak articles as a source of queries for detection of signals of disease emergence on the Internet

Elena Arsevska[1,2], Thierry Lefrancois[1,2], Mathieu Roche[3,4,5], Renaud Lancelot[1,2], David Chavernac[1,2], Sylvain Falala[1,2], Pascal Hendrikx[6], Barbara Dufour[7], [1]Cirad, Montpellier, France; [2]Inra, Montpellier, France; [3]Cirad, Montpellier, France; [4]Irstea, Montpellier, France; [5]AgroParisTech, Montpellier, France; [6]Anses, Lyon, France; [7]EnvA, Maisons-Alfort, France. Contact: elena.arsevska@cirad.fr

Timeliness and precision in detecting exotic animal infectious disease outbreaks is crucial for preventing their spread. In 2013, the French national platform for animal disease surveillance has set up an international epidemiological intelligence team (so-called VSI team) aiming at detecting, verifying and monitoring signals of disease emergence from different sources of information, including the Internet. We propose an innovative method for monitoring disease emergence on the Internet. It is based on 3 sequential steps: 1) web crawling, 2) automatic classification of disease outbreak documents by machine learning approaches, 3) extraction of information from documents (e.g., disease, number of cases, location, etc.).

To query the web, the choice of relevant terms is crucial. For this purpose, we used text mining together with a collective domain expertise following a Delphi method. This approach allowed highlighting the relevant terms to detect signals of disease emergence on the Internet. We have applied it to detect documents addressing African swine fever (ASF) outbreaks (i.e. 123 dispatches from Google, and 45 from PubMed) written in English language, obtained for the period 2011-2014 with the baseline query “African swine fever outbreak”.

Based on 2400 terms extracted with the text-mining approach, our automatic search system associated with the collective domain expertise (i.e. evaluation of 20 groups of terms by 21 specialists) identified 3 groups of highly specific terms to detect signals of ASF emergence: 1) haemorrhagic fever in *Suidae*, 2) mortality in *Suidae* and 3) swine fever. Implemented as complex queries, these groups of terms allowed finding previously undetected ASF outbreak articles with the baseline query (period 2011-14): 3 for each of groups 1 and 2, vs. 54 for group 3.

Monitoring disease emergence on the Internet is a promising method towards improved disease introduction risk assessment. Nevertheless, domain experts still play a central role. Our method is generic: we intend to evaluate it on data from other exotic infectious diseases and with real-time data stream. Should this evaluation be successful, the method might be routinely used by the VSI team.

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Serological diagnostic techniques for bovine viral diarrhea virus (BVDV) today in Argentina and its relevance in the context of a potential control program

Maria S. Perez Aguirreburualde[1], Andrea Pecora[2], Alejandra Ferella[2], Natalia Aznar[1], Marina Mozgovoj[2], Emilio Leon[1], Maria J. Dus Santos[2], [1]INTA, Buenos Aires, Argentina; [2]INTA, Buenos Aires, Argentina. Contact: solperezburu@gmail.com

The control of infectious diseases is inextricably linked to the ability of diagnostic tests to define the exposure of a population or individual to the agent in question. The use of serum neutralization (SN) for the detection of antibodies against BVDV is widely reported in literature and procedure manuals. Based on the simplicity most laboratories use cytopathic strains for the assay. Although the SN is considered the reference technique, partial cross-neutralization between different genotypes makes the parameter sensitivity specific for each genotype, which could imply an underestimation of the prevalence determined. No strain is ideal in all circumstances, in practice it is considered that the one to be selected detects the highest proportion of serological reagents in the local population. For this however, it is required to have the description of local isolates which is usually a missing. As with all SN tests, the running costs and waiting time for results are a disadvantage over ELISA tests. Purpose: Here we aim to evaluate the impact of the diagnostic technique to determine the serological status of herds. Methods and Results: The results obtained after analysis of the 1600 samples from 83 beef herds of Chubut province, show that at least 12 of those would had been wrongly categorized as negative, if samples would have been process only against genotype 1a. From the total of negative samples for genotype 1a, 17% and 30% were positive against genotype 1b and 2 respectively. This made the value of true negatives fall from 37% to 19% of the samples. The same samples were run through an experimental ELISA, and an agreement between both techniques was verified. Conclusions: Preliminary results from a survey conducted among laboratories of the country demonstrate that the majority of them just offer traditional diagnostic protocols using SN only against genotype 1a, and just a few use commercial ELISAs. For those, the recent import restrictions applied by the authorities for this kind of supply are a clear limitation. Relevance: In this context, we consider the absence of locally produced diagnostic kits is a major factor jeopardizing the feasibility of implementing a control program for BVDV.

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Assessment of CSF surveillance in a highly intensive swine industry: the case of south Brazil

Ana Lourdes A. A. Mota[1], Antônio Augusto R. Medeiros[2], Ildara N. Vargas[2], Fernanda C. Dórea[3], Sabrina G. Tavares[4], Flávio P. Veloso[4], Fernando Ferreira[5], **Vítor Salvador P. Gonçalves**[1], [1]Universidade de Brasília, Brasília, Brazil; [2]Agriculture Secretariat of Rio Grande do Sul, Porto Alegre, Brazil; [3]National Veterinary Institute, Uppsala, Sweden; [4]CIDASC, Florianópolis, Brazil; [5]University of São Paulo, São Paulo, Brazil. Contact: vitorspg@unb.br

Brazil is the fourth pork producer and exporter in the world. Most of the OIE listed diseases are exotic or have been eradicated from the country. The National Program for Swine Diseases includes surveillance for CSF in order to maintain the free status in 16 states, which hold most of the swine population and the country's export capacity. The two most southern states - Rio Grande do Sul (RS) and Santa Catarina (SC) - standout in production and exports of pork and are recognized by the OIE as free of CSF. Both states have an on-going active surveillance program, in accordance with federal guidelines set by the Ministry of Agriculture, in addition to the passive disease reporting system. The active surveillance has the following components: (1) serological monitoring of accredited breeding farms that sell genetic stock, twice a year; (2) serological surveillance of commercial farms triggered by mortality of piglets above a certain threshold or the presence of hemorrhagic lesions; (3) serological monitoring of breeding stock at the abattoir; (4) sero-surveys of non-commercial small-holdings every two years. The present work aims at developing an analytical model for evaluating the efficacy of such measures using available surveillance data from both states.The first stage included an assessment of surveillance sensitivity. We constructed scenario trees based on discussions with field and industry people and used data from 2013. The preliminary estimates of the sensitivity of components (2) and (3) combined are 90.3% and 80.3%, for RS and SC, respectively. Should the surveillance activities be maintained at the same level thereafter, each state would achieve a 95% probability of CSF freedom after two years, given a 1% probability of disease and an unknown prior probability of freedom.The project is now refining the data used for parametrizing the model, such as relative risks of different production systems, and collecting field data on biosecurity at the farm level. In addition, there is a need to collect data on the procedures followed by farm personnel and veterinarians, both on farm and at the abattoirs.The results will be used to shape up the surveillance strategy for CSF in Brazil.

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A Financial Analysis of the Justification for Subsidization of Disease Surveillance

Tim Carpenter[1], Fernando O. Mardones[2], Pablo Valdes-Donoso[3], [1]Massey University, Palmerston North, New Zealand; [2]Instituto de Medicina Preventiva Veterinaria, Facultad de Ciencias Veterinarias, Universidad Austral de Chile, Valdivia, Chile; [3]University of California, Davis, CA, Contact: t.e.carpenter@massey.ac.nz

Purpose:
To examine the economic importance of considering the infectious nature of disease transmission when constructing a national-level disease control program
Methods:
Theoretical relationships between the benefits and costs of disease surveillance and the disease prevalence were established to determine the optimal level of disease surveillance at the farm level. Using these relationships, we then examined the optimal level of disease surveillance that should be conducted at the regional level and compared that with the current surveillance alternative, using infectious salmon anemia (ISA) surveillance in Chile as a case study.
Using data previously collected at the farm and national levels, we constructed a stochastic, multi-level, simulation model to mimic the spread of ISA, given alternative disease detection levels, assuming six sampling time intervals and four sample sizes, by simulating 1000 ISA introductions for each of the 24 strategies.
Results:
Simulation results indicated that sampling frequency should be increased to every two weeks, which would result in a benefit of more than $652,000. Although the benefit decreased as the testing interval increased, there was also a benefit associated with testing more fish, e.g. $320,000 if 100 vs. 30 fish were tested at 20-week intervals.
Conclusions:
The economically optimal level of surveillance was quantified at the farm and country levels. As illustrated here, the optimal level of surveillance at the country level was much more active than that, which would have been occurred if it were left up to the individual producer. Epidemiologic and economic evaluations need to be conducted together in order to better understand the economics of disease control, and as illustrated here, the optimal level of disease surveillance. In order to reach this economically optimal level, it may be in a sociieties' best interest to subsidize the individual producers' disease control efforts.
Relevance:
Surveillance programs are often designed based on sample size calculations; however, as illustrated here, it is important to also take into consideration the economics of a disease, especially when the disease is infectious.

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Benefit-cost analysis of a global eradication programme for peste des petits ruminants

Bryony A. Jones[1], **Karl M. Rich**[2], Jeffrey C. Mariner[3], John Anderson[4], Martyn Jeggo[5], Sam Thevasagayam[6], Yi Cai[6], Andrew R. Peters[7], Peter Roeder[8], [1]Royal Veterinary College, University of London, Hatfield, United Kingdom; [2]Lab 863 Ltd, Edgware, United Kingdom; [3]Tufts Cummings School of Veterinary Medicine, Grafton, MA, [4]The Nelson Mandela African Institute of Science and Technology, Arusha, Tanzania, United Republic of; [5]Geelong Centre for Emerging Infectious Disease, Medical Faculty, Deakin University, Geelong, Australia; [6]Bill and Melinda Gates Foundation, Seattle, WA, [7]Scotland's Rural College (SRUC), Edinburgh, United Kingdom; [8]Taurus Animal Health, Headley Down, United Kingdom. Contact: karl@lab863.com

Purpose

Peste des petits ruminants (PPR) is an important cause of mortality and production loss among sheep and goats in the developing world. Despite concerted control efforts in a number of countries, it has continued to spread in Asia and Africa, placing an increasing burden on the livelihoods of livestock keepers and scarce veterinary resources in affected countries. Given the similarities of PPR with rinderpest, and the lessons learned from the successful global eradication of rinderpest, the eradication of PPR appears to be an appealing option to both eradicate an important disease and improve the livelihoods of the poor in developing countries.

Methods

We conducted a benefit-cost analysis of a proposed global PPR eradication programme to provide an economic justification for such a programme. Based on our knowledge and experience, we prepared a programme strategy, and then estimated the costs of the programme. The benefits of the programme were determined firstly from the averted mortality costs, based on an analysis of the literature. Second, we estimated the downstream impact of reduced mortality using a social accounting matrix. Third, we computed the avoided control costs based on current levels of vaccination.

Results

Our benefit-cost analysis provides a sound economic justification for PPR eradication. Based on a 15-year programme with total costs in discounted terms of USD 2.26 billion, we estimate discounted benefits of USD 42.1 billion, yielding a net benefit of USD 39.9 billion, a benefit cost ratio of 18.6, and an internal rate of return of 123%. As PPR mortality rates are highly variable, we conducted sensitivity analysis based on lower and higher mortality scenarios to provide upper and lower estimates.

Conclusions

All examined scenarios indicate that investment in PPR eradication would be highly beneficial economically.

Relevance

Removing one of the major constraints to small ruminant production would be of considerable benefit to some of the most vulnerable communities in Africa and Asia. Our analysis highlights that PPR eradication is biologically, technically, and politically feasible, and generates high economic returns.

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SURVEILLANCE FOR DEMONSTRATED-ABSENT PATHOGENS: 2 YEARS, 5 YEARS, 10 YEARS - WHEN CAN WE STOP?

Marta D. Remmenga[1], Lori Gustafson[1], Kamina Johnson[1], Ian Gardner[2], [1]USDA-APHIS, Fort Collins, CO, [2]University of Prince Edward Island, Charlottetown, PE, Canada. Contact: marta.d.remmenga@aphis.usda.gov

Purpose

Producers involved with live animal trade often conduct surveillance routinely to demonstrate freedom from disease, amassing large amounts of data over time. Despite their volume, historic datasets may be given limited regard, with a focus instead on ongoing testing. While ongoing surveillance is logical for pathogens of uncertain or endemic status, it makes economic and biologic sense to scale down surveillance for pathogens of long demonstrated absence. Additional surveillance system pressures include emerging diseases and new diagnostics at local and national levels. Surveillance systems need to adapt as industries explore new markets, products, and technologies by balancing competing demands for a fixed set of resources.

Methods

Methods to scale surveillance according to risk are discussed within the context of current OIE guidelines. Examples using historic data and risks of disease introduction to scale surveillance are explored. The varying reliance on the health status of the region and gains in surveillance efficiency are explained for each example.

Results and Conclusions

Results show that scaling back activities for pathogens of demonstrated absence and low risk of introduction give surveillance systems better capacity to adapt to changing needs. Despite this, there continues to be a reluctance to retire pathogens from routine surveillance. Example applications of the methods raise additional questions for discussion and demonstrate the need for greater understanding of the implications of the mathematical model assumptions by epidemiologists and decision makers.

Relevance

Ongoing surveillance may be necessary in open environments subject to pathways for new disease introduction. However, in closed environments where risks are mitigated, or otherwise deemed low to disease exposure, prospective surveillance plans could adjust sampling accordingly. Method development and acceptance drives effectiveness and efficiency in surveillance. Exploring how extensive the period of demonstration should be and how much reduction can be scientifically supported are questions that animal health officials across the globe will be interested in discussing.

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Optimising surveillance for sensitivity and cost-effectiveness - an example for Bluetongue

Simon R. Ruegg[1], Hurria Yassin[2], Yves Van der Stede[3], Rebekka Nafzger[1], Helmut Saatcamp[2], Sarah Welby[3], Gertraud Schüpbach[1], Katharina Staerk[4], [1]University of Bern, Bern, Switzerland; [2]Wageningen University, Wageningen, Netherlands; [3]Veterinary and Agrochemical Research Centre (CODA-CERVA), Brussels, Belgium; [4]SAFOSO AG, Bern, Switzerland. Contact: srueegg@vetclinics.uzh.ch

Purpose:
An increased risk of (re)establishment of several vector-borne diseases (VBD) in Europe may arise from globalisation due to increasing international trade and related movement of animals as well as the ongoing climate change. Recent outbreaks such as Bluetongue (BTV) and Schmallenberg virus confirm that this risk is real. Effective surveillance systems are essential to detect, control and monitor VBD. The decision on how much resources are spent for surveillance of a specific disease is the result of political, technical and financial considerations.

Methods:
In order to inform such decisions, we propose a combination of scenario tree modelling and incremental cost effectiveness analysis. This approach is illustrated with the example of demonstration of freedom from disease of BTV (serotype 8).
Passive, clinical surveillance was assessed, and for active surveillance five designs were compared: (1) a random sample, (2) risk-based surveillance targeting high risk herds, (3) voluntary vaccination with risk-based surveillance targeting non-vaccinated herds, (4) voluntary vaccination with risk-based surveillance targeting non-vaccinated herds at high risk, and (5) mandatory vaccination with risk-based surveillance targeting herds at high risk. These designs could be implemented using either PCR or ELISA on blood samples, or ELISA on bulk-tank milk (BMT).

Results & Conclusions:
It appeared that incurrence of BTV-8, a serotype with morbidities of 2.5% in cattle and 7.7% in sheep, would be detected with almost certainty within a year using just passive surveillance, consisting of the reporting of clinical suspect cases by owners and veterinarians and a subsequent PCR.
Best cost-effectiveness could be obtained for a given sample size, by sampling the maximal number of herds. Furthermore, BMT appeared to be the method of choice to actively demonstrate freedom from disease in populations dominated by dairy production. And finally, designs involving voluntary vaccination (assumed 10% protective coverage) only marginally reduced costs of surveillance.

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Comparison of different surveillance strategies for Bluetongue Part 2 - The effectiveness of active and passive clinical surveillance for early detection

Jörn Gethmann, Maya Gussmann, Franz J. Conraths, Friedrich-Loeffler-Institut, Greifswald - Insel Riems, Germany. Contact: joern.gethmann@fli.bund.de

Background
In August 2006, bluetongue virus serotype 8 (BTV-8), which had caused disease before in the sub-Saharan region, Asia and South America, was introduced into Central Europe. The virus hit an area with a high population density of BTV-naïve ruminants, suitable vectors (*Culicoides* spp.) and climatic conditions favourable for virogenesis and transmission. For this reason, the EU modified the existing active and passive surveillance systems aiming at early detection and proof of freedom from disease (Commission regulation (EC) No 1266/2007 of 26 October 2007 on implementing rules for Council Directive 2000/75/EC as regards the control, monitoring, surveillance and restrictions on movements of certain animals of susceptible species in relation to bluetongue).
Methods
In the present study, we tested different surveillance strategies for early detection and freedom from disease regarding their effectiveness and their costs to improve the cost-benefit ratio. We developed a combined simulation model based on the models of Gerbier et al. (2008), de Koeijer et al. (2011) and Santman-Berends et al. (2011) to simulate the bluetongue outbreaks in 2006 and 2007. Wesubsequently used the outcome of the simulation model to test different surveillance strategies for an early detection of Bluetongue disease that is active surveillance, passive surveillance or a combination of both. For active surveillance, we tested different levels of detection (0.5, 1, 2 and 5% on animal level).
Preliminaryresults
The preliminary results show that clinical surveillance is detects BTV-8 earlier than active surveillance for BTV-8. Hence, passive surveillance alone would be sufficient for an early detection of BTV-8.
Conclusions
These results are important for decision makers as the decision to suspend active surveillance can save money without losing information on the potential introduction of the disease.

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Biosecurity practices and the management of emergency animal diseases among beef producers in Australia

Marta Hernandez-Jover[1], Vaughan Higgins[1], Melanie Bryant[2], Luzia Rast[1], Connar McShane[3], [1]Charles Sturt University, Wagga Wagga, NSW, Australia; [2]Swinburne Business School, Melbourne, Victoria, Australia; [3]James Cook University, Townsville, Queensland, Australia. Contact: mhernandez-jover@csu.edu.au

Purpose: Prevention of emergency animal diseases (EAD) in Australia relies on strict offshore and border measures and disease surveillance and control programs onshore. Producers are crucial for disease control; however, there is limited information on producers' awareness of disease risks and their management practices. The aims of this study were to investigate how beef producers in Australia manage EADs risks and to explore knowledge transfer strategies for biosecurity and EAD prevention.
Methods: To achieve these aims face-to-face interviews with government and industry stakeholders (n=18) and a cross-sectional study among beef producers, using a postal survey (n = 182) and face-to-face interviews (n = 34), were conducted.
Results: Findings indicate that animal health system stakeholders have clearly defined responsibilities in biosecurity and EAD prevention and management. However, producers are uncertain about these roles, which can affect their willingness and trust to report animal disease and confusion about EAD management. Producers are aware of the sources of animal disease risk and prioritise herd health. However, EAD and biosecurity planning are a low priority as they perceive EAD events unlikely to occur. In addition, only moderate implementation of biosecurity practices, such as isolating incoming animals or keeping visitors' records, was reported. Furthermore, over 40% of producers had minimal knowledge of the meaning of EAD, with over 20% reporting no veterinary contact in the last five years and an additional 8.5% who had never contacted a veterinarian. In the event of an unusual disease, most producers would contact their private or government veterinarian; however, most would also treat themselves and some would do nothing and wait.
Conclusions and relevance: Results from this study suggest that there is a need for better coordination between stakeholders to encourage a shared biosecurity and EAD understanding and to communicate a consistent message to producers. The study also highlights the need for improving producer awareness of the importance of EAD prevention and biosecurity practices as well as the stakeholders' roles within the animal health system.

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Smallholder livestock producers in Australia -biosecurity and knowledge transfer

Marta Hernandez-Jover[1], Lynne Hayes[1], Jenny-Ann L. M. L. Toribio[2], Rob Woodgate[1], Luzia Rast[1], [1]Charles Sturt University, Wagga Wagga, NSW, Australia; [2]University of Sydney, Camden, NSW, Australia. Contact: mhernandez-jover@csu.edu.au

Purpose: Practices of smallholder livestock producers are perceived to pose biosecurity risks; however, these practices and the potential risks are not fully understood. The aim of the current study was to investigate biosecurity, disease management and communication networks of smallholder producers in Australia.
Methods: To achieve this aim a stakeholder consultation and a national cross-sectional study, using an electronic and postal survey, among smallholders keeping <50 cattle, sheep and/or pigs were used. Focus groups with smallholders, using participatory epidemiology approaches, were conducted to triangulate previous findings and to obtain in depth information on producers' practices and attitudes.
Results: Twenty-eight stakeholders representing government, industry and community groups participated in the consultation, which identified a decline in research and resources for smallholders, a lack of a formal definition of this sector and variations in knowledge of the sector and level of direct association. A total of 944 smallholders (16.0% response rate) responded the questionnaire and 20 producers participated in the focus groups. Extra income and home consumption were the main reasons for keeping livestock, with over 40% being involved in other agricultural and environmental activities. Although half of respondents had moderate to high understanding of the term biosecurity, implementation of biosecurity practices was limited and veterinary contact was low. In addition, smallholders were mainly concerned with endemic diseases, with emergency animal diseases being a low priority. Animal welfare and cost were the main reasons of disease importance. Smallholders identified veterinarians, family, livestock agents and other producers as player stakeholders, with perceived high interest and influence on their practices; whilst government agencies and industry groups were perceived as having low influence and interest.
Conclusions and relevance: This study will support the development of improved knowledge transfer strategies to engage smallholders with biosecurity and health management, using targeted methods delivered by trusted stakeholders.

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Carryover effects of bovine leukemia virus antibodies in samples from shared milk meters

Omid Nekouei, Javier Sanchez, Greg Keefe, University of Prince Edward Island, Charlottetown, PE, Canada. Contact: onekouei@upei.ca

Purpose: screening for infectious diseases of cattle using milk from the dairy herd improvement (DHI) sampling process is very convenient. However, when samples from shared milk meters are used, carryover of milk antibodies or other diagnostic targets can complicate the interpretation of the diagnostic test results for diseases (e.g. bovine leukosis). Objectives of this study were 1) to assess the potential for carryover of antibodies against bovine leukemia virus (BLV) in milk samples obtained from shared meters, and 2) to determine if adjustment of the test cut-off value would improve the test performance for meter-collected ELISA results.
Methods: in July 2013, eight dairy farms were randomly selected from herds with a wide range of BLV prevalence levels in Prince Edward Island, Canada. Within each farm, during the routine procedures of DHI sampling, two simultaneous milk samples, one hand-collected, and the other from the corresponding milk meter were taken from all lactating cows (n = 236) that were milked at the selected meters. The sequence of cows using each meter was precisely recorded. All samples were tested for BLV antibodies using a commercial ELISA. Antibody carryover potential was assessed in meter samples which were preceded by other cows sharing the same meters, using a linear model. Applying the hand sample results as the reference standard, a new cut-off was defined for meter-collected samples to optimize the test characteristics, using a ROC analysis.
Results & Conclusions: at the standard cut-off of the test, 46.6% of the hand-, and 57.6% of the meter-collected samples were positive. For low-titer cows (e.g. negatives), the likelihood of antibody carryover significantly increased as the titer of preceding cows increased, while this change was not significant for high-titer cows. A suspicious category for meter ELISA results was defined, and a retest was recommended for the cows falling into this category. This strategy effectively assisted in reducing the number of consequent false positive results.
Relevance: when DHI-collected samples are used, carryover can affect the interpretation of dichotomous test results, and may require adjustment of assay cut-off values.

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How do veterinarians frame farmers' and their own barriers to implementing biosecurity measures?

Orla Shortall, Annmarie Ruston, **Jasmeet Kaler**, University of Nottingham, Sutton Bonington, United Kingdom. Contact: jasmeet.kaler@nottingham.ac.uk

Purpose:
Biosecurity is seen as essential for dairy farm and industry profitability, reducing disease risks to the sector and to humans, as well as being beneficial for animal welfare. However, there is evidence of limited uptake of biosecurity measures in the dairy sector in the UK. Vets have been identified as a trusted source of biosecurity advice for farmers. However, limited work has been conducted on veterinarians (vets) perceptions of the barriers on implementing biosecurity measures on dairy farms.
Methods:
Interviews with 28 vets were conducted to explore vet perceptions of farmer and vet barriers to implementing biosecurity practices. Frame analysis was used to explore the themes identified. Frames are conceptual lenses through which we experience the world and frame analysis investigates how people order and understand particular aspects of reality. A online survey was conducted with expert vets and a choice modelling was conducted on veterinarians choices of most effective and practical measures.
Results:
Vets suggested the lack of farmer action was not due primarily to a lack of knowledge on the farmers' part, but rather that farmers do not perceive the disease risk of their own actions. There appeared to be a discrepancy between how vets assessed the risks and how farmers assessed them. It was suggested that there was not a biosecurity culture in the dairy sector. Difficulties in making the most of the vet-farmer relationship were also highlighted, as vets stated some farmers were wedded to the "test and treat" model of veterinary intervention.
Conclusions: The findings resonated with previous work on farmers' barriers, as a lack of time, money, knowledge and logistical problems on the farmers' side, and lack of time and a perception that farmers are not interested in biosecurity, on the vets' side.The in depth nature of the interviews allowed vets to expand on these factors and unearthed new perspectives into biosecurity.
Relevance:
The research sheds new light on vets' views of their own and farmers' barriers to uptake of biosecurity and points to ways in which vets would like to see the farmer-vet relationship develop in order to allow them to better implement biosecurity measures.

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Herd health programme for resource poor farmers in Gauteng Province

Noluvuyo R. Magadla, Gauteng Department of Agriculture and Rural Development, Johannesburg, South Africa. Contact: noluvuyo.magadla@gauteng.gov.za

Gauteng is mainly an urban province with only 4% of its population being rural. A number of township and informal settlements' residents practise small scale livestock production for home consumption, income generation or translocation of animals to the owner's home province. A limited number of farmers located in formal agricultural land are also classified as resource poor. To assist these farmers, a preventive animal health care project was launched in 2007 to raise awareness on veterinary and livestock production practises. This article highlights major constraints, successes, opportunities and improvements of the project since its inauguration. The objectives of the program were; to increase the efficiency and effectiveness of animal health care delivery for livestock productivity, safeguard public health, support and contribute to the national agricultural development strategy. This was based on four pillars; a disease prevention programme, farmer husbandry skills development program, basic clinical care and introduction of livestock identification for traceability and farm information system. Since the inauguration of the programme, livestock vaccinations have increased from under 1000 to 21041 cattle and 12808 small-stock in 2013/14. A database has been created with over 4500 cattle identified with fully traceable tags. Established stakeholder and intergovernmental collaborations have proven a success in assisting farmers with on-farm infrastructure development. The manual methods of farm management and animal movements have been improved through digital and communications technology. Ultimately a holistic and sustainable livestock production and health delivery programme for resource poor farmers was developed that meets the client's needs in an economical manner and still ensures that government responsibilities of delivery of services, food security, poverty eradication and redress of inequality are fulfilled.

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Assessing the impact of tailored biosecurity advice on farmer behaviour and disease risk in beef herds in England and Wales

Jacqueline M. Cardwell[1], Steven van Winden[1], Joanne Hardstaff[1], Wendy Beauvais[1], Alex Mastin[2], William de Glanville[3], John Fishwick[1], Dirk U. Pfeiffer[1], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]University of Salford, Salford, United Kingdom; [3]University of Edinburgh, Edinburgh, United Kingdom. Contact: jcardwell@rvc.ac.uk

Purpose:
The term 'biosecurity' encompasses many measures farmers can take to reduce the risk of pathogen incursion or spread. As the best strategy will vary between settings, veterinarians play an important role in assessing risk and providing biosecurity advice, but effectiveness requires farmer compliance. The aim of this study was to assess the effectiveness of tailored biosecurity advice packages in reducing endemic infections on UK beef suckler farms.

Methods:
In total, 116 farms recruited by 10 veterinary practices were followed for four years. Farms were randomly allocated to intervention (receiving specifically tailored advice) or control (receiving general advice) groups. A spreadsheet-based tool was used yearly to attribute a score to each farm relating to the risk of entry of five pathogens (bovine viral diarrhoea virus [BVDV], bovine herpesvirus-1, Mycobacterium avium paratuberculosis, Leptospira interrogans hardjo [L. hardjo] and bovine tuberculosis). Objectives of these analyses were to identify which risk score components were the best predictors of infection and to identify any trends for risk behaviour reductions during the study, as an indication of compliance. Polychoric correlations between score components were examined and multilevel mixed effects logistic regression used to identify key risk score components as infection predictors. Non-parametric tests for trend were used to identify patterns of behaviour and infection across study years and to compare these between intervention and control farms.

Results:
Significant reductions in BVDV and L. hardjo infections, and in risk scores for all five pathogens, were seen on intervention but not control farms.

Conclusions:
Results suggested that veterinary advice did have an impact on farmer behaviour and that tailored biosecurity advice packages do have potential to reduce pathogen incursion.

Relevance:
These findings, along with qualitative data from the same study, will allow refinement of the risk scoring tool and inform development of a collaborative approach to biosecurity between veterinarians and farmers, including adoption of cost-effective strategies effective across pathogens.

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The effects of covariation between the behavioral and physiological components of transmission on epidemic outcomes

Lauren A. White[1], James D. Forester[2], Meggan E. Craft[3], [1]University of Minnesota, St. Paul, MN, [2]University of Minnesota, St. Paul, MN, [3]University of Minnesota, St. Paul, MN, Contact: whit1951@umn.edu

Purpose: Transmission is contingent upon individual behavior that leads to contact between infectious and susceptible hosts, and the transmission efficiency of the agent, which depends on the physiology of the pathogen and host. Nonetheless, little is known about how interactions between individual variation in behavior and physiology scale-up to overall contact frequencies at a population level. The objective of this study is to evaluate how covariation between the behavioral and physiological components of transmission affect network properties, epidemic outcomes, and optimal sampling regimes for empirical studies in wildlife.
Methods: Here, we develop an individual-based, dynamic network model where individuals form or remove edges with conspecifics based on their individual behavior predispositions and on their infection status. This simulation will describe the complete, time-ordered network--one that represents the actual transmission pathways available to the pathogen in real-time. Next we will evaluate the efficacy of different sampling regimes by exploring how modeling predictions of epidemic duration and size vary when comparing the time-ordered network with time-aggregated networks that correspond to different sampling frequencies.
Results: We predict that allowing for dynamic interactions will be most important for pathogens of lower infectiousness and for those that induce the strongest sickness behaviors (e.g., fever, lethargy).
Conclusions: While disease models traditionally allow infection to spread across a static contact network, pathogens can change individual host behavior in ways that alter association patterns. Modeling studies will be critical in determining the degree of research effort necessary to fully capture the transmission process for contact network studies in wildlife.
Relevance: This study addresses several key questions for investigators: when to incorporate contact heterogeneity into studies and how well static networks can approximate real-time dynamics.

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The risk of *Salmonella* contamination of pig pens may be mitigated by hygiene and biosecurity practices: a study in England

Alasdair J. C. Cook[1], Simon Cousens[2], Robert H. Davies[3], [1]University of Surrey, GUILDFORD, United Kingdom; [2]London School of Hygiene & Tropical Medicine, London, United Kingdom; [3]Animal & Plant Health Agency (APHA) - Weybridge, Addlestone, United Kingdom. Contact: alasdair.j.cook@surrey.ac.uk

Purpose: *Salmonella* infection is found in a quarter of pigs slaughtered in England. Many producers operate their finisher accommodation on an all-in/ all-out basis. Pig pens should be cleaned and disinfected then left to dry between batches. The impact of these practices upon *Salmonella* varies. Data from a study of 46 finisher farms were used to estimate the association between three variables on *Salmonella* contamination of pens prior to re-stocking.

Methods: 1062 pens were selected randomly. Pen faecal/floor swabs were collected when pigs were sent for slaughter and prior to restocking. After pre-enrichment in buffered peptone water they were subcultured to DIASALM medium. Suspect growth was inoculated onto a Rambach agar plate and colonies confirmed by slide agglutination test. The prevalence previous batch (ppb) was calculated. Data were analysed at pen level by multiple logistic regression, using GEE with robust standard errors to account for within farm clustering.

Results:

The results suggest that an increasing prevalence of *Salmonella* in the previous batch is associated with an increased risk of pen contamination at re-stocking. Greater attention to cleaning and biosecurity is associated with a reduced risk of contamination at restocking. Only 33 of 46 farms reported the number of dry days and there is only weak evidence that increased dry days was associated with a reduced risk of contamination.

Conclusions: Conservatively, a high ppb increases the risk of pen contamination by a factor of 2 or more. Greater attention to hygiene and biosecurity may reduce the risk of pen contamination by 10% and increased dry days may reduce this risk by 5%.

Relevance: Veterinarians and pig producers often assume that between-batch cleaning and disinfection and leaving pens to dry will inevitably remove any residual *Salmonella* contamination but inadequate attention to cleaning, disinfectant concentration and pest control undermines this, especially when the prevalence of contamination in the previous batch is high. These results are compatible with an important reduction in risk if rigorous procedures are followed.

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What do cattle farmers tell us about their attitudes towards biosecurity and vaccination that can help veterinarians improve their work?

Imogen Richens, Wendela Wapenaar, Marnie Brennan, University of Nottingham, Sutton Bonington, United Kingdom. Contact: wendela.wapenaar@nottingham.ac.uk

Purpose
This study aimed to identify the motivators and barriers of farmers towards implementing biosecurity measures, including vaccination strategies.
Methods
Two researchers interviewed farmers across England, Scotland and Wales, focussing on vaccination and biosecurity practices. Inductive thematic analysis was used to identify key themes and topics highlighted by interviewees.
Results
Vaccination was used without much hesitation if there was a risk of disease entering a herd, or if disease was present in a herd. Farmers saw veterinarians as important advisors on implementation of vaccination strategies. It was interesting to find the working relationship between veterinarians and farmers important. This did not appear to be directly related to the frequency of veterinary visits, but was often related to trust of the person they were interacting with. 'My vet' was often distinguished from 'vets', indicating a perceived different role for veterinarians. These personal aspects were highlighted in various ways during interviews and appeared to be of higher importance than other aspects such as costs of veterinary services or products.
Most farmers believed that control of disease was possible, and that most actions undertaken were perceived to be based on some form of risk assessment. Biosecurity measures were more likely to be implemented if the disease threat was considered 'serious'. Additionally, farmers were more likely to consider using biosecurity measures if the benefits outweighed the costs, and if there was good evidence of efficacy when implementing the measures.
Conclusions
The farmers' perception of disease risk on farms, as well as the important role of veterinarians, appears to have a significant influence on the decisions being made by farmers.
Relevance
The findings of this research are vital considering emerging disease threats, the increasing emphasis on reduced use of antibiotics and a challenging economic climate for farmers and veterinarians. It is of key importance that veterinarians are aware of their clients' points of view and concerns relating to biosecurity and vaccination.

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Risk factors for large animal inpatient shedding of Salmonella enterica in a veterinary teaching hospital

Brandy A. Burgess[1], Paul S. Morley[2], [1]Virginia Tech, Blacksburg, VA, [2]Colorado State University, Fort Collins, CO, Contact: burgessb@vt.edu

Purpose: Widespread environmental contamination is commonly seen during epidemics of healthcare-associated infections attributed to Salmonella enterica. Additionally, patient isolates can have the same phenotype (i.e., serotype and susceptibility) as environmental isolates, suggesting animals to be a likely source. Previous reports focus on subsets of patients with results being minimally generalizable to the general hospital population. The objectives of this study were, 1) to determine factors associated with fecal shedding of Salmonella among large animal inpatients within the general hospital population; 2) do so in comparison to two different groups of patients - a group in which there is high confidence in negative status (having at least 3 negative cultures) and a group with potential for misclassification of shedding status (at least 1 negative culture); and 3) to demonstrate that the choice of comparison group can affect resultant associations.

Methods: Inpatients included in this case-control study had fecal samples collected and cultured, using standard techniques, as part of long-term infection control efforts. Data on factors of interest were collected retrospectively from electronic medical records. Multivariable conditional logistic regression was used to evaluate associations between animal factors and fecal shedding of S. enterica.

Results: During the study period, there were approximately 11,061 inpatients of which 5.9% (n=648) were fecal culture-positive for S. enterica. The majority of culture-positive inpatients were bovine (72%) and equine (22%) with the remaining being New World camelid and small ruminant. Overall, 69.4% of patient shedding could be attributed to systemic illness (i.e., population attributable fraction) in this study.

Conclusions: The findings of this study will provide a better understanding of factors associated with fecal shedding in the general large animal inpatient population, allowing for the implementation of evidence based preventive measures.

Relevance: Information from this study will be integral to risk management related to periods of epidemic as well as endemic disease associated with S. enterica.

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Epidemiological and economic analysis of Haemorrhagic Septicemia in India

Dwaipayan Bardhan[1], Sanjay Kumar[2], Med Ram Verma[1], [1]Indian Veterinary Research Institute, Bareilly, India; [2]Indian Veterinary Research Institute, Bareilly, India. Contact: dwaipayanbardhan@gmail.com

Purpose

Hemorrhagic Septicemia is one of the most widely reported disease in India. Scant literature is available documenting the epidemiology of the disease and the economic losses due to it. The present study aims to address this research gap.

Methods

The study uses a stratified multistage sampling technique, by dividing India into four major geographical strata, viz. east, west, north and south. Data on epidemiological and economic parameters pertaining to HS were collected from one representative state, having highest livestock population, from each region. A total of 2277 livestock rearing households were covered in the survey from a total of 48 villages in 16 administrative blocks from 8 districts of the 4 selected states. Once, the morbidity and mortality rates, as observed in the survey, were imputed upon the age group-wise population of each breed/species in each region, the total number of region-specific cases and deaths were obtained.

The total economic loss due to HS in bovines was worked out as sum of mortality loss, direct loss in milk yield, losses due to reproductive failure, loss in animal draught power, cost of treatment of affected animals and labour costs. Specific mathematical models were developed for the purpose of computing component-wise losses.

Results

Morbidity and Mortality due to HS were analyzed from different angles, viz. age, breeds/species, sex, region, season, herd size, lactation stage and order, etc. to have a better understanding of the predisposing factors associated with the disease. The total economic loss due to HS in India was estimated as **$2491 million**. Among different components, the maximum loss of about 53% was due to mortality, followed by treatment cost (29.5%), extra labour charges (10%), drop in work power (4.4%) and direct milk loss (3%). The share of buffaloes in total economic loss was highest (66%).

Conclusion

The study has revealed significant economic loss due to HS in India which is higher than national level economic losses reported for other important diseases in recent studies. This implies that HS, from policy perspective, is one of the most important diseases when it comes to mitigating losses due to diseases in dairy animals.

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Risk factors for the occurrence of different Eimeria species in two regions of India

Bhagyalakshmi Chengat Prakashbabu[1], Georgina Limon-Vega[1], Thenmozhi Venkatachalam[2], Damer Blake[3], Javier Guitian[1], Eimeria CIDLID[4], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]Tamil Nadu Veterinary and Animal Sciences University, Chennai, India; [3]Royal Veterinary College, Hatfield, United Kingdom; [4]BBSRC/DFID-funded Eimeria CIDLID consortium, Hatfield, United Kingdom. Contact: bchengat2@rvc.ac.uk

Purpose: India is the second largest poultry producer in the world. Coccidiosis is one of the biggest hurdles faced by the poultry industry in India, where only Infectious bursal disease and Newcastle disease have been found to be more costly. Few studies have investigated risk factors for coccidiosis in India, and even less is known regarding occurrence of the seven recognised *Eimeria spp*, a salient issue given that pathogenicity varies with species. *Eimeria spp* are categorised as; very highly pathogenic (*E necatrix*), high pathogenic (*E brunetti* and *E tenella*), medium pathogenic *(E acervulina* and *E maxima*) and low pathogenic (*E mitis* and *E praecox*).The aim of this study was to identify risk factors associated with presence of different *Eimeria spp* in four northern and four southern states in India. Faecal samples and data on farm characteristics and management were collected from 104 farms from the North and 134 farms from the South.
Methods: Faecal samples were analysed using microscopy and PCR to identify *Eimeria spp* present. Multiple correspondence analysis was performed on data collected in order to transform correlated variables into a smaller number of synthetic uncorrelated factors. Hierarchical cluster analysis (HCA) was used to identify typologies of poultry farms. The association between clusters and presence of different *Eimeria* species was enumerated by logistic regression.
Results: HCA revealed three distinct clusters in the studied regions. In the North, farms with non-indigenous broilers and a flock size between 451-4000 were at higher risk of being positive to all categories of *Eimeria spp* compared to farms with indigenous cross-bred layers with flock size >4000 and backyard farms with indigenous birds. In the South, backyard farms with indigenous breeds were at higher risk of most pathogenic *Eimeria spp* than farms with non-indigenous breeders and broilers with flock size >3125 and layer farms.
Conclusions: The study suggests that broiler farms with non-indigenous young birds and high flock size are at higher risk of coccidiosis.
Relevance: The findings of this study enables us to prioritise farms when designing control strategies for coccidiosis in Indian poultry systems.

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Use of a rHVT-NDV vector vaccine in backyard chickens in Newcastle disease endemic area, Gauteng, SA, 2014-2015

Peter J. Geertsma, Krpasha Govindasamy, Department of Agriculture, Gauteng Province, Pretoria, South Africa. Contact: peter.geertsma@gauteng.gov.za

Purpose: Vectormune ND®, Ceva-Biomune, USA (VM), a rVHT-NCD vector vaccine, has been used in commercial chickens and a vaccine recovery rate of more than 80% is expected. However it has not been used in backyard chickens in Gauteng before. A study was conducted in Tarlton where numerous NCD outbreaks in both commercial and backyard sectors occurred over the last 3 years. Water-based NCD vaccine in this population has been unsuccessful. This study aimed to (1) determine the association of the VM vaccine in backyard chickens to NCD anti-body titres (2) determine the protective efficacy of VM.

Method

81 Boschvelders (BV) were introduced into 13 Sites **(S1-S13)** in 14/07. 61 of the BVs and 45 local breed (LB) chickens were vaccinated, in 14/10, with VM after baseline blood samples were taken. All birds were tagged (61 BVs and 130 LBs). The cohort was sampled monthly and Haemagglutination Inhibition (HI) tests were done. Data was captured into MS ACCESS 2013, cleaned and analysed using EXCEL and RStudio. Univariate analysis was done and an ordinal logistic regression model (Epicalc) used.

Results

An outbreak of virulent NDV was confirmed on 14/12/11 in **(S2)**. 50 birds died.

A total of 21 of the study cohort were reported dead on 15/02/24. Of these 86% (18/21) were not vaccinated. 10/12 VM birds on S2 survived.

The RR of VM vaccinated (exposed) chickens dying to chickens of unknown vaccine status dying was 0.17 (95% CI = 0.06–0.5) in this endemic NCD area (when all other causes of death are ruled out) i.e. the vaccine had a protective efficacy of 83.5% (95% CI = 50.38 - 94.18). The conclusion from the ordinal logistic regression model is that the increase in Titre levels to NCD significantly increases with vaccination: OR 2.2 (CI:1.2 - 4.1, p-value 5.68e-03) and some locations: **(S10)** OR:5.0 CI: 1.2 - 22.2 , p-value 1.47e-02 2; **(S2)** OR 4.4, CI- 1.2 - 17.3, p-value 1.52e-02.

Conclusion

Chicken deaths were significantly associated with an unknown vaccine status. The vaccination is associated with increased titre levels indicating seroconversion. The use of VM prevented 84% of deaths in the vaccinated flock.

Relevance

A once-of VM vaccination in backyard chickens is effective and is a cost effective alternative to current control.

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Risk Factors and Potential for Risk Reduction on Urban Live Bird Markets - Results of a Multivariate Analysis of Longitudinal Environmental Surveillance in Jakarta, Indonesia

U. W. Hesterberg[1], M. Azhar[2], E. Wuryaningsih[2], F. C. Zenal[1], G. B. Utomo[1], J. Henning[3], L. Schoonman[1], P. Pudjiatmoko[2], E. Brum[1], J. McGrane[1], [1]FAO Indonesia (Food and Agriculture Organisation of the United Nations), Jakarta, Indonesia; [2]Ministry of Agriculture, Jakarta, Indonesia; [3]Queensland University, Brisbane, Australia. Contact: daktari4u@yahoo.de

Visits to Live Bird Markets (LBM) have long been identified as one of the main ways for humans to contract H5N1 HPAI or other Avian Influenza Viruses. In response to this, several countries have eliminated traditional wet markets or enforced temporary closure. In Indonesia LBMs are an integral part of the culture and are thriving. Since closure of the markets is not feasible, research on measures that can be implemented to reduce the health risk to consumers is required. The aim of our study was to evaluate if there are factors that reduce or increase the risk of LBM with regard to H5N1 HPAI presence and to formulate policy recommendations on how the risk could be reduced. The study used information from four cross-sectional risk factor and poultry movement studies that were conducted at LBM's in Jakarta between 2008 and 2013. These data were combined with test results from regular monthly environmental surveillance for H5N1 HPAI conducted in 89 of the total 260 markets. Data were analysed using Generalized Estimation Equations (GEE) and Random Effect Models adjusted for clustering at market level and repeated testing. The most important identified risk factor was the density of collector yards in the district in which the market was located (OR 25, $p<0.001$). Collector yards serve as assembly and redistribution points for poultry arriving from outside the greater Jakarta metropolitan area before they are delivered to LBMs. Other important significant risk factors were rainfall (OR 7.2, $p<0.001$) and the average distance from the district in which a market is located to the district of origin of the poultry (OR 1.96, $p<0.001$). The results provided further strong evidence on protective measures that can be taken to decrease the risk of HPAI H5N1 contamination in LBMs. These were slaughtering outside the market (OR 0.34, $p< 0.001$) and the separation of slaughter and sales areas within the markets (OR 0.31, $p<0.001$). The study provided the required evidence for the full implementation of the Jakarta Governor's Regulation No. 4/2007 on restructuring the market chain. The results also indicate that re-locating collector yards outside dense urban areas can reduce the HPAI risk for urban markets and thereby consumers.

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Herd clustering based on milk quality practices in dairy producers from Villa María (Córdoba, Argentina)

Claudina Vissio[1], Alberto Rampone[2], Sergio Dequino[3], Mónica Moretto[3], Alejandro Larriestra[1], [1]Universidad Nacional de Río Cuarto, Río Cuarto, Argentina; [2]Universidad Nacional de Villa María, Villa María, Argentina; [3]INTA, Villa María, Argentina. Contact: cvissio@ayv.unrc.edu.ar

Córdoba is the second largest milk producing province of Argentina and because of that it is necessary a better understanding of producer compliance toward the application of good cow management practices to produce milk of better quality. Purpose: to classify and characterize dairy farmers according to the good management practices and the quality of milk produced. Methods: The study population was a cluster of dairy farmers who provide milk for cheese manufacturing. Between March and May of 2013, all producer (n=100) were visited once. The day of the visit, information about farm facilities, milking routine and good practices were gathered using check list. In addition, a bulk milk sample was collected for somatic cell count (SCC). Results: Over 45 herd management variables were recorded. After the checks for collinearity, all non-correlated variables were subjected to Principal coordinate analysis and Hierarchical cluster analysis. The Gower was the measure of distance used to identify clusters. The final number of groups was defined based on technical views and using the Tibshirani test. The variables with higher discriminant power used to classify the farms were type of holding pen, whether or not the farmer applied foremilk stripping, dry teats properly and post-deeping teat seal; and the milking machine functionality, milk yield per cow and bulk milk SCC (ln cells/mL x 1000). The cluster analysis showed three groups of farms based on the variables before mentioned. The coordinate planes explained 46% the total variability and showed the clusters of farms further apart. Conclusions: The group of producers studied showed three well defined clusters based on the set of dairy farm good practices applied. The findings are in consistence with previous research, besides of the higher set of variables analyzed and the larger sample size considered. Relevance: These results will help to devise a technology transfer extension program customized according to the herd management type identified, instead of targeting using an average herd approach. In fact, that information can help to improve efficiency of such as programs, because of the awareness of the dairy farmer heterogeneity.

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Methods used to research farmers' attitudes toward cattle production: a rapid review

Heather O'Connor, Imogen Richens, Marnie Brennan, Pru Hobson West, Jasmeet Kaler, Nick Wright, Wendela Wapenaar, University of Nottingham, Sutton Bonington, United Kingdom. Contact: wendela.wapenaar@nottingham.ac.uk

Purpose
The purpose of this study was to use a rapid review methodology to identify and critically appraise the published literature investigating attitudes of farmers towards cattle production.
Methods
A comprehensive search of CAB Abstracts (OVID) was carried out using a specific search strategy.
Results
Studies were examined for a variety of factors, including topic investigated, the type of data collection method and the type of analysis conducted. Fifty-seven studies were identified that represented a range of topics, methods and analyses. There appeared to be a discrepancy between the data collection method and the subsequent type of data analysis in some of the studies. There was also variation in the quality of the studies as categorised by a bespoke critical appraisal tool. The predominant use of quantitative methods to analyse data that was collected qualitatively highlights the potential for the loss of data depth and richness.
Conclusions
The inclusion of attitudes, motivators and barriers of farmers towards a number of aspects of cattle production research has increased significantly over the past twenty years and covers a range of study topics and types. However the quality of these studies, when assessed using a novel critical appraisal tool, varies widely. This study demonstrates that the consistent reporting of methods and results using published guidelines is likely to significantly improve the quality of the published literature in this important area of research.
Relevance
Understanding farmers’ attitudes and opinions on key topics is important as they are major stakeholders in areas of animal health and welfare, food security and policy.

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Japanese encephalitis in a peri-urban pig slaughterhouse of Cambodia : a dynamical modeling approach to quantify the risk of transmission to humans

Maud Yakovleff[1], Julien Capelle[2], Raphael Duboz[1], Didot Prasetyo[3], Veasna Duong[4], S. Ong[4], San Sorn[5], Arnaud Tarantola[6], Philippe Buchy[7], **Veronique Chevalier**[8], [1]CIRAD/ Institut Pasteur Cambodia, Montpellier, Cambodia; [2]CIRAD/ Institut Pasteur Cambodia, Phnom Penh, Cambodia; [3]NAMRU, Phnom Penh, Cambodia; [4]Institut Pasteur, Phnom penh, Cambodia; [5]NaVRI, Phnom penh, Cambodia; [6]Institut Pasteur, Cambodia, Cambodia; [7]Institut Pasteur, Phnom Penh, Cambodia; [8]CIRAD, Montpellier, France. Contact: chevalier@cirad.fr

Purpose:
Japanese encephalitis virus (JEV) is the most important cause of acute encephalitis in Eastern/Southern Asia. The basic transmission cycle involves *Culex* mosquitoes, pigs, and Ardeid birds. Cambodia has been facing high population growth in urban areas, associated with an increase of pork consumption, and consequently, the implantation of pig slaughterhouse in peri-urban areas. Pigs that transit through Cambodian slaughterhouses use to come from the whole country, but also from Thailand and Vietnam where the disease is endemic.Depending on age, origin country and transportation duration, these pigs may arrive either susceptible, infectious or removed from JE infection. Due to thepresence of *Culex quinquefasciatus*, a JE competent mosquito vector, in peri-urban areas, and in a country where JE vaccination is not available countrywide, the risk of JE urban transmission is increasing.
Methods:
We developed a deterministic model consisting in two Susceptible Exposed and Infectious (SEI) models for two species of mosquitoes, one rural and one per-urban species, coupled with a Susceptible and Removed (SR) model for humans. To estimate the model parameters, we used (i) for pigs, a flow dynamic survey associated with a serological survey performed in the pilot slaughterhouse, (ii) for mosquito densities a longitudinal trapping survey in the same location, (iii) data from the literature. We performed a sensitivity analysis of this model.
Results:
According to this model and by choosing realistic values for the parameters, the slaughterhouse-induced annual incidence was estimated to be 0.14%, potentially resulting in 9 human cases a year. : the number of infected individuals - 2 mosquitoes species and humans - is very sensitive to pig JE prevalence at the slaughterhouse. These three output variables are also very sensitive to the average number of meals a mosquito of both species can have by unit of time, the probability that a mosquito feed on a pig (respectively on a human) and the infection rate of mosquitos by meal for both species
Conclusions:
Further investigations are needed to refine this risk and recommend prevention measures in Cambodian urban areas.

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Risk factors for Bovine Enzootic Haematuria among cattle in the Kingdom of Bhutan

Arata Hidano[1], Basant Sharma[2], Rinzin Pem[3], Ugyen Namgyel[3], Sangay Rinchen[2], Sangay Letho[4], Karma Wangdi[5], Karma Rinzin[6], Narapati Dahal[7], Kinzang Dukpa[8], Mark Stevenson[9], [1]EpiCentre, Massey University, Palmerston North, New Zealand; [2]RLDC Tsimasham, Chukha, Bhutan; [3]RLDC Wangdi, Wangdi, Bhutan; [4]RLDC Kanglung, Trashigang, Bhutan; [5]RLDC Zhemgang, Zhemgang, Bhutan; [6]Murdoch University, Murdoch, Australia; [7]Ministry of Agriculture and Forests, Thimphu, Bhutan; [8]National Centre for Animal Health, Thimphu, Bhutan; [9]University of Melbourne, Melbourne, Australia. Contact: A.Hidano@massey.ac.nz

Purpose:
Enzootic haematuria is a debilitating disease of cattle caused by chronic ingestion of bracken fern (*Pteridium esculentum*). Where fern is abundant and fodder and nutrition resources are limited, control of bovine enzootic haematuria (BEH) is difficult. We conducted a case-control study in Bhutan to identify modifiable risk factors for disease.

Methods:
A matched case-control study involving 16 of the 20 dzongkhags (provinces) of Bhutan was carried out between March 2012 and June 2014. In Bhutan, sodium acid phosphate and hexamine (SAP&H) is routinely administered to cattle diagnosed with BEH. All cattle greater than 3 years of age treated with SAP&H in 2011 were identified and BEH-positive (case) households defined as those with one or more BEH-affected animals.

BEH-negative households were defined as those that kept cattle and where BEH had not been diagnosed within the previous 5 years. Two BEH-negative households nearest each case household were selected as controls. A questionnaire was administered to the key decision maker, where available, in each case and control household to identify details of cattle management and feeding. Causal diagrams were developed and a conditional logistic regression model used to quantify the association between each of the exposures identified in the questionnaire and the presence or absence of BEH.

Results:
A total of 182 case and 360 control households were enrolled into the study. After adjusting by confounders, use of fresh fern and dry fern as a bedding for cattle increased the odds of a household being a case by a factor of 2.29 (95% CI 1.10 to 4.74) and 2.48 (95% CI 1.04 to 5.88), respectively. Free grazing in spring for 3 and 2 months increased the odds of a household being a case by a factor of 2.07 (95% CI 1.04 to 4.11) and 3.84 (95% CI 1.22 to 12.1) compared to those that did not free graze in spring.

Conclusions:
We identified cattle management practices that were associated with the presence of BEH that were readily modifiable.

Relevance:
Improving farmers' knowledge on BEH risk factors and modification of those risk factors should decrease the prevalence of BEH in endemic countries.

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Processes behind the adoption of on-farm strategies for Johne's disease control on Alberta dairy farms

Caroline Ritter[1], Keliesha Roth[1], Cindy L. Adams[1], David F. Kelton[2], Jolanda Jansen[3], Karin Orsel[1], Jeroen De Buck[1], Herman W. Barkema[1], [1]University of Calgary, Calgary, AB, Canada; [2]University of Guelph, Guelph, ON, Canada; [3]St. Anna Advies, Nijmegen, Netherlands. Contact: cmnritte@ucalgary.ca

Introduction/Purpose: The Alberta Johne's Disease Initiative (AJDI) is a voluntary control program for Alberta dairy farmers. A main purpose of the program is to decrease the herd prevalence of Mycobacterium avium subsp. paratuberculosis (MAP). Farm-specific risk assessments and management plans provide farmers with recommendations whose implementation would reduce the probability of MAP transmission. However, often AJDI participating farmers do not implement these recommendations. The aim of this study is to explore influences on farmers' decision making on whether or not to adopt JD specific management strategies.
Methods: A grounded theory approach was used for data collection and analysis. Farmers that did not implement a recommendation from the AJDI management plan were interviewed. A semi-structured interview procedure was used and conversations with farmers were audio-recorded. Transcripts were analyzed using the principles of iteration and constant comparison. Data collection and analysis will continue until no new information is generated and a grounded theory based on distinct categories is established.
Results: At the time of abstract submission the first eight interviews have been analyzed. Preliminary results indicate that farmers either lack ability or motivation to implement AJDI recommendations. Ability to adopt changes depends on how well the recommendation accounts for farm-specific resources and constraints. Motivation to adopt changes depends on 1) feeling of responsibility or pride, 2) expected or experienced (dis-) advantages of the change and 3) perception of the difficulty to overcome JD on the farm. More categories are expected to emerge with further interviews.
Conclusion/Relevance:
Farmers try to find a balance between preventing JD while taking into account different factors and competing aspirations. In order to successfully motivate farmers to adopt AJDI recommendations it is necessary to communicate efficiently by addressing their specific concerns and priorities. The probability that a farmer adopts a change is higher when the recommendation is tailored towards the individual farm.

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Modelling Porcine Epidemic Diarrhoea Virus (PEDV) spread in a pig densely populated area in France without population immunity

Nicolas Rose[1], Mathieu Andraud[1], Yannick Blanchard[2], Béatrice Grasland[2], [1]Anses, PLOUFRAGAN, France; [2]Anses, PLOUFRAGAN, France. Contact: nicolas.rose@anses.fr

Purpose:
A devastating epizooty of porcine epidemic diarrhoea (PED) has been striking the US since April 2013. In Europe, only sporadic cases due to mild strains have been reported in Germany, Italy, The Netherlands, France and Belgium to date. However severe outbreaks due to highly pathogenic strains similar to those circulating in the US have been reported in Ukraine recently. Seroprevalence studies carried out in different European countries (UK, Belgium, France, and Denmark) suggest that the immunity of the population in these countries against PEDV is low. The objective of the study was to assess the impact of an introduction of a highly pathogenic PEDV in a pig densely populated area in Europe using a modelling approach. The example of Brittany, one of the main pig production areas in France, is taken.
Methods:
A Spatio-temporal individual-based, stochastic model has been built to simulate the spread of the virus in the area. Data reporting geographical location of the herds, herd type and size, annual movements of animals between herds and frequency of contacts with vehicles and other mechanic vectors have been used for parameterisation. The model has been developed using the North American Animal Disease Spread Model.
Results:
Simulation results showed that a massive epizooty would be expected with similar characteristics as observed in the US. Shorter durations of herd infectiousness, as described for mild strains, resulted in limited sporadic cases as reported currently with those strains in Europe. The most efficient control measure was stamping out infected herds with a notification delay shorter than 10 days and with increased biosecurity. Limitations of animal movements reduced also significantly the epidemic size. When animal movements were not suppressed and only biosecurity was enhanced, the epizooty tended to move to an enzootic form.
Conclusions:
In the absence of immunity, the introduction of PEDV strains currently circulating in the US would have an important impact on the French swine population.
Relevance:
Rapid intervention would be required to limit the propagation of the virus in such a densely populated area.

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Spatial tools for the control of visceral leishmaniasis in Campo Grande, Mato Grosso do Sul, Brazil: incidence analysis and determination of vulnerable areas

Juliana Arena Galhardo[1], Gabriela Tjhio César Pestana Barros[1], Beatriz Crepaldi Aléssio[1], Lucas Fernandes Barros de Melo[1], Artur Kanadani Campos[2], José Eduardo Tolezano[3], Antonio Conceição Paranhos Filho[1], [1]Universidade Federal de Mato Grosso do Sul, Campo Grande-MS, Brazil; [2]Universidade Federal de Viçosa, Viçosa-MG, Brazil; [3]Instituto Adolfo Lutz, São Paulo-SP, Brazil. Contact: juliana.galhardo@ufms.br

Purpose: Due to geography, climate and unplanned urbanization, since 2002 Campo Grande has become an endemic area for visceral leishmaniasis. To increase disease control strategies, the analysis of incidence from 2007 to 2011 was carried out in urban regions and neighborhoods of Campo Grande using spatial analysis tools.
Methods: To determine the spatial relationship between neighborhoods and vulnerable areas for human visceral leishmaniasis (HVL), was developed a geographic information system in QGIS software and thematic maps were elaborated using the incidence by area/year. For the analysis of incidence, the indicator was constructed using the absolute incidence data available at the Brazilian Ministry of Health website and population data from 2007 to 2010 available at the Brazilian Institute of Geography and Statistics website. Population of the years 2008, 2009 and 2011 was estimated by the average annual rate of geometric growth.
Results: In the period 632 cases of HVL were reported, with neighborhood incidences varying from 0.0 to 11.22/10,000 inhabitants and an annual average of 1.67/10,000. Cases were recorded in all regions, but higher incidences were at Prosa, Anhanduizinho and Lagoa, concentrating 63% of the incidence. Segredo and Centro regions contributed with 21% and Bandeira and Imbirussu, east and west side of the city, may be considered vulnerable areas because there were low incidence rates. Eight neighborhoods showed the highest incidences in the period, ranging from 6.1 to 11.22. In 10 neighborhoods there were no recorded cases, being classified as vulnerable areas. Five of the eight districts with higher incidence are surrounding vulnerable areas.
Conclusion: HVL is spread in Campo Grande. The proximity of high incidence areas with vulnerable areas greatly increases the risk of transmission.
Relevance: Visceral leishmaniasis is endemic in Campo Grande and the use of geotechnology in health as a decision-making tool is of great importance for the implementation of measures of control and prevention, for better implementation of logistical, human and financial resources.

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Socio-economic factors influencing biosecurity measures of livestock producers in Japan

Kohei Makita, Yuki Nakahara, Takuto Watanabe, Yuto Tamura, Shingo Asakura, Rakuno Gakuen University, Ebetsu, Japan. Contact: kmakita@rakuno.ac.jp

Purpose: In Japan, the Standard of Rearing Hygiene Management (SRHM), which stipulates biosecurity measures for livestock producers to comply with, was strengthened in 2011, after outbreaks of foot-and-mouth disease and avian influenza. However, some producers still do not comply with some items in SRHM. The present study aims to understand socio-economic factors influencing hygiene practice of producers.

Methods: Hokkaido Prefecture, the principal agricultural production area, and Saitama Prefecture, peri-urban areas adjacent to Tokyo, were selected as study sites. Participatory appraisals were conducted with dairy, beef cattle, pig, layer, broiler, and sheep producers to understand their views on the factors influencing hygiene practice. Questionnaires were designed based on these results, and postal surveys were conducted. Only for broiler producers, country wide survey was conducted, because the majority was enterprises operating in multiple prefectures. A survey for sheep was conducted only in Hokkaido. After univariate statistics, four multivariable generalized linear models each for both sites and all the species were performed for socio-demographic, farm management, knowledge, and hygiene associated factors, respectively, selecting proportion of SRHM items complied (compliance rate) as response variable.

Results: As the items of SRHM are different among livestock species, simple comparison cannot be performed. However, the mean compliance rate was highest in broiler producers (91.7%, preliminary), and layer (64.8% in Hokkaido and 65.2% in Saitama), pig (75.4% and 53.6%), and sheep (66.1%) producers followed. The rate tended to be lower among dairy (61.5% and 56.0%) and beef cattle (59.1% and 57.0%) producers. Only in pigs, compliance rates were significantly different between two sites. Multivariable statistics found that the factors related with a capacity of owner or farm, knowledge on animal health, and attitude for hygiene were associated with compliance rate for all species.

Conclusions: Communication of hygiene knowledge and supports for producers with limited capacity may improve biosecurity further.
Relevance: This is relevant to biosecurity.

P001

Epidemiological investigations using internet-derived data: an example investigating the seasonality of the Middle East Respiratory Syndrome (MERS)

Peter A. Durr, Kerryne Graham, AAHL-CSIRO, Geelong, Australia. Contact: peter.durr@csiro.au

Purpose:
The Middle East Respiratory Syndrome (MERS) was identified in September 2012, and since then has been responsible for over 900 confirmed infections, principally in the Arabian Peninsula. While the viral cause of the disease was quickly established, the source of the outbreak, and the relative role of domestic and wildlife reservoirs remains controversial.
Methods:
There have been few studies on the epidemiology of the MERS, due in part to the lack of a consistent dataset of the epidemic. To overcome this, we undertook a data integration of all available data sources, principally from internet reports from international and national public health authorities. This enabled us to investigate the role of seasonality in community exposed - as versus health care facility exposed - cases of the disease.
Results:
Using the internet derived data, we were able to derive plausible date of infection, despite the raw data generally only providing dates of confirmation of the disease. This enabled us to confirm a marked spring (March-May) seasonality of community exposed cases for 2014. The signal for seasonality was less marked for 2012 and 2013, but this was probably due to variable reporting in these years.
Conclusions:
The confirmation of the seasonality of community exposed MERS cases throughout the Arabian Peninsula supports hypotheses that either spillover or transmission has a strong ecological or climatic driver. Out study should assist the targeting of surveillance efforts to specific windows of transmission.
Relevance:
Using the internet as source of data for epidemiological studies is becoming increasingly common in public health. Nevertheless, there is a danger of using naïve “data mining” techniques without a good understanding of the infection dynamics of the disease being investigated. A realistic compromise is to use the internet as the primary source of the data, but apply careful data cleaning guided by experts to derive a robust dataset suitable for further analysis.

P002

Modernisation of meat inspection by use of risk assessments

Lis Alban[1], Jesper Valentin Petersen[1], Anne-Kristine Bækbo[1], Tanja Østergaard Pedersen[2], Marianne Halberg Larsen[2], [1]Danish Agriculture & Food Council, Copenhagen V, Denmark; [2]Department for Veterinary Disease Biology, Frederiksberg, Denmark. Contact: lia@lf.dk

Meat inspection has remained more or less unchanged for a century. However, in most intensive livestock production hazards such as *Mycobacterium* and *Brucella* are no longer present. Instead, *Salmonella* and *Yersinia* constitute the most important swine-related hazards and these hazards cannot be dealt with during ordinary meat inspection. Therefore, meat inspection is up for debate about how to make it more risk-based, to introduce in practice a chain perspective and how to give the food business operator the responsibility for food safety. We will show how we use risk assessment as a way to evaluate step-by-step what the effect would be of omitting each of the classical steps in meat inspection including palpation and/or incisions into the carcass and the various organs. We use the OIE approach to risk assessment and combine it with collection of samples from abattoirs including laboratory investigation, slaughterhouse statistics, literature and expert opinion. Moreover, we collaborate with all stakeholders about how to identify new ways of detecting lesions in a visual-only system. Currently, focus is on chronic cases of pyaemia/osteomyelitis in finisher pigs and sows. According to the Danish legislation, such carcases should be subjected to de-boning to avoid presence of osteomyelitis not found in the rework area. Currently, 40,000 pigs are subjected to de-boning in Denmark per year, and the associated costs amount to approx. €3 million. The questions are: 1) is the meat fit for human consumption? 2) Is de-boning necessary or do the meat inspectors find what they should find in the rework area? And 3) which alternative practices could replace de-boning? We will show how we evaluate this by use of a cross-disciplinary approach involving industry, academia and veterinary authorities. The project involved samples from 100 finisher pigs and 100 sows with chronic pyaemia. For each case, we took samples from the abscesses and the muscle on the distal part of the right foreleg. As a control group, we collected muscle samples from 60 finishers and 60 sows, which were fully accepted at meat inspection. This study is of relevance for other countries discussing how to modernize meat inspection.

P003

Epidemiological characterization of the evolution of animal rabies in Chile, 2003-2013.

Raúl A. Alegría-Morán[1], Daniela Miranda[1], Alonso Parra[2], Lisette Lapierre[1], [1]University of Chile, Santiago, Chile; [2]Ministry of Health, Santiago, Chile. Contact: ralegria@veterinaria.uchile.cl

Purpose:
Because of its high lethality, rabies is a zoonotic disease of great impact in public health. According to the World Health Organization Chile has the status of country free of human rabies transmitted by dogs. The last case of human rabies was reported in 2013, without fatal outcome but it was not possible to identify the viral variant involved. The aim of this study was to analyze the epidemiological evolution of animal rabies in Chile, for the period 2003-2013.

Methods:
An epidemiological characterization and description of the registered cases from the National Program for Prevention and Control of Rabies of the Ministry of Health was carried. During the period 2003-2013, a total of 927 cases were reported. A descriptive statistics (mean and positivity percentage) and descriptive mapping for the characterization of the evolution of the disease, recording origin of the sample, number of cases per region, animal reservoir implicated and viral variant was made.

Results:
927 positive cases were recorded, presenting an average of 84 cases per year. 920 (99.2%) cases came from passive surveillance, while 7 (0.8%) cases were reported by active surveillance; with a total positivity, through the years, of 77.02% and 1.37% respectively. Positivity was reported mainly in the central zone (88.1%), composed by Valparaiso (19.1%), Metropolitana (40.6%), Del Libertador General Bernardo O'Higgins, Maule (11.8%) and Bio-Bio regions, concentrated in urban centers, in contrast with rural areas, where the number of cases were lower. Main positive reservoirs were bats (99.8%), specifically Tadarida Brasiliensis and viral variant 4 was the most commonly diagnosed. Only two cases were reported in domestic species (dog and cat).

Conclusions:
Wildlife rabies in bats remains endemic in Chile, concentrated in urban areas. The main reservoirs are insectivorous bats, particularly T. brasiliensis. Moreover, the cycle of classical rabies (caused by the canine variant) continues interrupted.

Relevance:
It is crucial that the population is kept informed about the rabies and how to prevent it, because there are significant opportunities for presentation of new cases in bats, dogs and even people.

P004

Descriptive analysis of participatory epidemiology experts and uses for animal health

Alberto Allepuz[1], Katinka de Balogh[2], Daniel Beltran-Alcrudo[2], [1]Universitat Autónoma de Barcelona (UAB) / Centre de Recerca en Sanitat Animal (CReSA),, Barcelona, Spain; [2]Food and Agriculture Organization (FAO), Rome, Italy. Contact: alberto.allepuz@uab.cat

Purpose:
In the last years, different studies have used Participatory Epidemiology (PE) methodologies on animal health, but there is no compilation available of who, how, when and where have been employed.
Methods:
Therefore, in order to identify the main experts/institutions working on the topic and the main uses of PE, we performed a search of the whole range of relevant materials, i.e. peer-reviewed papers, PhD reports, conference proceedings, manuals, training material, and past and present projects. The search of peer reviewed papers covered the period between 1980 and December 2014 using the PubMED bibliographic database. The inclusion of the studies based on their relevance was assessed by screening the titles and abstracts (and the full text in some cases). All the above-mentioned relevant materials were searched in websites such as 'Participatory epidemiology' or the 'Participatory epidemiology network for animal and public health'. Past and present projects where PE was used as a methodology were retrieved from focal points at a selection of institutions, universities, research groups and NGOs.
Results:
Results from this search showed that the number of PE activities was very limited until 2000, after which the number of activities has considerably increased. Most of the PE activities focused in Africa (66%), followed by south-east Asia. The high number of institutions with only one PE activity may be due to the fact that PE is an emerging discipline and several institutions are beginning to work in the topic. The more frequent identified uses were 'Surveillance' followed by 'Disease control' together with 'Descriptive epidemiology' and 'Disease survey' activities. Avian influenza, foot and mouth disease and food-borne diseases were the most frequently diseases covered.
Conclusions and relevance:
Through this study, we were able to make an inventory regarding PE uses and experts in the animal health context. Further steps could be to explore how PE could be used in the One Health context, a critical analysis of the weaknesses of the methodology and a discussion among experts about the PE definition, the main gaps, current needs and follow-up steps.

P005

Relationship between on farm risk factors and Toxoplasma gondii infection in farm animals: An extended literature review

G. Schares[1], M. Opsteegh[2], M. Mass[2], M. Georgiev[3], **Georgina Limon**[3], J. Guitian[3], P. Maksimov[4], F. J. Conraths[1], D. Aubert[5], A. Bales[6], B. Bangoura[7], R. Blaga[8], A. Burrells[9], V. Djokic[10], O. Djurkovic-Djakovic[11], I. Klun[12], F. Katze[9], A. Györke[6], E. Pozio[13], F. Spano[13], I. Villena[5], J. van der Giessen[2], [1]Friedrich-Loeffler-Institute, Isle of Riems, Germany; [2]National Institute for Public Health and the Environment, Bilthoven, Netherlands; [3]Royal Veterinary College, Hatfield, United Kingdom; [4]Friedrich-Loeffler-Institute, Ise of Riems, Germany; [5]USC EpiToxo and Agency for Food, Environmental and Occupational Health and Safety, Paris, France; [6]University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, Romania; [7]University Leipzig, Leipzig, Germany; [8]National Veterinary School of Alfort, JRU BIPAR, Maisons-Alfort, France; [9]Moredun Research Institute, Edinburgh, United Kingdom; [10]National Veterinary School of Alfort, Maisons-Alfort, France; [11]University of Belgrade, Belgrade, Serbia; [12]University of Belgrade, Belgrade, Serbia; [13]Istituto Superiore di Sanità, Rome, Italy. Contact: glimon@rvc.ac.uk

Toxoplasmosis is caused by the protozoan Toxoplasma gondii and is one of the most important zoonotic diseases worldwide. The need of more accurate data on potential risk factors, at farm level, for animals to become infected has been recently highlighted by the European Food Safety Authority

Purpose: An extended literature review using the systematic review approach was conducted to identify studies which looked at risk factors of T. gondii infection in production animals.

Methods: Studies published in English, French, Spanish, Dutch, German and Italian were considered. The review was restricted to the most important domestic food-producing animals in Europe: cattle, pigs, sheep, goats, horses and chickens, European husbandry systems and peer reviewed papers published since 1994.

Results: A total of 111 studies were included and provided information on various putative risk and protective factors for T. gondii infections in farm animals including definitive host related factors, management practices, specialization and factors characterizing the likelihood of fodder or water contamination.

The presence of cats increased the risk of infection as revealed in a number of studies in pigs and small ruminants. Most studies assessing the potential role of rodents identified a risk effect. Most studies suggested that outdoor access increased the risk of infection in pigs. A low level of management intensity in small ruminants revealed conflicting results. Degree of specialization played a role in chickens. Surprisingly, studies assessing a potential role of contaminated water as a risk factor for infection did not reveal a consistent association.

Conclusions: The review shows that further studies are necessary to solve conflicting findings and to complete knowledge especially in cattle, equids and in poultry.

Relevance: The findings of this review have been used to design cross sectional studies in various European countries as part of an EFSA consortium.

P006

Pathogenic Leptospira in rodents and water in critical areas of Nicaragua

Byron Flores[1], Jessica Sheleby-Elias[1], Nabil Halaihel[2], William Jirón[1], Tania Pérez-Sánchez[3], Hector Fuertes[2], **Ana Muniesa**[3], Christiane Düttmann[1], Ignacio de Blas[3], José Luis Muzquiz[3], [1]Universidad Nacional Autónoma de Nicaragua, León, Nicaragua; [2]Universidad de Zaragoza/ ALQUIZVETEK SL, Zaragoza, Spain; [3]Universidad de Zaragoza, Zaragoza, Spain. Contact: ana_muniesa@hotmail.com

Purpose: Leptospirosis is considered the most widespread zoonosis in the world. In Nicaragua the disease is endemic and critical geographic regions were established based on various risk factors indicators. Asymptomatic carriers, such as rodents, would act as infection source to other animal species. Humans become infected by direct contact with urine contaminated soil, water or food. The aim of the present study was to identify pathogenic Leptospira in rodents and water from critically affected areas of Nicaragua.
Methods: Sampling was carried out in the Departments of Chinandega, Chontales, Jinotega, Estelí, León and Matagalpa. A total of 435 samples were processed: 170 samples from rodents and 265 water samples from distinct waters sources (water supply, ponds, basins, wells and rivers) were included in this study from areas with confirmed cases of human leptospirosis. Direct isolation of pathogenic Leptospira was done in specific isolation media: Ellinghausen, McCullough, Johnson and Harris Plus 5-fluorouracil (EMJH-5FU). A real-time PCR was also performed for specifically detecting pathogenic Leptospira species as described by Levett et al. (2005).
Results: Results obtained revealed the presence of Leptospira in 21.80% (CI95% = 15.26, 28.26) of the captured rodents showing significant differences in prevalence between different Departments ($p<0.001$). April and May had the highest frequency of positives ($p<0.001$). A 10.94% (CI95% = 6.99, 14.89) of the water samples tested positive with significant differences ($p=0.026$) from distinct sources, with the highest prevalence present in domestic water reservoirs. April (41.70%) and May (30.60%) showed the highest prevalence ($p<0.001$) and significant difference were observed within Departments ($p=0.008$) with the highest prevalence for Department of Leon (17.40%).
Conclusions: Human leptospirosis could be correlated with water contamination, mainly from the domestic reservoirs in homes with presence of infected rodents.
Relevance: Monitoring of rodents and water sources for Leptospira are needed and specific measures and protocols should be to be developed in order to minimize its prevalence in Nicaragua.

P007

Comparative genomics of drug resistant Salmonella enterica isolated from dairy cattle and humans.

Richard Pereira[1], Laura Carroll[1], Laura Carroll[1], Henk Den Bakker[1], Julie Siler[1], Margaret Davis[2], William Sischo[2], Thomas Besser[2], Martin Wiedmann[1], Lorin Warnick[1], [1]Cornell University, Ithaca, NY, [2]Washington State University, Pullman, WA, Contact: rvp25@cornell.edu

Purpose: The objective of this study is to use whole genome sequencing to compare the genome of S. Typhimurium, S. Newport and S. Dublin isolated from dairy cattle and humans in Washington State and New York State from 2008 to 2012 .

Methods: A total of 90 drug-resistant Salmonella isolates were selected for this study, 44 from Washington State (20 from dairy cattle and 24 from humans) and 46 from New York State (22 from dairy cattle and 24 from humans). Selection of isolates by location, source and serotype was stratified by year and was dependent on availability of isolates meeting these criteria. All isolates were tested for antimicrobial resistance to 12 drugs using Kirby-Bauer disk diffusion, and all isolates were resistant for at least one drug. DNA isolation and sequencing was conducted at Cornell University. Sequence reads were annotated using the SRST2.

Results: Preliminary results from sequencing revealed that the most common drug classes for which resistance genes were detected were aminoglycoside, sulfonamide and tetracycline. Aminoglycoside and tetracycline were the two most common drug classes for which two or more resistance genes for each class were identified within the same isolate. Further analysis is being conducted to compare the genomic findings for phylogeny and drug resistance determinants by location, source and serotype stratified by year. SNP data will be obtained by comparing isolates between themselves and will be used to build a maximum likelihood tree. Additional analysis will also be conducted by comparing isolates against well characterized Salmonella reference genomes and by conducting analysis to evaluate time-measured phylogenies' evolutionary relatedness (using BEAST).

Conclusions: The results of this study will evaluate overlap in phylogeny and antibiotic resistance genetic determinants in Salmonella, helping estimate potential hazards of Salmonella from dairy cattle to human health.

Relevance: Salmonella enterica are some of the most common bacterial pathogens of both cattle and humans. A persistent concern is the spread of Salmonella from food animals to humans through the food chain. This worry is greater when Salmonella is multidrug resistant.

P008

Motivators and barriers towards positive health behaviour in the British veterinary profession

Charlotte Robin[1], Robert Christley[1], Fiona McMaster[2], [1]University of Liverpool, Neston, United Kingdom; [2]Anglia Ruskin University, Cambridge, United Kingdom. Contact: charlotte.robin@liverpool.ac.uk

Purpose:
Zoonoses account for a large proportion of infectious diseases worldwide. As one of the initial points of contact, veterinary professionals are at high risk of exposure. Infection control practices aim to reduce infection risk, yet limited data are available regarding attitudes towards these practices. This study aimed to identify motivators and barriers for infection control practices in the British veterinary profession.

Methods:
1000 veterinary practices were randomly selected from the Royal College of Veterinary Surgeons database, and contacted with a postal questionnaire. The questionnaire contained open and closed questions, covering veterinary experience, risk perceptions, infection control practices and management of zoonotic cases.

Results:
252 (12.6%) questionnaires were returned, 54.0% by veterinary surgeons and 46.0% by veterinary nurses, 93.9% of whom were female. The mean number of years in practice was 20±0.7 years, and all veterinary nurses and 90.6% of veterinary surgeons qualified from UK institutions.
18.7% of respondents were unaware of any standard operating procedures for zoonotic diseases at their practice, and although all practices provided personal protective equipment (PPE), 15.5% of respondents were not given PPE training.
All respondents indicated perceived risk would influence their decision to use PPE. Training or practising outside the UK was associated with risk being reported as an important motivator to use PPE (P=0.03). Safety concerns were most frequently cited as influencing the decision about PPE use, with 55.9% stating it would be a deterrent. Number of years in practice was associated with time constraints being identified as a deterrent for use of PPE (P=0.03).

Conclusions:
Awareness of infection control practices was high, but attitude varied and several motivators and barriers towards compliance were identified.

Relevance:
Identification of what motivates or discourages veterinary professionals to comply with infection control practices, in conjunction with a deeper understanding of their perceptions of the risks they encounter during their work will help promote positive health behaviour within the profession.

P009

Have your say about Hendra - a qualitative study to explore horse owners' knowledge and perception of Hendra virus

Anke Wiethoelter[1], Kate Sawford[1], Nicole Schembri[2], Melanie Taylor[2], Navneet Dhand[1], Nina Kung[3], Barbara Moloney[4], Therese Wright[4], Hume Field[5], Jenny-Ann Toribio[1], [1]The University of Sydney, Sydney, Australia; [2]University of Western Sydney, Sydney, Australia; [3]Queensland Department of Agriculture, Fisheries, and Forestry, Brisbane, Australia; [4]NSW Department of Primary Industries, Orange, Australia; [5]EcoHealth Alliance, New York, NY, Contact: anke.wiethoelter@sydney.edu.au

Purpose: Hendra virus (HeV) is a zoonotic disease of sporadic occurrence in Australia caused by spillover from flying foxes to horses, and from horses to people. HeV vaccination of horses and property management measures are highly recommended and publicised to prevent spillover events. Since health behaviour models have shown that uptake of such risk mitigation strategies is largely influenced by risk perception, we investigated horse owners' knowledge and attitudes on a range of HeV related topics.

Methods: Our mixed methods research study comprised a qualitative interview study with horse owners from various horse industry backgrounds in Australia. Semi-structured face-to-face interviews were conducted in high HeV risk areas, covering experience with HeV, risk perception and mitigation, as well as HeV information-seeking behaviour. Interviews were recorded and transcribed verbatim. Transcripts were analysed with NVivo using thematic analysis.

Results: Several main themes emerged from the 24 interviews with 27 horse owners (24-84 years old, 59% female). All interviewees were aware of HeV outbreaks in their area, common clinical signs in horses, and recommended management practices. Attitudes towards HeV vaccination were mostly polarised; ranging from "*a relief to have*", "*the right thing to do*" and "*duty of care*", to resentment and mistrust largely driven by factors such as safety concerns ("*still in its trial stages*"), cost ("*can't afford it*"), booster schedules, and compulsory horse vaccination for attendance of some events. Veterinarians play a central role in HeV communication pathways as one interviewee described: "*We have the vet out every few months for something, so we can always ask them questions about the Hendra as well. They have been very forthcoming with any information they have. They're vets, so I suppose we trust them.*"

Conclusion & Relevance: Despite the broad awareness of HeV, the attitude polarisation towards the vaccination potentially threatens effective HeV risk management. The results of this study will help to inform targeted communication strategies and HeV policy development for this zoonosis of great veterinary and public health significance.

P010

Estimation of the incidence of human brucellosis in an endemic setting: case study in Jordan

Imadidden I. M. Musallam, Javier Guitian, Royal Veterinary college, Herts, United Kingdom. Contact: Imusallam@RVC.AC.UK

Purpose: To estimate the incidence of Brucella spp. seropositivity in the central governorates in Jordan using blood samples submitted to the central medical laboratory in Amman city.
Methods: Blood samples submitted to the central medical laboratory in the period March - December 2014 were categorized into two groups; group 1 included blood samples that were submitted for the diagnosis of diseases that have clinical presentations similar to brucellosis (Acute febrile illnesses). Group 2 included blood samples that were submitted for diagnosis of diseases that have clinical presentations non-overlapping with those typical of acute, sub-acute or chronic brucellosis. A systematic random sample (n=125) from each group was selected and tested for Brucella spp. antibodies; firstly by Rose Bengal Test (RBT) and then confirmed by iELISA (anti-Brucella IgM ELISA; NovaLisa, NovaTec Immundiagnostica GmbH, Germany). An individual was considered as positive if it tested positive to both RBT and iELISA (series interpretation). Information on selected risk factors was obtained by means of a telephone questionnaire and the association between them and seropositive status assessed. The estimated seroprevalence, adjusted for the assumed performance of the testing strategy, was converted to rate per 100,000 person- year.
Results: the median of age for both groups was 26 years, the estimated true seroprevalence in group 1 was 10.6%, (95%CI: 9.5 - 23.8) and in group 2: 5.4 (95% CI: 2.1 - 13.2), while the estimated incidence was 125.64 (95% CI: 68.5 - 197.5) and 66.98 (95% CI: 27.3 - 122.5) case/ 100000 population.
Conclusions and Relevance: Human brucellosis remains a major public health problem in Jordan, where the disease is hugely underestimated. Our estimates suggest that Jordan is among the countries with highest reported incidences of human cases, which is compatible with the endemicity, at high levels, of brucellosis among Jordan’s ruminant populations.

P011

Relationship between cattle and zoonotic tuberculosis

Luis G. Higareda[1], Sara E. Herrera[2], Gabriela Aguilar[1], Feliciano Milián[1], [1]Universidad autónoma de Queretaro, Queretaro, Mexico; [2]Centro de Investigación y Asistencia y Diseño en Tecnología del Estado de Jalisco, Guadalajara, Mexico. Contact: luishigareda@hotmail.com

Tuberculosis is a reemergent disease caused by Mycobacterium tuberculosis in humans and M. bovis in cattle, which also affects a wide host range of domestic and wild species. The main route of infection for humans is by consumption of raw milk and fresh chees; M. bovis infection is related to extra pulmonary tuberculosis. In México, the prevalence of zoonotic tuberculosis in the general population is unknown. Because of this, the purpose of this study was to evaluate the relationship between cattle and zoonotic tuberculosis throughout a retrospective study of cases reported on a high risk area (≈ 16%) of tuberculosis in cattle. A total of 120 human cases reported between 2010 and 2013 in the study area were included in the study. Data was analyzed with a bivariate analysis to identify potential risk factors. Those variables with a p-value of 0.20 were later included in a logistic regression model to obtain adjusted odds ratios. The cumulative incidence rate was 5.8/100,000, 56.5% (68/120) of the cases were diagnosed as extra-pulmonary tuberculosis. Being 18 years-old and younger had 5 times more chances of having tuberculosis. Patients with diabetes and with chronic obstructive pulmonary disease are 4 times more likely to become sick with extra-pulmonary tuberculosis. Only 2 of 120 cases were confirmed by culture, one of them was M. bovis. Surprisingly, extra pulmonary tuberculosis is greater than pulmonary tuberculosis in the study area. This frequency is much greater than that reported in the literature; therefore, the hypothesis is that M. bovis may be involved. From five urine samples, one isolate was obtained by culture, which turned out to be M. bovis, confirming the presence of this pathogen in extrapulmonary infections. More studies are underway in this region to confirm the presence of M. bovis in human cases of tuberculosis. These studies have the purpose of call the attention of authorities in animal health to increase efforts to reduce the prevalence of tuberculosis in cattle to reduce the risk to public health.

P012

Dairy cattle management factors that influence on-farm density of European starlings in Ohio, 2007 - 2009

Genet Medhanie[1], David Pearl[1], Scott McEwen[1], Michele Guerin[1], Claire Jardine[2], **Andrea Thomas-Bachli**[1], Jeffery LeJeune[3], [1]University of Guelph, Guelph, ON, Canada; [2]University of Guelph, Guelph, ON, Canada; [3]The Ohio State University, Wooster, OH, Contact: athomas@uoguelph.ca

Purpose
The objective of this study was to identify farm management factors and farm structural features that influence the density of European starlings (Sturnus vulgaris) on dairy farms.
Methods
The number of starlings from barns, feed storage and manure storage areas was recorded from 150 dairy farms in summer and fall 2007 - 2009. Risk factors from a questionnaire administered during these two farm visits were assessed for possible association with the number of starlings per milking cow (starling density). Zero-inflated negative binomial models were fitted using these data.
Result
Year of visit, feeding method (i.e. whether the feeding was on an aisle, bunk or other) and feeding site (i.e. whether cows were fed indoors or outdoors), feeding method and site, manure removal frequency, and distance from the closest roost site were significantly associated with starling density. Starling density was significantly higher on farms visited in 2007 compared to those visited in 2008 and 2009. A significant interaction effect between feeding method and feeding site was identified. The effect of different feeding methods varied depending on whether they were used indoors or outdoors, but generally feeding outdoors increased starling density on the farm. The likelihood of zero starling counts in farms that removed manure from barns weekly or less frequently was higher compared to those that removed manure daily or after every milking. The odds of a zero starling count decreased with increasing distance of a farm from the closest night roost.
Conclusion
The major risk factors associated with the number of starlings per milking cow on dairy farms in Ohio were related to feeding and manure management practices.
Relevance
Identifying risk factors that expose farms to starlings would assist in developing non-lethal strategies that minimize the number of birds and reduce the potential transmission of cattle and zoonotic pathogens. Consequently, identifying dairy farm management and environmental factors that attract European starlings to dairy farms has potential animal and public health implications.

P013

Using spatial scan statistics applied to survival time data to investigate the utility of dead corvid and mosquito surveillance programs in Ontario, 2002 - 2008.

Andrea Thomas-Bachli[1], David Pearl[1], Elizabeth Jane Parmley[2], Olaf Berke[1], Ian Barker[2], [1]University of Guelph, Guelph, ON, Canada; [2]University of Guelph, Guelph, ON, Canada. Contact: athomas@uoguelph.ca

Historical data on West Nile virus (WNv) in Ontario has not been compared with respect to the most sensitive and timely information for surveillance. Three surveillance programs; found dead corvid testing, trapped mosquitoes tested in speciated pools, and reported human cases, were explored retrospectively for the years 2002-2008. During each summer, found dead corvids submitted by the public were tested within each PHU until a small number of positive results were detected. Therefore, traditional risk-based methods are not appropriate for investigations using these data. Instead, we developed exponential parametric models using survival time data on the first-positive cases within each PHU. Socio-demographic and geographic associations with the time-to-detection of WNv were explored using survival analyses. Adjusted survival times based on the model coefficients were derived. Spatial scan statistics using the exponential survival-time model were employed to identify clusters of PHUs with faster WNv detection in comparison with the remaining PHUs in Ontario. Clusters of PHUs with fast detection of WNv in space-time, using unadjusted and model-adjusted data, were compared geographically and temporally for each surveillance modality. Statistically significant ($p<0.05$) space-time clusters of PHUs with fast time-to-detection were found using each surveillance stream. There was geographic overlap between clusters of PHUs using first-positive dead birds, mosquito pools and human cases during years in which significant clusters were detected. The dead corvid program outperformed the mosquito program in terms of timeliness during the first years of surveillance. Survival model-adjusted clusters of first-positive dead corvids demonstrated improved detection of human case clusters during some years. Spatial scan statistics can be utilized to detect WNv activity using survival time information. Dead corvids appear to provide the most timely indication of WNv activity in Ontario using this technique. Model-adjusted scan statistics show promise in the detection of clusters that are not biased by underlying socio-demographic and geographic characteristics.

P014

Prevalence, clinical presentation, and operation characteristics of Mycoplasma bovis outbreaks in farmed bison (Bison bison) in Western Canada

Ana L. Bras[1], Herman W. Barkema[1], Murray Woodbury[2], Carl Ribble[3], **M. Claire Windeyer**[1], [1]University of Calgary Faculty of Medicine, Calgary, AB, Canada; [2]Western College of Veterinary Medicine, Saskatoon, SK, Canada; [3]University of Calgary Faculty of Medicine, Calgary, AB, Canada. Contact: c.windeyer@ucalgary.ca

Purpose: The North American bison industry has grown steadily in recent years, largely because bison meat is seen as a natural alternative to beef. However, bison producers have recently began to face an emergence of disease caused by Mycoplasma bovis. A total of four case reports of M. bovis disease in bison have been published, but to date, there is no literature reporting the epidemiology of M. bovis in farmed bison. The objectives were to determine the prevalence of disease caused by M. bovis infection in farmed bison herds throughout Western Canada, describe the clinical presentation of the disease, and evaluate the association between the development of M. bovis disease and herd-level risk factors.
Methods: Bison producers in Western Canada (Manitoba, Saskatchewan, Alberta, and British Columbia) listed as members of the Canadian Bison Association in 2013 and 2014 were contacted for a telephone survey.
Results: A total of 202 of the 441 eligible (43%) bison producers completed the survey. Twelve farms (6%, 95% CI: 3-10%) had a laboratory-confirmed diagnosis of M. bovis with disease onset between May 2009 and Jan 2015. Case herds had a median of 11% of cows older than 3 years (IQR: 1-19%) and 2% of yearlings (IQR: 0-11%) with clinical signs of M. bovis disease during the first year of the outbreak. Clinical signs of M. bovis persisted in a herd for a median of 12 weeks (IQR: 7-24 weeks). Among risk factors assessed, being a mixed operation (e.g. cow-calf herd that also purchased animals to background or finish), having a larger herd size (mean 944, 95% CI: 417-2142 in case herds, and mean 151, 95% CI: 133-174 in control herds), and purchasing animals from multiple sources (e.g. auction and directly from another producer) were associated with M. bovis outbreaks ($p < 0.05$).
Conclusions: Mycoplasma bovis has affected numerous bison operations in Western Canada over the past 5 years, especially among large mixed operations that purchased bison from multiple sources.
Relevance: The economic impact of this disease in affected bison herds makes it imperative to broaden our knowledge about the epidemiology of M. bovis among farmed bison herds, as well as develop prevention and control strategies.

P015

Prevalence of and risk factors for gastrointestinal parasitism in farmed bison (Bison bison) in Western Canada

M. Claire Windeyer[1], Hermen W. Barkema[1], Thom B. Oostenbrug[2], Ana L. Bras[1], Murray Woodbury[3], Libby Redman[4], John S. Gilleard[4], [1]University of Calgary Faculty of Medicine, Calgary, AB, Canada; [2]Utrecht University, Utrecht, Netherlands; [3]Western College of Veterinary Medicine, Saskatoon, SK, Canada; [4]University of Calgary Faculty of Medicine, Calgary, AB, Canada. Contact: c.windeyer@ucalgary.ca

Purpose: A majority of farmed bison in Canada are raised in the western provinces, largely in pasture-based systems. However, little is known about the epidemiology of gastrointestinal parasites in bison. The objectives of this study were to: 1) describe the prevalence of gastrointestinal parasites on bison operations in Western Canada; and 2) investigate risk factors associated with parasite burden.
Methods: Information about herd demographic and management practices was collected using semi-structured face-to-face interviews. A total of 269 fecal samples were collected: 72 pooled samples from 43 operations, and 197 individual samples from ≥15 bison on 10 of those operations. Fecal egg counts (FEC) were performed using a standard 2 or 3-slide McMaster technique. Multivariable logistic regression assessed herd-level factors associated with high parasite burden (≥200 eggs per gram (EPG) in pooled samples).
Results: The proportion of samples positive for Eimeria spp. was 80% (n=215), Trichostrongylid spp. was 64% (n=172), Moniezia spp. was 9% (n=24), Nematodirus spp. was 6% (n=15), Capillaria spp. was 5% (n=13), Trichuris spp. was 4% (n=11), Strongyloides spp. was 2% (n=5), and Toxocara spp. was 0% (n=0). Among positive samples, median (interquartile range) EPG was 425 (425-1105) for Eimeria spp., 40 (17-102) for Trichostrongylid spp., 93.5 (17-280) for Moniezia spp., 17 (8.5-34) for Nematodirus spp., 51 (34-85) for Capillaria spp., 85 (17-119) for Trichuris spp., and 17 (17-17) for Strongyloides spp. Herds that dewormed at weaning had 8x higher odds ($p < 0.001$; CI: 2.3-30.5) of a high burden. Herds that had access to running water had a 15x lower odds ($p= 0.03$; CI: 1.4-167) of a high burden.
Conclusions: The most prevalent gastrointestinal parasites were Eimeria and Trichostrongylid nematodes. Herd-level odds of high burden were associated with deworming practices and water source; however, further research is needed to understand practices to reduce parasite burden in farmed bison.
Relevance: Gastrointestinal parasites may have substantial health and production impacts on livestock. Gaining greater knowledge of their epidemiology in farmed bison may improve control strategies.

P016

Bushpigs in Madagascar: at the crossroad of wildlife, livestock, human and ecosystem health

Ranto Ramy-Ratiarison[1], Antoine Rouillé[2], Julie Ravaomanana[3], Eric Rakotomalala[1], Vladimir Grosbois[4], **Sophie Molia**[4], Rianja Rakotoarivony[1], François Roger[4], Ferran Jori[4], Miguel Pedrono[5], [1]Université d'Antananarivo, Antananarivo, Madagascar; [2]Université de Rennes, Rennes, France; [3]FOFIFA-DRZV, Antananarivo, Madagascar; [4]CIRAD, Montpellier cedex 5, France; [5]CIRAD, Antananarivo, Madagascar. Contact: sophie.molia@cirad.fr

PURPOSE:
Bushpigs (Potamochoerus larvatus) are a significant source of cheap proteins in several rural areas of Madagascar. We aim to identify diseases of bushpigs in those areas, explore their role as sources of pathogens for livestock and humans, and understand how hunting and trade may affect epidemiological risks.
METHODS:
Our integrated approach includes 1) epidemiological studies (investigate the presence of African swine fever, cysticercosis, hepatitis E, and internal parasites in blood samples, organs and faeces from bushpigs); 2) ecological studies (use transect surveys to quantify the presence of bushpigs around forests and GPS collars to map movements and contacts with domestic pigs); 3) socioeconomic studies (conduct questionnaire surveys among pig farmers, hunters, and butchers). Generalized linear mixed models test the association between potential risk factors and prevalence of pathogens, abundance of bushpigs or frequency of hunting/trade.
RESULTS:
Preliminary results obtained in sakalavae territory showed that 1) prevalence was high for internal parasites (especially Ascaris suum and gastrointestinal strongyles), sporadic for cysticercosis and null for African swine fever and hepatitis E; 2) abundance of bushpigs increased in savannahs as compared to dry forests during the fruiting period of monkey orange (Strychnos spinosa); 3) 85% of hunted bushpigs were captured alive with traps and brought back to villages where they stayed until they were sold or slaughtered for food. Other results are in progress.
CONCLUSION:
Based on our preliminary results, we recommend limiting free-ranging of domestic pigs in areas close to dry forests with bushpigs, especially during the fruiting period of monkey orange. Awareness campaigns should also inform hunters and consumers of bushpig meat about the need to properly cook meat potentially infested with cysticerci and about the risk of disease transmission through contacts between pigs and bushpigs.
RELEVANCE:
Interdisciplinary approaches enlarge the understanding of health risk determinants. Recommendations based on our results will help increase food security and safety in rural areas of Madagascar.

P017

Epidemiological study of Campylobacter spp. colonisation of wild game pheasants (Phasianus colchicus) processed in Approved Game Handling Establishments in Scotland

Alessandro Seguino[1], Cosmin Chintoan-Uta[2], Darren J. Shaw[1], Sionagh Smith[1], [1]The University of Edinburgh, Edinburgh, United Kingdom; [2]The University of Edinburgh, Edinburgh, United Kingdom. Contact: alex.seguino@ed.ac.uk

Purpose:
Campylobacteriosis in humans due to C. jejuni and C. coli is the most common bacterial diarrheal disease worldwide. Control measures currently focus on the reduction of Campylobacter in chickens, as 60-80% of human cases can be attributed to poultry meat. However, C. jejuni and C. coli have also been reported in a range of livestock and wildlife species, including live pheasants. Pheasants reach the consumer's table as a by-product of the shooting industry. Approximately 3.5 million game birds are shot in Scotland every year; however only 700,000 are received at Scottish Approved Game Handling Establishments (AGHEs) for veterinary inspection. Despite this volume of wild game entering the food chain, there is a lack of information concerning the risk of campylobacteriosis in humans arising from consumption of wild game meat and the role wild game birds may have as a reservoir of infection. This study's aims were to determine the prevalence of Campylobacter in wild game pheasants processed in AGHEs in Scotland, to identify sequence types (ST) present and to evaluate their impact on public health.

Methods:
Two hundred and eighty seven caeca and 59 skin samples were collected from pheasant carcases during the hunting season 2013/2014. Laboratory isolation of Campylobacter was performed using standard culture methods; positive caecal samples were subjected to PCR and Multi Locus Sequence Typing (MLST).

Results:
36.5% of 287 caecal samples were Campylobacter positive while all 59 skin samples were negative. C. coli and C. jejuni accounted for 62.7% and 37.3% of positive samples tested (n=99), respectively. Nineteen STs of Campylobacter were recovered from MLST (n=80). ST828 (n=19) was most common, followed by ST827 (n=12) and ST19 (n=7).

Conclusions:
The STs found in pheasants are overall more common in livestock than chickens, raising the possibility of cross-infection between pheasants, cattle and sheep in the field. STs 827 and 19 are common in humans and primarily associated with livestock, while ST828 is chicken-associated.

Relevance:
This study suggests that wild game birds are a reservoir of Campylobacter and helps in the understanding of risk to humans of pheasant meat consumption.

P018

Validating tests for Neospora caninum exposure in wildlife populations without a gold standard.

Karla Moreno-Torres[1], Barbara Wolfe[1], Mark Moritz[2], William Saville[1], Rebecca Garabed[1], [1]Ohio State University, Columbus, OH, [2]Ohio State University, Columbus, OH, Contact: moreno-torres.1@osu.edu

Purpose:
Surveillance for wildlife diseases is crucial to understanding and controlling infectious diseases in human, wildlife, and livestock populations. However, validation of laboratory tests that are used to screen diseases in wildlife populations is based mainly on studies in domestic animals. Consequently, the use of these tests in wildlife populations may lead to inaccurate estimates of population parameters. Fortunately, Bayesian latent class analysis (LCA) can be used to estimate the true prevalence of pathogens and specificity and sensitivity of tests in wildlife populations in the absence of a gold standard.

Methods:
We demonstrate this method by evaluating the accuracy of the cELISA kit (VMRD®) used in estimating true prevalence of Neospora caninum in three wildlife populations.

Results:
Our results show that the apparent prevalence of N. caninum from the test results is not equal to the true prevalence in bison, white-tailed deer and Père David deer populations in Southeastern Ohio, USA. True prevalence estimates were not different between Père David deer and white-tailed deer, but the true prevalence in the two deer populations differed from the true prevalence in the bison population. This suggests some species difference in the epidemiology of N. caninum for these co-located populations.

Conclusions:
Bayesian LCA methods are used as in this example to overcome the constraints on validating tests in wildlife species.

Relevance:
The ability to accurately evaluate disease status and prevalence in a population allows us to better understand and determine the epidemiology of multi-host pathogen systems at the community level.

P019

Molecular and statistical analysis of Campylobacter spp. carriage and antimicrobial resistance in mammalian wildlife and livestock species from Ontario farms (2010)

Mythri Viswanathan[1], David L. Pearl[1], Eduardo N. Taboada[2], E. Jane Parmley[3], **Andrea Thomas-Bachli**[1], Claire M. Jardine[4], [1]University of Guelph, Guelph, ON, Canada; [2]Public Health Agency of Canada, Lethbridge, AB, Canada; [3]Public Health Agency of Canada, Guelph, ON, Canada; [4]University of Guelph, Guelph, ON, Canada. Contact: athomas@uoguelph.ca

Purpose: The objectives of this study were to assess risk factors for the carriage of Campylobacter and antimicrobial resistant Campylobacter among livestock and mammalian wildlife on farms in Ontario, and to determine if Campylobacter subtypes are exchanged between wildlife and livestock based on molecular subtyping.
Methods: Using data from a cross-sectional study of 25 farms in 2010, we assessed associations between Campylobacter and antimicrobial resistant Campylobacter carriage and the following explanatory variables using mixed logistic regression models: animal species, farm type, type of sample (livestock or wildlife), and Campylobacter species; the model included a random intercept for the farm where samples were collected. Isolates were subtyped using Campylobacter-specific 40 gene comparative fingerprinting assay.
Results: A total of 92 livestock samples and 49 raccoon samples were collected with 72% and 41% testing Campylobacter positive. Livestock isolates were significantly more likely to have antimicrobial resistance (AMR) to ≥1 antimicrobial tested compared to wildlife isolates. C.jejuni was significantly more likely to exhibit AMR to ≥1 antimicrobial tested compared to C. coli. However, resistant C. jejuni isolates were resistant to only tetracycline while C. coli showed multi-drug resistance, ≥2 antimicrobials tested. Fecal samples from livestock were significantly more likely to test positive for Campylobacter than wildlife samples. Relative to dairy, swine had significantly increased odds of testing positive for Campylobacter. The odds of shedding Campylobacter jejuni was significantly greater in beef compared to dairy and raccoons. Fifty unique subtypes of Campylobacter were identified, but only one subtype was found in both wildlife and livestock.
Conclusions: The sharing of Campylobacter species between livestock and wildlife was uncommon based on identical subtype similarity and AMR patterns.
Relevance: Understanding the transmission dynamics of Campylobacter spp. can indicate a point of pathogen entry into the food production system and can help inform effective strategies to reduce Campylobacter spp. transmission.

P020

Factors associated with the contact between backyard pigs and feral swine in the State of Rio Grande do Sul

A. A. R. Medeiros[1,2], Gustavo Sousa Silva[1], Diego Viali dos Santos[1,3], Brayan Alexandre Fonseca Martinez[1], Ana Paula Serafini Poeta[1], **Luís Gustavo Corbellini**[1], [1]Universidade Federal do Rio Grande do sul, Porto Alegre, Brazil; [2]Secretaria Estadual da Agricultura e Pecuária do Rio Grande Do Sul, Porto Alegre, Brazil; [3]Ministério da Agricultura, Pecuária e Abastecimento, Porto Alegre, Brazil. Contact: lgcorbellini@hotmail.com

Purpose: There are increasing number of reports of attacks and damage caused by the presence of feral swine in Rio Grande do Sul, causing negative impacts on the native vegetation, predation of wildlife, and the likelihood of transmitting diseases to humans and animals. This study aims to identify the presence the feral pigs and assess factors associated with the contact with the domestic pigs.
Methods: The study was conducted in the years 2012 and 2014 using a purposive sampling, intended primarily to demonstrate and document the absence of classical swine fever virus in the farms within a free zone. A total of 640 subsistence farms were sampled throughout the state. An epidemiological questionnaire was applied in these farms to identify attack and/or the presence of wild boar in the vicinities of the property (response variable).A Poisson regression model was used to identify factors associated with the presence of wild boar in these farms through the estimates of prevalence ratio (PR).
Results: Variables retained in the final model ($p<0.05$) were: farms located near forest reserves (PR=3.27); 2) farms located near indian reserves and rural settlements (PR=3.28); 3) farms raising outdoors pigs (PR=2.29); and 4) farms raising wild boars (PR=2.92).
Conclusions: Factors associated with the presence of feral swine in backyard pig farms were linked primarily with environmental variables. Properties near forest reserves, indigenous reserves and rural settlements, had higher prevalence ratio (PR). This is explained by the need of refuge areas for maintenance and stabilization of these feral animals, increasing the probability of contact with domestic pigs raised close by these areas.
Relevance: This is the first study aimed to identify factors associated with the contact between wild and domestic pigs in Brazil, and it is expected to support decision makers on the implementation of health policies aimed at mitigating the risk of contact between domestic animal species production with wild animals, thus minimizing the likelihood of transmission pathogens between them.

P021

Badgers and their interaction with cattle and farmyards - data from remote satellite tracking in the Republic of Ireland

Teresa MacWhite[1], Peter Maher[2], Enda Mullen[3], David Kelly[4], **Margaret Good**[2], Nicola Marples[5], [1]Department of Agriculture, Food and the Marine, Dublin, Ireland; [2]Department of Agriculture, Food and the Marine, Dublin, Ireland; [3]Department of Arts, Heritage and the Gaeltacht, Dublin, Ireland; [4]Trinity College, Dublin, Ireland; [5]Trinity Colleg, Dublin, Ireland. Contact: margaret.good@agriculture.gov.ie

Purpose:
European badgers, *Meles meles,* are wildlife vectors of TB caused by *Mycobacterium bovis*. The proximity of badgers to cattle, their use of farmyards and pastures containing cattle, is of fundamental importance in understanding transmission possibilities for *M. bovis* between a wildlife reservoir and cattle on farms.
Methods:
During this study the positions of free-ranging badgers were recorded up to eight times a night, using collars fitted with GPS (Global Positioning System) units.
Data on their use of farmyards and a series of paddocks with and without cattle present were investigated over a three month period.
The data on badger movements were plotted against the location and type of farmyard in the study area, and the grazing records on a farm, Badger usage of each paddock when it had and when it had not cattle present was investigated and compared.
Results: This study demonstrated that badgers in this area, generally avoided all types of farmyards but particularly those where cattle were present and further established convincingly for the first time that free ranging badgers avoid entering paddocks containing cattle.
Conclusions:
Direct contact between individual badgers and cattle is unlikely to be a major route of *M. bovis* transmission between these species. Therefore alternative strategies for controlling cross-infection between badgers and cattle might focus on other likely routes of transmission such as possible abnormal behaviour of badgers with advanced generalised TB, and indirect routes of transmission.
Relevance: Badger movement patterns play a key role in the transmission of *M. bovis* both within the species and to other susceptible hosts, especially cattle which can therefore have a significant economic impact on cattle farmers.

P022

Impact of endemic infectious diseases in swine production: Influenza A virus and porcine reproductive and respiratory virus

Julio Alvarez[1], Javier Sarradell[2], Barry Kerkaert[3], Montserrat Torremorell[1], Dipankar Bandyopadhyay[4], Robert Morrison[1], Andres Perez[1], [1]University of Minnesota, St Paul, MN, [2]Facultad de Veterinaria, Universidad Nacional de Rosario, Casilda, Argentina; [3]Pipestone Veterinary Services, Pipestone, MN, [4]University of Minnesota, Minneapolis, MN, Contact: jalvarez@umn.edu

Purpose:
Studies measuring the impact of influenza A virus (IAV) and porcine reproductive and respiratory syndrome virus (PRRSV) in pigs have traditionally focused on their effect on breeding herds and have relied on post-mortem detection of the pathogens when the impact was measured in growing pigs. In this study, we evaluated the association between the presence of IAV and PRRSV in breeding herds, and the subsequent post-weaning mortality observed in the cohorts of growing pigs that tested positive for the viruses at weaning.

Methods:
Detection of IAV and PRRSV was assessed by RT-PCR on oral fluid samples from suckling piglets in nine sow farms. Production data including mortality close out data from 177 batches of growing pigs weaned within one week of the IAV and PRRSV testing were analyzed to measure the association between IAV and/or PRRSV test results and mortality recorded for a given batch. A Bayesian mixed effects negative binomial multivariable regression model was used to account for the effect of potential confounders.

Results:
There was a significant association between IAV and PRRSV on post-weaning mortality, with season and number of days on feed also associated with the outcome. A large heterogeneity between flows was observed, highlighting the potential effect of other management-related characteristics.

Conclusions:
Detection of IAV and PRRSV in piglets prior to weaning was associated with an increase in postweaning mortality. Therefore the impact of these viruses in growing pigs should be taken in consideration when measuring the effect of the viruses in breeding herds.

Relevance:
Combination of production data (routinely recorded in wean to finish farms) with surveillance testing performed in breeding farms can help to further quantify the impact of endemic pathogens in breeding herds and demonstrate the potential of prevention strategies. The analytic approach used here can be extended to other pathogens and production systems.

P023

Surveillance of Swine Influenza in Florida and Caribbean

Dhani Prakoso[1], Maureen T. Long[1], Gregory C. Gray[2], Gary L. Heil[2], Elise Lee[3], Jun J. Liu[1], Sarah E. Beachboard[1], Nanny Wenzlow[1], Gretchen H. Delcambre[1], Rosina C. Krecek[3], William L. Castleman[1], Gabriele A. Landolt[4], Patti C. Crawford[5], [1]University of Florida, Gainesville, FL, [2]University of Florida, Gainesville, FL, [3]Ross University, Basseterre, Saint Kitts and Nevis; [4]Colorado State University, Fort Collins, CO, [5]University of Florida, Gainesville, FL, Contact: dprakoso@ufl.edu

Purpose:Swine influenza (SIV) is an acute respiratory disease in pigs caused by a virus from a family member of Orthomyxoviridae. Severe bias exists in sampling of intense swine from production locales; large areas of the Americas where swine are raised contribute little to our understanding of SIV in pastoral communities. We hypothesized that the open management of smaller farms with open housing in Florida and the Caribbean provided less chance of swine influenza being detected. Testing would result in a finding of limited nasal shedding of other swine pathogens compared to that reported for swine from large production facilities.

Methods:SIV was studied in three types of swine housing in Florida and the Caribbean where small farms predominate: 1) livestock shows in which humans and finishing swine are co-mingled, 2) smaller farms with open management on St. Kitts, 3) finished swine presented to a small local slaughter plant. Nasal swab sampling and testing of swine included SIV and subsets of these samples were tested for classical swine fever (CSF), porcine respiratory and reproductive virus (PRRS), and porcine circovirus (PCV) by real-time PCR. Convenience samplings were conducted from 2010-2012. Swine swab samples were taken from swine at the University of Florida quarantine and slaughter house facilities (414 samples), three county fairs in Florida (600 samples), and St. Kitts (500 samples) for a total of 1514 swine.

Results:None of the samples tested positive for SIV, PRRSV or CSF. Seven of 100 samples of Florida swine tested positive for PCV.

Conclusions:This initial study demonstrates that swine from pastoral communities arrive at fair grounds and slaughter facilities free of SIV. On small farms with open air stalling, little SIV and other pathogens are detected. Continued testing of co-mingling events is also important for the small swine farm industry since the prevalence of pathogens may be highly dissimilar to other management strategies.

Relevance: This small study will be utilized to demonstrate in the form of white papers through the Florida swine industry that testing of swine in high contact with humans is actually of benefit to the industry.

P024

Phenotypic Characterization of Salmonella Phages on free-range swine compared to Salmonella Phages from Industrial production systems

Dácil Rivera[1], Christian Cáceres[1], Rocio Salas[2], Francisca Di Pillo[2], **Christopher Hamilton-West**[2], Andrea I. Moreno Switt[1], [1]Universidad Andres Bello, Santiago, Chile; [2]Universidad de Chile, Santiago, Chile. Contact: christopher.hamilton@veterinaria.uchile.cl

Purpose. Salmonella is an important zoonotic pathogen, in Chile is the leading cause of foodborne illnesses with more than 3000 cases reported annually. A number of foods are sources of Salmonella, including animal-derived, produce, and processed. Among animal-derived food, swine is usually contaminated with Salmonella. Studies of the ecology of Salmonella on swine in Chile have shown a big difference in the prevalence of Salmonella on free-range swine compared to industrial systems. While phages are important drivers of Salmonella diversity; our knowledge of them is very limited. The main goal of this study was to characterize the diversity and the phenotype of Salmonella phages on two study areas, free-range versus industrial.

Methods. We isolated Salmonella phages from 20 samples from swine obtained from free-range farms and 20 samples from industrial swine production in Central Chile. We used as host for phage isolation strains representing serovars Enteritidis, Typhimurium, Heildelberg, and Agona. We characterized the host range on the isolated phages using 25 strains representing different serovars and Salmonella strains isolated on the same systems in Chile.

Results. S. Enteritidis was the host that allowed the isolation of most of the phages, 75% of the samples were isolated on Enteritidis host on industrial systems and 55% on free-range. Phages represented diverse morphologies, ranging from small plaques of approx. 1 mm to large plaques of approx. 3-4 mm, indicating a wide diversity on the isolated phages. Host range characterization showed phages with narrow and wide host range on both systems.

Conclusions. Salmonella phages are widely distributed on free-range and industrial systems; while S. Enteritidis is not a common serovar in swine, our findings indicate that phages lysing this serovar are very common in Chile. Our results demonstrate the importance of phages in the ecology of Salmonella on animal production systems.

Relevance. This is the first study that compares Salmonella phages on free-range and industrial systems; in addition, this study is very novel for Chile where phage ecology is completely unknown.

P025

The spatial dynamics of porcine epidemic diarrhea (PED) spread in Miyazaki prefecture, Japan

Yosuke Sasaki[1], Julio Alvarez[2], Satoshi Sekiguchi[1], Masuo Sueyoshi[1], Satoshi Otake[3], Andres Perez[2], [1]University of Miyazaki, Miyazaki, Japan; [2]University of Minnesota, St. Paul, MN, [3]Swine Extension & Consulting Inc., Niigata, Japan. Contact: yskssk@cc.miyazaki-u.ac.jp

Purpose: Porcine epidemic diarrhea (PED) was detected for the first time in 7 years in Japan in October 2013 in Okinawa prefecture, and spread into Miyazaki prefecture, one of the regions with a highest farm density in the country, by December. The objective of the study here was to assess the spatial dynamics of PED spread during the first 6 months of the epidemic (December 2013-July 2014) in Miyazaki.
Methods: Geographical information and farm capacity of every farms in the prefecture (n=511) was obtained from a government database containing demographic information for livestock producers. In addition, data on PED detection was obtained from the Miyazaki Livestock Hygiene Service Center. For spatial or spatio-temporal analyses, the Cuzick-Edwards (CE) test, the Knox test, the directional test, and the permutation model of the scan statistic were implemented.
Results: Cumulative incidence of PED was 15.8% (81/511) during the study period. The highest density of positive farms was observed in the most populated areas of the prefecture. The CE test revealed an extensive degree of spatial clustering, with clustering of positive sites being significant ($p<0.01$) until the 13th level of neighborhood. The observed-to-expected ratio of cases was maximized at short spatio-temporal distances, with values above 4 when the thresholds were set at 2 kilometers and 10 days, respectively (Knox test detected, $P<0.01$). A significant ($P<0.01$) direction of spread was detected towards the northeast direction (average angle 35.0°). The permutation model detected four different significant ($P<0.01$) clusters coincidently with different stages of expansion of the epidemic wave.
Conclusions: The strong spatio-temporal clustering of PED cases during the first 6 months of the epidemic in Miyazaki is consistent with results obtained from the U.S., which has also been recently affected by PED, demonstrating the rapid spread of the virus in naïve populations.
Relevance: These results will help to understand the epidemiological dynamic of PED infection and, ultimately, to establish realistic objectives for the prevention or control of the disease.

P026

African swine fever has low spread potential in the Finnish domestic pig population

Tapani Lyytikäinen, Jonna Kyyrö, Leena Sahlström, Finnish Food Safety Authority, Helsinki, Finland.
Contact: tapani.lyytikainen@evira.fi

Purpose: African swine fever (ASF) has been recently found near the Finnish borders in wild boar populations and sometimes also in domestic pig populations in Russia and the Baltic states. In Finland the disease has not
been observed, but for contingency purposes the spread potential of the disease
needs to been known.
Methods: The spread was simulated by a Finnish animal disease spread model.Model parametrisation mostly followed an earlier Finnish classical swine fever risk assessment (Raulo & Lyytikäinen 2006) and a study of ASF simulations by Nigsch et al. (2013). Monte Carlo simulation consisted of 100000 simulated outbreaks that were started in random order from every Finnish pig farm (n=2340) under the conditions of 2009. Only the spread by operations of domestic pig production were simulated.
Results: The probability of an epidemic outbreak appeared to be low (0.23) and the number of infected farms in case of further spread was on average 2.6. As a consequence, there would be 3 non-infected pig farms in the protection zone (< 3 km radius) and 14 pig farms in surveillance zones (3-10 km radius) for each infected farm. The probability of an epidemic outbreak was the highest on farrowing farms and the lowest on finishing farms. The spread potential did not vary much between Provincial veterinary officer -districts, except that the potential of spread was lower in Åland and Lapland due to lower pig farm density.
Conclusions: The results indicate that the EU measures are adequate to control the spread of ASF in Finland and the risk for an extended outbreak that escalates out of control is very small. The ASF outbreak would obviously have other consequences that have economic importance such as difficulties for exports.
Relevance: The results are consistent with the earlier study with more coarse simulation of ASF spread in Finland (Nigsch et al. 2013).

P027

Estimation of the reproduction rate (R) of Porcine reproductive and respiratory syndrome virus in two endemic farrow-to-finish farms.

Emanuela Pileri, Gerard Eduard Martin-Valls, Ivan Diaz, Meritxell Simon-Grife, Ariadna Garcia, Jordi Casal, **Enric Mateu**, Centre de Recerca en Sanitat Animal, Cerdanyola del Vallès, Spain. Contact: enric.mateu@uab.cat

Purpose: The objective of the present work was to study transmission of porcine reproductive and respiratory syndrome virus (PRRSV) in two non-vaccinated endemic farrow-to-finish farms in order to estimate the reproduction rate (R).
Methods: In each farm (F1 and F2) a batch of pigs was followed from weaning to slaughtering age (n=85 and n=75, respectively). In F1, blood samples were weekly collected from 3 to 13 weeks of age, and then animals were bled at 15, 17 and 24 weeks of age. In F2, blood sampling was done weekly from 3 to 21 weeks of age. The pen allocation of each individual pig during the observational period was recorded. A commercial ELISA (Idexx PRRS X3 Ab Test®) was used for the detection of PRRSV antibodies. Based on serological results, the transmission parameters beta (on a weekly basis) and R were calculated for each pen, for each farm and for the whole group of observations. For this estimation it was assumed that the infectious period was 4 weeks and afterwards pigs were considered immune.
Results: In F1, seroconversions were observed from 10 weeks of age except for three pigs. Cumulative incidence (CI) reached 94.0% at 24 weeks of age and therefore, 14 weeks were needed to achieve transmission to almost all pigs. In this case, the beta and R parameters were 0.88 [0.72; 1.04] and 3.53 [2.89; 4.18], respectively. In F2 seroconversions started at 15 weeks of age being all pigs seropositive after 20 weeks. In this farm, the virus spread to all finishing pigs in 5 weeks, so beta and R parameters were 1.33 [1.10; 1.57] and 5.34 [4.41; 6.26] respectively. When results from F1 and F2 were combined, the beta parameter was 1.02 [0.85; 1.18] per week.
Conclusions: As shown by the data, R may vary substantially but its value would be compatible with a relatively slow transmission and therefore, moderate increases in the vaccine efficacy could be enough to stop the spread of the virus in these type of farms.
Relevance: R value for PRRSV under natural conditions is little known. Estimation of R as presented here can be useful to understand the potential of vaccine stop transmission of PRRSV between pigs.

P028

Comparison of laboratory accession data and premises-level data for understanding the epidemiology of swine enteric coronavirus diseases (SECD) in the United States.

Brian McCluskey, Julie Wallin, Celia Antognoli, Sarah Tomlinson, Fred Bourgeois, USDA, APHIS, VS, Fort Collins, CO, Contact: brian.j.mccluskey@aphis.usda.gov

Purpose: Two swine enteric coronaviruses, Porcine Epidemic Diarrhea virus and Porcine Deltacoronavirus entered the United States in 2013 resulting in high morbidity and case fatalities. This study compares the collection methods and value of laboratory accession data voluntarily submitted from participating National Animal Health Laboratory laboratories with premises-level data submitted after mandatory reporting requirements for SECD were established by the USDA. Methods: Following the identification of Porcine Epidemic Diarrhea virus in May 2013, test accession data was voluntarily submitted to the USDA's Veterinary Services for compilation, analysis and national reporting. Test accession data included sample test date, State from which sample was purportedly submitted, age class of animals tested and test result. Data was submitted primarily through individual spread sheets from participating labs. Validity of voluntarily submitted data was not assessed by the laboratories or by the USDA.

In June 2014, the USDA required the reporting of SECD to federal and State animal health officials. Required data elements included premises identification number (PIN); date of sample collection; type of unit being sampled; test methods used to make the diagnosis; diagnostic test results; and the name and contact information of the veterinarian submitting the samples. HL7 messaging was implemented by laboratories conducting over 85% of the testing in the United States so that almost real time data was being delivered to the USDA. Positive test results were confirmed to be associated with clinical signs by USDA and State field epidemiologists. All data submitted through messaging or spreadsheets was validated by field epidemiologists or data analysts.

Results: Comparison of voluntary and mandatory data revealed significant discrepancies in incidence estimates and in the accuracy in reporting of geographic distribution of disease. Conclusions: Accurate premises based data facilitates the development and implementation of disease control measures with a particular emphasis of targeting these measures to compartments or geographic areas where they will be most effective.

P029

Risk analysis tool developed to assist with decision-making on prevention of swine diseases. Application to Porcine Epidemic Diarrhea in Caribbean countries.

Maria Irian Percedo Abreu[1], Jordi Casal[2], Javier Guitian[3], Cristobal Zepeda[4], Victor Gongora[5], Gillian Ellis[6], Maria Teresa Frias[7], Ana Alba Casals[2], Francisco Calvo[8], **Jennifer Pradel**[9], [1]CENSA, Mayabeque, Cuba; [2]CReSA, Barcelona, Spain; [3]RVC, London, United Kingdom; [4]USDA-APHIS-IS, Mexico, Mexico; [5]Belize Poultry Association, San Ignacio, Belize; [6]Ministry of Agriculture and Fisheries, Kingston, Jamaica; [7]CENSA, Mayabeque, Cuba; [8]Avia GIS, Zoersel, Belgium; [9]CIRAD, Petit Bourg, Guadeloupe. Contact: jennifer.pradel@cirad.fr

Purpose

Classical Swine Fever (CSF) and Teschovirus Encephalomyelitis (TE) have been identified as priority diseases for the Caribbean because of their sanitary, economic and social repercussions in affected countries, together with their high diffusion potential. After the emergence of Porcine Epidemic Diarrhea (PED) in the USA in 2013 and its further dissemination to other countries in the Americas and the Dominican Republic, the Steering Committee of the Caribbean Animal Health Network (CaribVET) added PED as a new priority for the region. This work aimed to develop a tool for risk analysis (RA) of swine diseases introduction/dissemination at national levels and applicable to the Caribbean region.

Method

This tool was initially developed for CSF and TE, and revised and adapted in 2015 for PED. The trilingual tool is a user friendly Excel Spreadsheet including the guidelines and questions for the risk assessment, are divided in three sections: 1) Release assessment of the pathogen from the affected country, 2) Exposure (dissemination) assessment of the susceptible pig population and 3) Consequences assessment of the pathogen introduction.

Results

A flexible RA tool has been designed. In section 1, the disease situation of the affected country and routes of pathogens introduction in the exposed country are considered. In section 2, the sanitary vulnerability in the exposed country is analyzed (control in external quarantine, performance of surveillance and diagnostic system, structure of the swine industry). Section 3 includes assessment of potential disease impacts in different swine production sectors. Values of scores for each criterion have been defined by an expert group for the disease being evaluated and the tool has been tested and validated in two Caribbean countries at risk.

Conclusion

Harmonization of sanitary risk assessment at national levels contributes to improve regional prevention and control strategies.

Relevance

The use of this tool is expected to trigger communication of threats and vulnerability detected with all stakeholders involved in the swine industry and to facilitate decision-making process to solve the problems identified in the countries.

P030

Human inflicted skin lesions in slaughter pigs - apparent prevalence and associations with management

Jens Frederik Agger[1], Henrik E. Jensen[2], Kristiane Barington[2], Soeren S. Nielsen[1], [1]University of Copenhagen, Frederiksberg, Denmark; [2]University of Copenhagen, Frederiksberg, Denmark. Contact: jfa@sund.ku.dk

Skin lesions in pigs at slaughter have raised public and political concern during recent years. Therefore a study was undertaken to: a) characterize the pathological types of lesions and their physical causes; b) estimate the apparent prevalence and associations with pig id-method, disease, gender, and transport loading time; and c) identify risk factors in the management for the occurrence of human inflicted skin lesions.

The study was based on three types of data. In a prospective longitudinal study of 8 months, data were collected from tissue samples from 97 injured pigs, and slaughter and meat inspection data from 5 million pigs at two large abattoirs. Interviews with farmers about management and delivery procedures at slaughter were conducted in a case control study including 69 farms. Data were analyzed with estimation of apparent prevalence and multivariable logistic regression using the likelihood ratio test and deviance to judge model fit.

The patho-anatomical reviews revealed that all 97 pigs had human inflicted contusions - with forms and extent associated with sticks, iron chains and tattoo hammers. The apparent prevalence in the meat inspection data was 0.007 % (356 cases).

Univariable analyses showed 3.5 times higher risk among pigs id-marked with a tattoo hammer compared to non-marked pigs (P=0.06). Male pigs had 1.3 times higher risk than female pigs. There were no clear associations between disease and skin lesions. Multivariable analyses showed an association only with the number of pigs in the delivery to the slaughterhouse. There was 2.6 times higher risk of human inflicted skin lesions in deliveries with 162-245 pigs compared to deliveries with 1-43 pigs.

The case-control study identified that hired labor using both chasing boards and chasing sticks increased the odds of human inflicted skin injuries 48 times compared to when the farmer himself managed movement of pigs from path to truck using a chasing board only.

It is concluded that delivery size should be further investigated, and delivery of pigs should be managed without the use of tattoo hammer and chasing stick.

This will further contribute to the welfare of pigs on their final journey to the slaughterhouse.

P031

Bayesian analysis for modelling contamination of trucks used in the shipment of pigs infected with porcine reproductive and respiratory syndrome virus

Krishna K. Thakur[1], Crawford W. Revie[1], Daniel Hurnik[1], Zvonimir Poljak[2], Javier Sanchez[1], [1]University of Prince Edwrad Island, Charlottetown, PE, Canada; [2]University of Guelph, Guelph, ON, Canada. Contact: kthakur@upei.ca

Background: Porcine reproductive and respiratory syndrome (PRRS) is a major disease in the swine industry. PRRS virus is primarily transmitted by direct and indirect contact between farms and through aerosol. Recent studies have suggested a high degree of truck sharing used for the shipment of pigs between farms. Other studies have highlighted the importance of trucks in the spread of PRRS virus.
Purpose: In the present analysis, a Bayesian approach was applied to quantify the likelihood that a shared truck used in the shipment of pigs would be infected with PRRS virus at the end of a given day, and to evaluate the efficacy of cleaning and washing protocols in reducing virus transmission during shipment.
Methods: PRRS virus-infected farms from which trucks shipped pigs were deemed to be the sources of infection. A quantitative stochastic model was built using data related to the prevalence of PRRS virus positive herds, number of times a truck is typically shared on any given day, shipment size, animal-level PRRS prevalence and virus shedding, travel time between farms, and the efficacy of three different cleaning and disinfection procedures.
Results: The model resulted in a mean probability of 0.394 that a truck would be infected at the end of a day, without considering the number of previous uses of the truck or whether or not it had been washed and disinfected. The action of washing trucks on its own resulted in a negligible decrease (less than 5%) in the probability that a truck would be infective; washing and disinfection resulted in a moderate decrease (58%), while washing and disinfection, followed by drying had the highest impact (90%).
Conclusion: Findings from this study suggest that under current biosecurity practices, where only around one third of the trucks are completely cleaned and disinfected between successive shipments, and that for more than half of the shipments made on any given day the same truck is used by more than two farms, a substantial risk may exist for the spread of PRRS virus as a consequence of sharing trucks.
Relevance: Findings from this study may have value to the swine industry in Canada as producers can make informed decision regarding the sharing of trucks among farms.

P032

Detection of Salmonella spp in poultry and swine backyard production systems from central Chile

Raúl A. Alegría-Morán, Francisca Di Pillo, Nicolas Bravo, Andres Lazo, Santiago Urcelay, Christopher Hamilton-West, University of Chile, Santiago, Chile. Contact: ralegria@veterinaria.uchile.cl

Purpose:
Characteristics and conditions of backyard production systems (BPS) transform them into potential maintainers of priority zoonotic agents, like avian influenza virus and Salmonella spp, highly important agents because of their impact in both animal and public health. The purpose of this study is to detect the presence of circulating Salmonella spp on backyard production systems (BPS) with poultry or swine breeding in central Chile.

Methods:
i) Cloacal and rectal samples were obteined (poultry and swine, respectably) from 263 BPS from 15 provinces from the regions V, RM and VI (equivalent to 1,405 samples). ii) Fecal content was then inoculated in test tubes with 5mL of peptone water (APT, Difco®) supplemented with 20 mg/mL of Novobiocin (Sigma®), incubated for 18 to 24 hours at 37° C. Then subcultured on modify semisolid Rappaport Vassiliadis (MSRV, Oxoid®) agar, supplemented with 20 mg/mL of Novobiocin (Sigma®) and incubated for 24 to 48 hours at 41.5° C. Samples compatible with growth and/or diffusion were subcultured by exhaustion on Xylose Lysine Deoxychocolate (XLD, Difco®) agar and then incubated for 24 hours at 37° C. Confirmation of compatible colonies was made by conventional PCR for the detection of invA gene.

Results:
27 (10.27%) positive BPS has been detected, compatible with the bacteriological diagnostic of Salmonella spp, equivalent to 37 (2.65%) positive samples. Being the provinces of Cordillera, Quillota, San Antonio and Melipilla the provinces that presents higher levels of positivity (25, 22, 20 and 17% respectively) and the provinces of Los Andes, Maipo and Talagante the only provinces with 0% of positive samples. From positive BPS, sample positivity has been observed in hens (64.9%), ducks (10.8%), turkeys (2.7%), swine (8.1%) and environmental samples (13.5%).

Conclusions:
There is evidence for the circulation of Salmonella spp on poultry and swine BPS, from central Chile, being detected on hens, ducks, turkeys and swine systems.

Relevance:
This becomes the first evidence of province and regional levels of Salmonella spp on BPS from central Chile.

P033

Baseline study of Yersinia enterocolitica in Swedish pig farms

Thomas Rosendal[1], Therese Råsbäck[2], Anna Aspán[2], Katarina Järnevi[2], Susanne André[2], Axel Sannö[3], Elina Lahti[1], [1]National Veterinary Institute, Uppsala, Sweden; [2]National Veterinary Institute, Uppsala, Sweden; [3]Swedish University of Agricultural Sciences, Uppsala, Sweden. Contact: thomas.rosendal@sva.se

Purpose:
Yersiniosis is an important foodborne illness caused by *Y.enterocolitica* that is reported in 1.4/100000 persons annually in the EU and 2.54/100000 in Sweden with a relatively high reported hospitalization rate. The main reservoir of the bacterium is the pig. The farm level prevalence of *Y. enterocolitica* has been measured from 16-64% and the contamination of carcasses at slaughter is also very common (15-74%). In Sweden, due to the very low prevalence of *Salmonella* in domestic animals, yersiniosis may be the most important food borne illness from pork. The present study will investigate the farm- and -pen level prevalence of *Y. enterocolitica* in Sweden and will also biotype the strains in order to identify known human pathogenic types.

Methods:
Four pen level fecal samples were collected from each of 105 pig farms with slaughter aged pigs during the fall of 2014. A survey was completed by the sampler that included questions about cleaning, biosecurity, feeding a housing systems. All isolates of *Y. enterocolitica* will be biotyped and characterized for the presence of virulence factors. Risk factor analysis will be completed to identify potential management strategies that are associated with the presence of this pathogen on farm.

Results:
Y. enterocolitica was identified from 32 of the sampled farms. In 10 farms either 3 or 4 of the sampled pens were positive for *Y. enterocolitica*,in 22 farms 1 or 2 pens were positive. The month that the samples were collected did not appear to have an impact on the status for *Y. enterocolitica* in the samples. Ongoing work will reveal any significant associations between production type and status. The results of biotyping will determine the presence of types of high human pathogenicity.

Conclusions:
Y. enterocolitica is present is the swedish domestic pig population at a prevalence similar to other pig producing regions in the world.

Relevance:
The results of this research are an important step in understanding the distribution and risk factors for the presence of pathogentic *Y. enterocolitica* in pigs in Sweden.

P034

Kennel cough in shelter dogs: prevalence of pathogens and antibacterial resistance

Jenny Stavisky[1], Andrew Waller[2], Janet Daly[1], Amy Charbonneau[2], Darren Hermes[2], Simon Priestnall[3], [1]University of Nottingham, Sutton Bonington, United Kingdom; [2]Animal Health Trust, Newmarket, United Kingdom; [3]Royal Veterinary College, London, United Kingdom. Contact: svzjhs@nottingham.ac.uk

Infectious respiratory disease ("kennel cough") is common in dogs housed in close contact. It is a particular problem in rescue shelters where significant morbidity may occur. In addition to its direct impact on welfare, kennel cough can delay the rehoming of affected animals, which reduces throughput, posing a significant financial burden for rehoming organisations. Although disease is typically mild, outbreaks of severe disease characterised by haemorrhagic pneumonia with high mortality, have been described. *Streptococcus equi* subsp *zooepidemicus* has been implicated in several of these outbreaks. The aim of this study was to determine the prevalence of *Streptococcus* zooepidemicus in shelter dogs with kennel cough, and to assess the prevalence and antibacterial resistance patterns in other potentially pathogenic bacteria present.

Shelters across the UK were recruited and provided with sampling and prepaid postage materials. Oropharyngeal swabs were taken from dogs with clinical signs of kennel cough (cough, nasal discharge). Data collected included clinical score, length of stay, vaccines and medications administered. Routine bacterial culture was performed for all samples, and sensitivity assessed using an antibacterial panel. A total of 565 samples were returned from 32 shelters (median 5, IQR 3, 9). One large shelter supplied 314 samples (55.6% of the total). Of the samples, 351 (62.1%) yielded a potentially pathogenic bacterial culture. In the positive samples, the most commonly identified species included *Escherichia coli* (99/351, 28.2%) and *Pseudomonas aeruginosa* (49/351, 14%). Four samples proved to be *Streptococcus zooepidemicus*, an overall prevalence of 0.7% (95% CI 0.2-1.9%). Of the 351 culture-positive samples, 322 (91.7%) showed some antibacterial resistance, and 284 samples (80.9%) showed multiple drug-resistance. Resistance was most common against clindamycin (282/351, 80.3%).

These results highlight the diversity in bacterial pathogens associated with kennel cough in shelters. *Streptococcus zooepidemicus* was rare in this study. Multiple antibacterial resistance is common in these environments, which has important implications for treatment.

P035

Effect of prednisone omission from a multidrug chemotherapy protocol upon treatment outcome in dogs with peripheral nodal lymphomas

Michael O. Childress, José A. Ramos-Vara, **Audrey Ruple-Czerniak**, Purdue University, West Lafayette, IN, Contact: aruplecz@purdue.edu

Purpose: To determine the impact of omitting prednisone from a combination chemotherapy protocol upon outcome and treatment-related toxic effects in dogs with nodal lymphomas.
Methods: A randomized prospective clinical trial that included 40 dogs with untreated, histopathologically-diagnosed primary nodal lymphomas was utilized. Dogs were randomly assigned to treatment with a combination of L-asparaginase, cyclophosphamide, doxorubicin, vincristine, and prednisone (L-CHOP), or to a similar protocol which excluded prednisone (L-CHO). Overall response rate, progression-free survival time, overall survival time, and toxic effects of therapy in the two groups were compared using statistical methods. Cancer- and treatment-related variables associated with progression-free and overall survival times were determined.

Results: Eighteen dogs received L-CHOP and 22 received L-CHO. The complete remission rate for dogs receiving L-CHOP was 72% (13/18), and that for dogs receiving L-CHO was 68% (15/22; P = 0.784). Median progression-free survival time for dogs receiving L-CHOP was 306 days, and that for dogs receiving L-CHO was 131 days (P = 0.117). Median overall survival time for dogs receiving L-CHOP was 420 days, and that for dogs receiving L-CHO was 254 days (P = 0.330). Serious treatment-related adverse events, chemotherapy dose reductions, and treatment delays were more common in the dogs receiving L-CHO than in those receiving L-CHOP, although these differences were not significant (P = 0.286, 0.073 and 0.106, respectively).

Conclusions: Prednisone omission from a multidrug chemotherapy protocol does not appear to significantly affect clinical outcome in dogs with peripheral nodal lymphomas.
Relevance: Dogs with lymphomas are typically older, and may therefore have comorbid conditions or require treatment with medications which would contraindicate the use of glucocorticoid therapy. In these cases, the omission of prednisone may not significantly alter the clinical outcome.

P036

Epidemiological characteristics of animal bites to humans, notified in health services in Quinta Normal County, Santiago, Chile. 2012.

Santiago Urcelay, Lisette Lapierre, Constanza Cubillos, University of Chile, Santiago, Chile. Contact: surcelay@uchile.cl

Purpose:
Animal bites represent an important public health issue as well as an economic impact for the health services and the security sense for the affected people. There are few studies about this topic in Chile, which are very much need to public preventive programs. The aim of this study was to perform an epidemiological characterization of animal bites occurred during 2102 in the Quinta Normal County, Santiago, Chile. In addition, the average cost of medical care resulting from these events in public health centres were calculated.

Methods:
Data were collect from hospital and health centres located in the Quinta Normal County and the animal information concerning the event were collect from a survey that was answer by the affected people. Survey cases were classify in three categories according to the severity of the injury.

Results:
From 517 records of animal bites cases, 408 were caused by dogs. No association was find between dog´s breed, animal origin and the location of where the aggression took place and severity of the injury. Costs associated to treatment and hospital staff that attended each case reached US$ 1,033 for slight bites, US$ 1,147 for serious bites and US$ 7,215 for extremely serious bites.

Conclusions:
In conclusion, The amount of dog bites represent an important cost to public health services, which could be higher if we considered those event not recorded at these services or attended at private health services.

Relevance:
The implementation of a responsible pet’s possession program and the establishment of suitable laws, among other measures, are imperative steps to accomplish the control of the mentioned situation.

P037

How do dogs encourage and motivate walking? Results from RESIDE

Carri Westgarth[1], Matthew Knuiman[2], Hayley Christian[2], [1]University of Liverpool, Liverpool, United Kingdom; [2]The University of Western Australia, Perth, Australia. Contact: carri.westgarth@liverpool.ac.uk

Purpose:
Not all dog owners walk their dog regularly and thus there is a need to identify intervention strategies for increasing dog walking, for both human and animal health. The most important factors associated with dog walking are the perceived support and motivation the dog provides for walking. Dog-related factors (e.g., dog size, age, health) have had mixed findings. The aim of this study was to re-examine a well-characterised dog walking dataset and model dog-related demographic and behavioural factors that contribute towards this strong sense of encouragement, obligation and motivation to walk the dog, which we call 'The Lassie Effect'.

Methods:
Data from a cross-sectional survey of 629 dog owners participating in the RESIDE study in Western Australia were analysed. The outcome variables of interest included 'Dog encouragement to walk' and 'Dog motivation/obligation to walk' and were collected using the Dogs And Physical Activity (DAPA) Tool. Multivariable logistic regression analyses were used to examine dog-related, cognitive and owner-demographic factors associated with each of these two outcomes.

Results:
Larger dog size; increased level of attachment to dog; knowing dog enjoys going for a walk; belief exercise keeps dog healthy; and social support from family to go walking in past month was associated with higher odds of 'Dog encouragement to walk' and 'Dog motivation/obligation to walk'. Perceived dog-specific barriers to walking with dog daily; child being the main person who walks with the dog; and children at home <18yrs (barrier) was associated with lower odds of 'Dog encouragement to walk' and 'Dog motivation/obligation to walk'. In addition, the belief walking reduces barking was associated with higher odds, and dog overweight; dog too old/sick; spouse/partner being the main person who walks with the dog was associated with decreased odds of 'Dog motivation/obligation to walk' only.

Conclusions:
Dog-related factors can affect the pathway to dog walking behaviour, and there may be separate factors influencing encouragement and maintenance of dog walking.

Relevance:
Interventions to promote dog walking need to address these factors.

P038

Factors associated with daily walking of dogs

Carri Westgarth[1], Hayley Christian[2], Robert Christley[1], [1]University of Liverpool, Liverpool, United Kingdom; [2]The University of Western Australia, Perth, Australia. Contact: carri.westgarth@liverpool.ac.uk

Purpose:
Regular physical activity is beneficial to the health of both people and animals. The role of regular exercise undertaken together, such as dog walking, is a public health interest of mutual benefit. However not all dog owners regularly walk with their dogs. Exploration of barriers and incentives to regular dog walking by owners is now required so that effective interventions to promote it can be designed.

Methods:
This study explored a well-characterised cross-sectional dataset of 276 dogs and owners from Cheshire, UK. Dog-demographic, owner-demographic, management, behavioural and environmental factors associated with the dog being walked once or more per day were analysed using multivariable logistic regression.

Results:
Factors independently associated with daily walking included: number of dogs owned (multiple (vs. single) dogs negatively associated); size (medium and possibly large dogs (vs. small) positively associated); and number of people in the household (more people negatively associated). Furthermore, a number of factors related to the dog-owner relationship and the dog's behaviour were associated with daily walking, including: having acquired the dog for a hobby (positively associated); dog lying on furniture (positively associated); dog lying on laps (negatively associated); growling at household members (negatively associated); and playing chase games with the dog (negatively associated).

Conclusions:
These findings are consistent with the hypothesis that the strength and nature of the human-dog relationship incentivises dog walking, and that behavioural and demographic factors may affect dog walking via this mechanism.

Relevance:
Future studies need to investigate how dog demographic and behavioural factors, plus owner behavioural factors and perceptions of the dog, influence the dog-human relationship in respect to the perceived support and motivation a dog can provide for walking.

P039

Trends in popularity of some morphological traits of purebred dogs in Australia

Kendy T. Teng, Paul G. McGreevy, Jenny-Ann Toribio, Navneet K. Dhand, University of Sydney, Camden, NSW, Australia. Contact: tten7180@uni.sydney.edu.au

Purpose:
The morphology of dogs can provide information about an individual's predisposition to some disorders. Therefore, trends in popularity of dog morphology over time provide clues about potential disease pervasiveness in the future. This study aimed to investigate trends in some morphological traits of Australian purebred dogs, including dog height, dog size and cephalic index (skull width divided by skull length), by analysing a 28-year-long (1986-2013) Australian National Kennel Council (ANKC) dog registration dataset.

Methods:
For every year, the numbers of dogs registered within 181 breeds were drawn from ANKC registration statistics. Height and weight data for breeds were obtained from the ANKC studbook or, if not available in the breed standards, from the Encyclopedia of Dog Breeds. The weights for each breed were used to assign breeds to one of the four size groups (small, medium, large, giant). Mean cephalic index data for 80 breeds were drawn from a peer-reviewed paper. Weighted regression analyses were conducted to examine trends in the traits by using them as outcome variables, year as the explanatory variable and numbers of registered dogs as weight. Linear regression investigated dog height and cephalic index, and multinomial logistic regression studied dog size.

Results:
The results suggested that both weighted minimal height ($\beta = -0.07$, s.e. = 0.027, $p < 0.001$) and maximal height ($\beta = -0.10$, s.e. = 0.030, $p < 0.001$) decreased significantly over time, and that the weighted mean cephalic index increased significantly ($\beta = 0.17$, s.e. = 0.030, $p < 0.001$). Multinomial logistic model results indicated that odds of registration of medium and small breeds increased by 5.3% and 4.2%, respectively, relative to large breeds and by 12.1% and 11.0%, respectively, relative to giant breeds ($p < 0.001$) for each 5-year block of time.

Conclusions:
Over the 28-year period, shorter and smaller dogs became relatively popular, compared to taller and larger dogs, and mean cephalic index of dogs increased.

Relevance:
Significant trends in the morphology of Australian dogs identified by our study provide valuable predictive information on the prevalence of diseases in dogs.

P040

Mathematical Modeling of Infectious Disease: The Interaction of Science and Social Science in Disease Response

Christine Crudo[1], William Sischo[2], Douglas Call[3], [1]Washington State University, Pullman, WA, [2]Washington State University, Pullman, WA, [3]Washington State University, Pullman, WA, Contact: ccrudo@wsu.edu

Purpose: The purpose of the mathematical model developed in this study is to show the impact that communication and policy have on disease containment efforts, especially if they are sensitive to the biological characteristics of the disease.

Methods: The model was constructed using a basic Susceptible-Infected-Removed Model. It was then expanded to contain additional compartments for individuals with higher susceptibility rates as well as compartments to account for asymptomatic individuals. The parameters for the model include biological inputs for the disease and social inputs to describe the policy and communication responses.

Results: The model demonstrates that policies must be sensitive to disease biology in order to be effective and that combining an effective communication strategy with a containment policy will further decrease the rate of infection.

Conclusions: The model serves as a tool for understanding how to respond to an infectious disease outbreak based on the biological characteristics of the disease in question. It effectively shows the importance of incorporating social science elements of policy and communication into disease response. Relevance: The Intervention Impact Model has the potential to change the way that governments and public health officials respond to infectious disease outbreaks in the future because it demonstrates the importance of a strategy incorporating policy and communication into the biological elements of disease. And demonstrates that effective strategies must be based in the biological characteristics of the disease and the knowledge gained from the model can save lives in future disease outbreaks be increasing disease response effectiveness.

P041

Simulating the Spread of Antimicrobial Resistant Bacteria in the Pig Pen

Kaare Græsbøll[1], Søren S. Nielsen[2], Nils Toft[1], Lasse E. Christiansen[3], [1]Technical University of Denmark, Frederiksberg C, Denmark; [2]University of Copenhagen, Frederiksberg C, Denmark; [3]Technical University of Denmark, Kgs. Lyngby, Denmark. Contact: kagr@dtu.dk

Background:
Antimicrobial resistance is an increasing challenge. For example, 40% of *Escherichia coli* in Danish pigs are resistant to treatment with tetracycline. Previous simulation models for antimicrobial resistance have focused on one susceptible and one resistant population of bacteria. Here we wanted to include multiple bacterial strains and multiple pigs in the pig pen.

Purpose:
The simulation model was part of a project including a field trial with +2,000 pigs receiving different doses of antimicrobials (AM), and several *in vitro* experiments used to determine growth rates of different bacterial strains in present of AM. The aim of the present study was to investigate which factors determine the spread of antimicrobial resistant bacteria (AMRB) within a pig pen using a newly developed simulation model.

Methods:
The model simulates AM dependent growth of individual bacterial strains (e.g. *E. coli*) in individual pigs, and dynamic effects of the excretion and uptake of bacteria from the common pen environment. It was experimentally verified that several bacterial strains co-inhabit the pig intestines, and the model structure was therefore constructed to support a dynamic equilibrium of several strains.

Results:
These experiments inform a novel mathematical model that incorporates both multiple pigs and multiple strains. The mathematical model is available as an interactive educational WebApp, www.kagr.shinyapps.io/MiniResist. We investigated how the transmission parameters affect the spread of bacteria between pigs, and how AMRB with fitness reduction may survive in the pig population.

Conclusions:
The model suggests mechanisms for survival of multiple bacterial strains in a dynamical equilibrium, and defines the limits for the fitness cost reduction allowable for resistant bacteria to survive.

Relevance:
Most importantly we observe non-linear effects of the excretion and intake parameters on the AMRB population that highlights a current knowledge gap, which should be explored by further experiments. The model also predicts that a higher dose of AM in shorter time leads to a lower level of resistant bacteria.

P042

Evaluation of the effect of control measures on the within farm transmission of porcine endemic diarrhea (PED) using mathematical model

Kiyokazu Murai, Sachiko Moriguchi, Yoko Hayama, Sota Kobayashi, Toshiyuki Tsutsui, Takehisa Yamamoto, National Institute of Animal Health, Tsukuba, Japan. Contact: mtbook@affrc.go.jp

Purpose: Porcine endemic diarrhea (PED) is a viral infectious disease causing severe diarrhea in piglets. In Japan, a large scale epidemic was occurred from 2013 to 2014 winter season and more than 800 farms found infected. To examine the effectiveness of control measures to PED transmission within a farrow to finish farm, we developed a deterministic compartment based mathematical model.
Methods: Pig population was divided into several compartments by production stages, pig houses and infection stages. Production stages were consist of breeding sows, suckling piglets and fattening pigs. The farm had three pig houses. Breeding sows were kept in breeding house and moved to farrowing house before giving birth to their piglets. After weaning, sows were returned to breeding house and piglets were moved to fattening house. After the fattening period, fattening pigs were removed for slaughter. Infection stages were defined as susceptible, latent, subclinically infectious, clinically affected and recovered. Clinical stage of piglets was subdivided into mildly and acutely affected. Infection was a result of exposure to contaminated environment of pig houses. Excretion from clinical and subclinical pigs caused increase of virus in their environment while amount of virus decreased by natural decay or disinfection. Disease transmission between pig houses was caused by movement of infected pigs and mechanical transmission of virus. Disease transmission after infection of a sow in breeding house was simulated for 200 days by one day time step. Effect of farm size, vaccination and biosecurity measures was also examined.
Results: Infection was temporally observed but limited in breeding house in small farm (30 sows). In large sized farm (400 sows), temporal infection was also occurred in the other two houses and death of suckling piglets occurred in the farrowing house. In this case, infection continued in fattening house at the end of simulation period. Although the biosecurity measures seemed not enough to prevent the disease transmission within farm, vaccination was shown to be effective to reduce the length of epidemic and the number of death of piglets.

P043

Development of FMD transmission simulator in Japan

Yoko Hayama, Takehisa Yamamoto, Norihiko Muroga, Sota Kobayashi, Kiyokazu Murai, Toshiyuki Tsutsui, National Institute of Animal Health, Tsukuba, Japan. Contact: hayama@affrc.go.jp

During a large-scale FMD epidemic occurred in Japan in 2010, the national and local animal health authorities were confronted with difficulties in smooth implementation of control measures such as culling and disposal of animals on farms. Then, the emergency vaccination was conducted to contain the further disease spread. The epidemic provided many lessons in deciding and implementing optimal control measures promptly and effectively in momentary changing the epidemic situation. The objective of this study is to develop an FMD transmission simulator to allow decision makers to evaluate the effectiveness and efficacy of control strategies upon the simulated outbreaks. This presentation introduces the structure and function of the simulator. This simulator contains a spatial, stochastic simulation feature to generate between-farm transmission in a selected area. To run the simulator, farm information including farm sizes, animal species and locations, is required. Parameters concerning the transmission process and control measures are also necessary. The transmission process used in this simulator is composed of two parts, namely transmission before the movement restrictions and that after movement restrictions. Long-distance transmission via movements and local spread were considered for the transmission before restrictions and only local spread was considered for that after movement restrictions. Long-distance transmissions were generated reflecting the movement patterns of animals, humans and vehicles in the area. Local spread was produced by transmission kernels estimated from the previous FMD epidemics in Japan in 2010 and those in Europe in 2001. Control measure scenarios include prompt culling, preemptive culling and vaccination. For simulating these scenarios, culling or vaccinating capacities and prioritization of farms to be culled or vaccinated can be defined in advance. Simulation outputs include epidemic size, economic impact and required human resources in graphs and tables as well as maps showing how the disease spread. The simulator is being elaborated to be more user-friendly as decision makers can make full use of the system without difficulties.

P044

Whole genome sequencing in support of the molecular epidemiological investigation of muskox die-offs associated with the bacterium Erysipelothrix rhusiopathiae

Karin Orsel[1], Taya Forde[1], Susan Kutz[2], Roman Biek[3], Jeroen De Buck[1], Hannah Trewby[4], Layne Adams[5], Frank van der Meer[2], Ruth Zadoks[4], [1]University of Calgary, Calgary, AB, Canada; [2]University of Calgary, Calgary, AB, Canada; [3]University of Glasgow, Glasgow, United Kingdom; [4]University of Glasgow, Glasgow, United Kingdom; [5]Alaska Science Center, Anchorage, AK, Contact: karin.orsel@ucalgary.ca

Muskoxen, *Ovibos moschatus,* found across much of Arctic Canada, are important ecosystem components and are a source of food and income, as well as a focus of cultural activities, for northern peoples. Since 2010, multiple unusual summer mortality events have occurred in muskoxen on the Canadian Arctic Archipelago, raising concerns about the health of this species and its environment. *Erysipelothrix rhusiopathiae*, a zoonotic bacterium not previously reported in the Arctic, was consistently isolated from multiple tissues of sampled carcasses. The objectives of this study were to genetically characterize the isolates and to determine whether the deaths could be attributed to a single strain. Whole-genome sequencing was performed on multiple isolates from 13 muskox carcasses collected on Banks and Victoria Islands between 2010 and 2013, which encompass over 200,000km^2. To provide context, these sequences were compared to other *E. rhusiopathiae* isolates (n=82) from various host species on a global scale, including recently isolated strains from muskox carcasses in northwestern Alaska (n=6). Paired-end reads were mapped to the *E. rhusiopathiae* reference genome to detect single nucleotide polymorphisms (SNPs) which were used to generate a maximum likelihood phylogeny to examine genetic relatedness. Among the global collection of isolates, around 15,000 core SNPs were detected across the 1.8 MB genome. The isolates from Alaskan muskoxen each differed from one-another by a few hundred SNPs. In contrast, extremely little variability was found among the muskox isolates from Banks and Victoria Islands: with the exception of one divergent isolate, these isolates differed from their inferred common ancestor by a maximum of 16 SNPs, suggesting a single outbreak and prolonged transmission. Based on the limited variability found, further work is required to determine how a single bacterial strain could have spread relatively rapidly across this vast area.

P045

The role of stocking constraints on the cost-effectiveness of vaccination against foot-and-mouth disease: the case of Scotland

Thibaud Porphyre[1], Harriet Auty[2], Mark E. J. Woolhouse[1], George J. Gunn[2], **Karl M. Rich**[3], [1]Centre for Immunity, Infection and Evolution, University of Edinburgh, Edinburgh, United Kingdom; [2]Epidemiology Research Unit, Scotland's Rural College (SRUC), Inverness, United Kingdom; [3]Lab 863 Ltd, Edgware, United Kingdom. Contact: karl@lab863.com

Purpose

In developed country settings, a crucial debate has revolved around the merits of stamping out versus vaccination strategies to control foot-and-mouth disease (FMD), particularly given the tradeoffs associated with the loss of export markets under the latter. However, an overlooked issue concerns the logistics of a vaccination policy itself. For instance, in case of a large outbreak, it remains an open question as to whether sufficient vaccine stocks and delivery capacity for such stocks could be mobilized adequately to cost-effectively arrest the spread of disease. If delays in vaccine delivery are large, it is possible that the effects of these delays could not only undermine the success of a vaccination campaign but also impose significant costs on scarce veterinary resources.

Methods

In this paper, we analyze the potential impact of vaccination constraints on simulated outbreaks of FMD in Scotland. We use an epidemiological simulation model to consider different scenarios of capacity constraints and their effects on disease evolution and direct costs. Based on an initial seeding of five infected premises in a high risk area for disease spread, we examine the distribution of cases and costs associated with various capacity and restocking scenarios.

Results

When initial stocks are small (e.g. 100,000 doses), large restocking delays are of particular importance. While there was little difference in average costs whether restocking occurred 14 or 28 days after order, delays of 56 days and higher rapidly increased the direct costs of control. These delays in restocking nearly doubled the average days of disease duration, causing sharp losses associated with export bans in particular.

Conclusion

While maintaining high initial levels of stocks reduced the cost associated with an outbreak relative to no vaccination, one needs to consider the opportunity cost with maintaining large vaccine inventories.

Relevance

An important implication of the analysis concerns the tradeoffs between the optimal level of vaccine stocks pre-outbreak and the ability to obtain more during an outbreak, as well as the viability of a vaccination policy itself.

P046

Modelling the risk of Bluetongue virus 4 to Scotland

Paul R. Bessell[1], Kate R. Searle[2], Ian G. Handel[3], Bethan V. Purse[4], Barend M. D. C. Bronsvoort[1], [1]The Roslin Institute, Edinburgh, United Kingdom; [2]Centre for Ecology and Hydrology, Edinburgh, United Kingdom; [3]The University of Edinburgh, Edinburgh, United Kingdom; [4]Centre for Ecology and Hydrology, Wallingford, United Kingdom. Contact: paul.bessell@roslin.ed.ac.uk

Purpose:
In recent years there have been annual incursions of bluetongue virus (BTV) into Western Europe. Of particular concern during 2014 was an incursion of BTV serotype 4 into the Balkans area that resulted in high morbidity and mortality in sheep. Should BTV-4 overwinter then it could spread during 2015 and potentially reach Scotland. Previous studies have demonstrated that Scotland is at risk of vector borne diseases but is highly sensitive to the timing of introduction and the temperature. This is supplemented by recent studies that demonstrated that the midge vectors of BTV are more likely to feed on cattle compared to sheep. In this study we model the impact of BTV introduction to Scotland given different timings of introduction, different temperatures and optimise vaccination strategies given spread extent and feeding preferences.

Methods:
In this paper we develop a spatially explicit stochastic simulation model for the spread of BTV-4 within and between farms in Scotland. Due to uncertainty in the transmission parameters of BTV-4 and to allow for temperatures varying from the mean, we ran a number of scenarios to vary these parameters. This incorporated midge feeding preferences, varied the timing of BTV introduction and the location sites of introduction. We then explore the impact of vaccination of different groups of animals in different locations.

Results:
Under most scenarios, relatively few sheep become infected (fewer than 100). Under a worst case scenario in which the virus is well adapted to spread at low temperatures and the temperatures are 1OC warmer than average then a median 220,000 sheep become infected if BTV is introduced to the south west in mid-May. By vaccinating 487,000 cattle in the south of Scotland, this number of infected sheep is reduced by 150,000; 1,880,000 sheep must be vaccinated to achieve the same reduction.

Conclusions & Relevance:
By considering vector feeding preferences alongside control strategies, large savings can be measures to effectively control BTV and the measures can be implemented more efficiently. This is particularly the case in Scotland where the relative marginality means that spread will be spatially and temporally contained.

P047

Spread potential of bluetongue in Finland and feasible alternatives for eradication

Tapani Lyytikäinen, Jonna Kyyrö, Leena Sahlström, Finnish Food Safety Authority, Helsinki, Finland.
Contact: tapani.lyytikainen@evira.fi

Purpose: Finland is a northern country with short summers. Finland has not experienced a bluetongue (BT) outbreak. However, knowledge of the spread potential of BT is required for contingency plans. The last BT outbreak reached southern Sweden but did not cross the Finnish border.
Methods: The spread was simulated by a Finnish animal disease spread model. Model parametrisation mostly followed the Koeijer et al. (2011) model parameterised for the spread of BT in Germany in 2006. According to the assumptions of the model of Koeijer et al (2011), the vector active season would be 91 days in the temperature conditions of Helsinki in 2009. Additionally the Finnish model also contained spread
by direct animal movement, modelled according to Turner et al. (2012). The developed Monte Carlo simulation consisted of 100000 simulated outbreaks that were started in random order from every Finnish cattle and sheep farm (n=19104).
Results: Bluetongue showed a low ability for spread as the probability of an epidemic outbreak was 0.24 and the average size of an epidemic outbreak was 2.8 infected farms if only one farm acted as the primary infected farm. These results are a co-product of Finnish temperature conditions, short vector active season and low farm density.
Conclusions: Optimal risk management measures should be selected with the low spread potential in mind. A goal to rapidly vaccinate the population within the vector active season might not be the most cost effective risk management strategy. Probably a slower vaccination campaign during the vector free season in conjunction with other health care operations would cause a similar effect at lower cost. Culling on infected farms and monitoring of risk farms may also be a potentially cost effective way to eradicate disease due to low the number of infected farms and small proportions of sheep farms in Finland.

P048

A system dynamics model of beef calf flow from farms in the southeastern United States

Robert W. Wills, David R. Smith, Min Wang, Richard H. Bailey, Mississippi State University, Mississippi State, MS, Contact: wills@cvm.msstate.edu

Purpose:
Beef calves from the southeastern United States are recognized as a relatively inexpensive but high health risk source of cattle for feedlots predominantly in the Great Plains. Stocker systems provide a means to increase entry weights and reduce disease risk at the feedlot. Nevertheless, many calves flow directly from the farm or sale barn to the feedlot. The goal of this research was to use system dynamics modeling to learn how morbidity and mortality within different segments of the production system affect the flow patterns of cattle moving through the market chains.

Methods:
A system dynamics model was developed to study the flow of beef calves produced in the southeastern states of the US and marketed to feedlots for final finishing. The model focused on sale barn to feedlot flows compared to sale barn to stocker to feedlot flows. Inputs for the model included on-farm cattle numbers and production measures, inputs for breakeven points at different market points, growth and production estimates in the different segments, and cattle prices at different market points. Of particular interest was the impact of segment specific morbidity and mortality and antimicrobial use on breakeven points.

Results:
The model revealed that although health and production benefits were achieved through the sale barn to stocker to feedlot flow, there may not be sufficient feedback loops (economic signals) from the feedlot to the farm or sale barn to support disease control measures that would improve health of cattle and reduce reliance on antimicrobials in the control of disease.

Conclusions:
The behavior of the beef cattle marketing system over time in response to economic and disease variables was simulated through the development of a system dynamics model. The approach permits the investigation of methods to improve feedback, both in economic and epidemiologic terms, from the feedlot to the farm.

Relevance:
The system dynamics model that was developed in this research can be used as a platform to explore how cattle producers, feedlot owners, and other stakeholders may improve profitability through establishing marketing flows that contribute to the improved health of calves.

P049

Estimation of local-spread transmission probability for foot-and-mouth disease

Masako Wada[1], Tim Carpenter[1], Naomi Cogger[1], Mark Stevenson[2], [1]Massey University, Palmerston North, New Zealand; [2]The University of Melbourne, Victoria, Australia. Contact: M.Wada@massey.ac.nz

Purpose:
Over the last decades, a number of attempts have been made to develop simulation models for foot-and-mouth disease (FMD), an economically important livestock disease, to help better decision making regarding control and eradication strategies. FMD is a highly contagious disease, of which the majority (> 80%) of transmissions are believed to be attributable to 'local spread,' a mechanism of spread without any clear linkage other than geographical proximity between infectious and susceptible populations, which is challenging to parameterise. Here we describe a method to estimate transmission kernel parameters that best represented local spread, using past epidemic data that have limited quantifiable information.

Methods:
Using the field (farm-level) data for the FMD epidemics, pairwise data were simulated by imputing missing data and randomly allocating a source for each infected premises based on the standardised probability estimated by one-dimensional kernel smoothing method. Then, the daily hazard of infection for different distance strata and different phases of epidemic was estimated by Kaplan-Meier survival analysis.

Results:
The transmission kernels ranged from 0 to 0.03 (infection/day), which varied by time, distance, phase and epidemic. The range was comparable with the results from other studies using complete data.

Conclusions:
Despite limitation in the quantifiable data, our method can be used to approximate local spread probabilities, which vary by multiple epidemiological factors.

Relevance:
The variations in the pattern of local spread found here can be useful in examining the sensitivity of an optimum control strategy. Results of this analysis will be useful for modelling and decision making for FMD control; while the methodology presented here will be applicable to other diseases.

P050

Simulation model of bovine brucellosis transmission in Argentine farms

María N. Aznar[1], Nicolas Rose[2], Luis E. Samartino[3], Claude Saegerman[4], Emilio E. León[3], [1]INTA/University of Liège, Hurlingham, Argentina; [2]Anses Ploufragan-Plouzané Laboratory, Ploufragan, France; [3]INTA, Hurlingham, Argentina; [4]Epidemiology and risk analysis applied to veterinary sciences - University of Liège, Liège, Belgium. Contact: aznar.maria@inta.gob.ar

Bovine brucellosis is endemic in Argentina, both in dairy and beef farms. The National Control and Eradication Program establishes compulsory vaccination of heifers and restrictions of cattle movements for reproductive reasons (only authorized if animals test negative).Purpose:to evaluate different brucellosis preventive and/or control strategies in Argentine dairy and beef farms.Methods: a stochastic, individual-based model in discrete time (time-step=1day) was built using Visual Basic to write the code and MS Access to indicate the inputs and analyze the results. The model simulates: a. the structure and the dynamics of a cattle herd; b. the spread of *Brucella abortus* within the herd; c. the effect of introducing animals for replacement; d. the vaccination effect; e. the effect of test and slaughter strategy. Stochastic modelling was done using Monte Carlo simulations. Different scenarios were simulated:
I) Base population: type of production (daily *vs* beef), herd size (big *vs* small), type of mating (continuous *vs* seasonal).
II) Disease: high *vs* low prevalence.
III) Replacements: internal *vs* external origin (unknown origin with and without sanitary controls; certified origin with and without sanitary controls).
IV) Vaccination: *Brucella* strain 19 *vs* RB51.
V) Diagnostic tests: the main ones were included, with its sensitivity and specificity values. They were combined in different strategies (parallel *vs* serial) and performed at different frequency throughout a year.
VI) Culling of reactors: immediately after the serologic result *vs* not immediately.Results: the main outputs of the model allowes identifying several key important measures: the number of vaccinations, diagnostic reactions and culls performed before reaching eradication and the time required to eradicate. Conclusions: the strategy that reaches eradication in the shortest time or at the lower cost can be identified, according to the initial scenarios. Relevance: this tool will help policy makers to choose the best preventive and/or control strategies, according to the context, improving the implementation of the National Control and Eradication Program.

P051

Comparison of American Food Quality Assurance standards to those of the Canadian Food Quality Assurance System

Vanessa E. Yeager, **Gay Y. Miller**, University of Illinois, Urbana, IL, Contact: gymiller@illinois.edu

Porcine Epidemic Diarrhea virus (PEDv) emerged in North America (NA) in March 2013. U.S. PEDv losses (8 million pigs; over 9,000 cases) are greater than Canadian losses (~90 cases). We hypothesize such differences may be explained by differences between Canada's quality assurance (CQA) standards vs U.S. pork quality assurance standards (PQA). These standards (measured farm assessments by qualified advisors) include biosecurity standards which are important for exclusion/protection from diseases such as PEDv and also for foodborne risks from pork.

The objective of this study was to conduct a preliminary exploration of differences that exist between the CQA and PQA, and if they may help explain the differences risks from pork or PEDv incidences. An investigator (Yeager) spent a 2-week period working with CQA in 2014 observing Canadian on-farm CQA assessments.

Preliminary investigation finds CQA audits more assessment categories than PQA. CQA is composed of 14 main assessment categories assessing 35 aspects of the Canadian pork industry. PQA is comprised of 3 main assessment categories, assessing 16 aspects of the American pork industry. The CQA site assessment has a 50-page questionnaire. Direct 'yes' or 'no' questions are asked as well as open-ended questions "What would you do if..." and "Describe your protocol for⋯". The PQA site assessment has 16 aspects in 2 pages in a check-off box format with boxes for 'acceptable', 'action plan', and an assessor comment box. The corrective action form of the PQA and CQA (for entry if needed) differ in the number of follow-up questions. Both PQA and CQA request description of the event(s) to be corrected/improved, with CQA including 3 follow-up questions on how the event happened, was rectified, and will be prevented. The observed CQA time for completion was higher (3-4 h range) than mean time for PQA (2 h).

Differences exist between CQA and PQA that suggest differences in biosecurity practices and disease risks. These findings are relevant since all producers and countries work benefit from decreased risks of disease introduction and spread for important diseases that influence swine productivity and foodborne illnesses associated with pork products.

P052

Lead content in game meat - is there an impact of ammunition?

Christine Müller-Graf, Annett Martin, Thomas Selhorst, Antje Gerofke, Helmut Schafft, Monika Lahrssen-Wiederholt, Matthias Greiner, Federal Institute for Risk Assessment, Berlin, Germany. Contact: Christine.Mueller-Graf@bfr.bund.de

The uptake of lead via food consumption can have a detrimental effect on health. In 2010 EFSA concluded that it would not be appropriate to derive a provisional tolerable weekly intake (PTWI) for lead as no threshold for a number of critical endpoints could be elicited.
Game meat has been identified as a source of lead intake and additional regular and high consumption of meat from animals killed with lead-based ammunition can potentially lead to a considerable increase in the lead levels of certain subgroups. A project on “Food Safety of Game Obtained Through Hunting” was initiated in Germany as a cooperation between the Federal Institute for Risk Assessment, the ministry, Federal States, hunting associations and the game meat association to obtain more data on the concentration of lead in game meat and factors contributing to the lead burden. In this project animals from three regions with different soil lead content were shot with either lead-based or lead-free ammunition. Mainly roe deer (n= 1254) but also wild boar (n = 854) were investigated and samples were taken from the haunch, saddle as well as meat close to the wound channel, which is still marketable. Because of the high number of samples which were below detection levels, tobit regression was used to deal with the excess number of zeros. Results showed that lead content in game meat shows considerable variation, especially in animals shot with lead ammunition. Here, very high values could be occasionally found especially in samples close to the wound-channel. The lead levels were found to be lowest in the haunch, higher in the saddle and highest close to the wound channel. Overall, a statistically significant difference was found between the game meat obtained with lead-based and lead free ammunition taking into account different background levels. As a result, there is a potential risk for a subgroup of children and pregnant women who consume a large amount of game meat shot with lead-based ammunition.

P053

Evaluation of generic E. coli as an indicator of Campylobacter spp. control during broiler chicken processing

Roy D. Berghaus[1], Stephan G. Thayer[1], Bibiana F. Law[2], Rita M. Mild[2], Charles L. Hofacre[1], Randall S. Singer[3], [1]University of Georgia, Athens, GA, [2]University of Arizona, Tucson, AZ, [3]University of Minnesota, St. Paul, MN, Contact: berghaus@uga.edu

Purpose: Generic E. coli has been recommended as one possible indicator of microbiological process control during broiler chicken processing. The objective of the current study was to determine whether reductions in E. coli counts between rehang and post-chill sampling locations were predictive of reductions in Campylobacter prevalence and MPN.
Methods: A total of 54 broiler flocks from two different companies were sampled during the current study. Six birds were sampled from each flock at rehang (after defeathering but before evisceration) and another six birds were sampled after immersion chilling. Whole carcass rinses were performed and quantitative cultures were completed for E. coli and Campylobacter.
Results: Generic E.coli was cultured from all 54 (100%) flocks, while Campylobacter spp. were isolated from 17 (31%) flocks. The overall percentages of samples positive for E.coli at rehang and post-chill were 100% and 96.6%, respectively. And the overall percentages of samples positive for Campylobacter at rehang and post-chill were 23.8% and 14.5%, respectively. Mean E.coli counts for culture positive samples decreased from 5.61 log10 cfu/carcass at rehang to 3.15 log10 cfu/carcass post-chill. Mean Campylobacter MPNs for culture positive samples decreased from 5.35 log10 MPN/carcass at rehang to 2.97 log10 MPN/carcass post-chill. Despite having similar overall mean load reductions between rehang and post-chill sampling locations, there was not a significant relationship between the magnitude of the reduction in E. coli and the magnitude of the reduction in Campylobacter at the flock level.
Conclusions: Generic E. coli may provide some indication of the overall effectiveness of processing interventions but it is not a suitable surrogate for estimating the magnitude of reductions in Campylobacter spp. at the individual flock level.
Relevance: These results have implications for routine monitoring of pathogen control programs during poultry processing.

P054

Process control to prevent beef contamination with non-O157 Shiga toxigenic Escherichia coli (STEC) in abattoirs in Mexico and Central America

Byron Chaves[1], Alejandro Echeverry[1], Mark Miller[1], Nelson Huerta-Leidenz[2], Maria Rubio[3], Rosa Ramirez[4], Gilberto Ordaz[4], Lyda Garcia[5], Ansen Pond[6], Todd Brashears[1], **Mindy Brashears**[1], [1]Texas Tech Unviersity, Lubbock, TX, [2]U.S Meat Export Federation-Mexico, Mexico D.F, Mexico; [3]Universidad Nacional Autonoma de Mexico, Mexico D.F, Mexico; [4]Universidad Autonoma de Yucatan, Merida, Mexico; [5]The Ohio State Unviersity, Columbus, OH, [6]Darling International, Des Moines, IA, Contact: mindy.brashears@ttu.edu

Purpose: To estimate the prevalence of non-O157 STEC on beef hides and carcasses and to evaluate in-plant strategies for the control of STEC bacteria in abattoirs in Latin America
Methods:Hides and carcasses were paired and followed through production. Sponge samples were collected on the foreshank area on hides, pre-evisceration carcasses, and carcasses after the final decontamination with lactic or peroxyacetic acid. The BAX® PCR platform was used to determine the presence of molecular markers for the target non-O157 STEC.
Results: STEC were present on hide, pre-evisceration and post-intervention samples collected at two non-TIF facilities in Mexico in 97, 74 and 68% (n=195) and in 100, 100, and 75% (n=60), respectively, whereas a TIF plant revealed 100, 50, and 0% prevalence (n=90) during the same period. In Honduras and Nicaragua (n=80), the prevalence of STEC markers ranged from 23 to 90% on hides and from 0 to 7% in pre-eviscerated carcasses. No STEC were found after application of a 2.5% lactic acid carcass spray. Lastly, in three plants in Costa Rica, a seasonal difference was observed for the prevalence of STEC on hides, ranging from 27 to 97% (n=180). Pre-eviscerated carcasses were contaminated at rates between 27 and 77%, and no carcasses were positive after the application of a 180-220 ppm peroxyacetic final acid spray.
Conclusions: The data demonstrate that hides are heavily contaminated and may be a major point of STEC entrance into the meat supply. However, control measures in some facilities prevented significant contamination of dressed carcasses, ensuring a safe product.
Relevance: Our data show that facilities have different capabilities to control STEC on dressed carcasses. High prevalence values estimated on dressed carcasses in non-TIF facilities in Mexico warrant further studies and the implementation of better control strategies to protect public health.

P055

Prevalence, distribution and seasonality of Shiga toxin-producing Escherichia coli (STEC) O157 and non-O157 in feces of commercial feedlot cattle in USA.

Natalia Cernicchiaro, Charley Cull, Diana Dewsbury, Lance Noll, Pragathi Shridhar, T.G. Nagaraja, David Renter, Kansas State University, Manhattan, KS, Contact: cernicn@gmail.com

Although there has been extensive research on STEC O157 in cattle, information on the frequency, distribution and seasonality of STEC non-O157 in the cattle reservoir and their production environment is limited. The objective of this study was to determine variability in feedlot- and pen-level prevalence as well as seasonal effects of seven STEC serogroups (O26, O45, O103, O111, O121, O145, and O157) and their associated virulence genes (stx1 and/or stx2, and eae) in feces from commercial feedlot cattle in the United States. To evaluate prevalence and seasonality, 24 pen-floor fecal samples were collected from each of 24 pens of ready-to-harvest cattle, in both summer 2013 and winter 2014, at a commercial feedlot. To assess differences in distribution, eight commercial feedlots in Nebraska and Texas were sampled in summer 2014. Up to 16 pen-floor fecal samples were collected from each of 4 to 6 pens per feedlot, per visit, for a total of three visits. Fecal samples were subjected to culture- and molecular-based detection methods. Generalized linear mixed models were used to estimate prevalence accounting for the hierarchical structure of the study. Model-adjusted sample-level prevalence estimates of STEC O26, O103, O145, and O157 during summer 2013 were 1.0, 1.6, 0.8, and 41.4%, respectively. Serogroups O26, O45, O103, and O121 were isolated from cattle feces in winter but no virulence genes of interest were detected. In summer 2014, all study feedlots and 23.0% of pens tested positive for STEC non-O157, whereas sample-level prevalence estimates ranged from 0.0% for STEC O121 to 18.7% for STEC O157. Although statistically significant ($P < 0.05$) seasonal differences in the prevalence of STEC O103 and O157 were found, STEC non-O157 were rarely detected in cattle feces tested in summer, and STEC isolates were not identified in winter months. No differences were found in prevalence estimates between states, however most of the variability occurred within pens. Prevalence estimates at different hierarchical, geographical and seasonal levels provide a much needed microbiological foundation for risk assessment models of STEC and other foodborne pathogens along the beef chain.

P056

Presence of Salmonella in retail meats collected in Mexico

Byron Chaves[1], **Alejandro Echeverry**[1], Ansen Pond[2], Shanna Motl[3], Martha Maradiaga[1], Lyda Garcia[4], Mark Miller[1], Mindy Brashears[1], [1]Texas Tech Unviersity, Lubbock, TX, [2]Darling International, Des Moines, IA, [3]Tyson Foods, Inc., Springdale, AR, [4]The Ohio State Unviersity, Columbus, OH, Contact: alejandro.echeverry@ttu.edu

Purpose: To estimate the prevalence of Salmonella in retail raw beef and pork products in Mexico

Methods: Between 2009 and 2013, a total of 2567 beef and 466 pork samples were collected in Cancun (n=456), Guadalajara (n=318), Merida (n=526), Mexico City (n=786), Monterrey (n=379), and Veracruz (n=568). Samples were collected in open city markets (CM, n=1697), and supermarkets (SM, n=1336). Samples were transported back to Texas Tech University for analysis for Salmonella presence via BAX® PCR platform. Isolates were obtained from BAX® positive samples.

Results: The overall prevalence of Salmonella in beef and pork products was 14.4% (370/2567) and 9.7% (45/466), respectively. Samples collected in CM were more frequently contaminated (4.2%, 407/1697) than those collected at SM (0.6%, 8/1336). Prevalence of Salmonella in ground pork (GP, 13.9%, 20/144) was higher than in whole pork (WP, 7.5%, 24/322). In the case of beef, 15.1% (353/2334) of whole products (WB) contained Salmonella compared to 7.3% (17/233) of ground products (GB). Salmonella prevalence remained constantly low in SM. However, values varied greatly in CM across cities. Salmonella presence in WB ranged from 1.2% (2/171) in Monterrey to 67.3% (169/251) in Merida. In GB, values ranged from 0% (0/74) in Monterrey to 40% (12/30) in Guadalajara. Salmonella prevalence in WP and GP varied between 0 and 30%, being lowest in Monterrey and highest in Guadalajara for both types of products.

Conclusions: The prevalence of Salmonella in retail beef and pork throughout Mexico varies. Samples collected in SM contained Salmonella at a prevalence value similar to that of the US. Samples collected in CM presented a much higher prevalence likely due to the lack of adequate refrigeration and the fact that most samples come from non-TIF inspected facilities.
Relevance: Our data show that there is a need for food safety education for meat handlers in city markets. Basic sanitation measures need to be implemented at municipal abattoirs, during transportation, and retail handling in order to decrease the prevalence of Salmonella.

P057

Challenges associated with validation of heat treatment processes used in pet food and pet treats to eliminate *Salmonella*

Amy R. Parks, Mark F. Miller, Lacey M. Guillen, Kathleen G. Fermin, Alejandro Echeverry, Mindy M. Brashears, Texas Tech University, Lubbock, TX, Contact: amy.parks@ttu.edu

Purpose:
Since 2014, there have been 11 *Salmonella* associated recalls in pet food and treats in the United States. Additionally, *S.* Infantis in dry dog food resulted in an outbreak with 49 individuals sickened. With the proposed Food Safety Modernization Act, pet food and treat producers will have to implement hazard analysis and risk-based preventive controls including the validation of current processes against pathogens like *Salmonella*. The objective was to validate multiple heat treatment processes to reduce *Salmonella* in pet food and treats.

Methods:
To validate, product (kibble, jerky, bones) was obtained from pet food facilities and inoculated with a *Salmonella* cocktail at approximately 7 log cfu/ml. The products were subjected to standard processing conditions (cooking, smoking or drying) in a pathogen processing laboratory. Samples were collected over time and plated for *Salmonella* survival. When samples were below the enumeration limit, they were subjected to pre-enrichment and isolation methods.

Results:
Each heat treatment resulted in a significant ($p < 0.05$) reduction in *Salmonella*. It is critical to not only achieve a significant reduction, but also a 7 log reduction with no residual surviving cells. While most treatments achieved the 7 log reduction, many processes resulted in survivors below the enumeration limit.

Conclusions:
It is essential that moist heat be applied at the beginning of the processes to ensure the destruction of *Salmonella*. Heat cycles with high humidity for longer times at the beginning of the cycle resulted in greater reduction with no residual survivors, while those without moist heat were more likely to have residual *Salmonella* survivors even for extended heat cycles. We have observed frequently that while a 7-log reduction may be achieved, *Salmonella* can survive in pet products. Post processing validation is crucial and a secondary control measure may be implemented to ensure complete destruction of the pathogen.

Relevance:
These data have an impact on the pet food industry and provide increased knowledge about *Salmonella* destruction in commonly used processes, which can lead to a reduction in *Salmonella* associated pet food recalls and outbreaks.

P058

Maet and meat products as a risk factor for food safety and imapct on public health

Marina Pavlak[1], Barica Rašić[2], Lidija Kozačinski[3], [1]Faculty of Veterinary Medicine , University of Zagreb, Zagreb,, Croatia; [2]Veterinary ambulance, Oriovet d.o.o., Lužani, Croatia; [3]Faculty of Veterinary Medicine , University of Zagreb, Zagreb,, Croatia. Contact: marina.pavlak@vef.hr

Purpose: The main objective of this study was to estimate the prevalence of pathogens in meat and meat products, to analyse some groups of foods as a risk for public health in order to assess the need for the organization and implementation of the food safety management.
Methods: At the Department of Hygiene, Technology and Food Safety of the Faculty of Veterinary Medicine University of Zagreb, 669 samples of meat and meat products (176 samples of fresh meat, 493 samples of sausages and cured meats) collected under official control and veterinary inspection procedures in Zagreb County were analyzed. Risk assessment was calculated using odds ratio and significant differences were made by logistic regression analysis at the level of 95% confidence interval.
Results: Meat and meat products were microbiological positive in 15,25 %. Odds ratio between fresh meat and meat products was 1,41 (CI 95% od 0,9 do 2,23) and between cured meat and sausages 2,24 (CI 95% od 1,21 do 4,16) (P<0,05). The highest number of isolated bacteria in fresh meat was related to the Staphylococcus. aureus (7,39%), aerobic mesophilic bacteria (5,68%), *Enterobacteriaceae* (5,11%) and *Salmonella* spp. (5,68%). In the meat products significantly highest number of isolated bacteria was related to the aerobic mesophilic bacteria (6,69 %), enterobacteria (5,27 %) and S. aureus (4,93 %). Exposure to an increased number of aerobic bacteria was 4.14 times higher in sausages than in other meat products.
Conclusions: According to market risk assessment, the most public food risk was exposition to the chicken meat. The exposure to the not-healthy chicken meat was 6,22 (CI 95 % od 1,34 do 29,01) times higher than to the beaf and 3,08 (CI 95 % od 0,67 do 14,11) times higher than to the pork (P<0,05).
Relevance: Food safety risk assessment is still one of the most important epidemiological activities in the field of public health, aiming to consumer protection and developing to food safety management which will reduce the risk and thus contribute to better customer protection.

P059

Global Transcriptome Analysis of Lactobacillus animalis NP51 exposed at different Temperatures

Diana I. Ayala, Kendra Nightingale, Mindy Brashears, Texas Tech University, Lubbock, TX, Contact: diana.ayala@ttu.edu

Lactobacillus animalis NP51 is a bacterium of interest in food industry because of its ability to inhibit foodborne pathogens and spoilage. The addition of this microorganism as probiotic to animal feed is generally recognized as safe (GRAS) for use in cattle. The aim of this study was to use RNA-seq to determine the transcriptional profile of Lactobacillus animalis NP51 at different temperatures 25°C (environment temperature), 39°C (host temperature-bovine), and 45°C (animal feed temperature). The bacterial strain was grown overnight at 37°C for 18h; overnight cultures were diluted into fresh medium and incubated at 25, 39, and 45°C until mid-logarithmic phase was reached. Total RNA extracted from two biological replicates of each temperature was rRNA depleted; individually bar-coded RNA-Seq libraries were prepared and sequenced on a MiSeq instrument. Raw data sets were assembled using de novo assembly. DNAStar Array Star software was used to analyze transcript levels. To obtain the quantitative amounts of expression, host temperature was set up as control. By comparing 25°C to the control, 572 genes were identified as differentially expressed, 488 genes showed reduced expression while 84 increased expression. At 45°C, 54 genes were differentially expressed, 23 showed reduced expression and 31 showed increased expression. The differentially expressed genes at both temperatures include the down-regulation of PTS gene expression, used for the uptake of carbohydrates; the late competence protein ComGA required for the competence-related block in chromosome replication, and the upregulation of the EmrE multidrug resistance protein. This study provides important information about the transcriptional differences of Lactobacillus animalis NP51 at low and high temperatures providing the basis for the characterization of genes with a potential role in the inhibition of foodborne pathogens.

P060

Preliminary investigation of Campylobacter in ground beef at retail

Katelyn A. Ortega, Guy H. Loneragan, Paden M. Ortega, Lacey S. Guillen, Kendra Nightingale, Jessie L. Vipham, Mindy M. Brashears, Texas Tech University, Lubbock, TX, Contact: katelyn.ortega@ttu.edu

PURPOSE:
Determine a baseline prevalence for resistant and susceptible *Campylobacter* in retail ground beef in Lubbock, Texas during the spring 2013.
METHODS
A total of 178 ground beef samples were collected in the spring of 2013 across 7 stores in Lubbock, Texas. Samples were enriched, incubated, and screened for the presence of *C. coli, C. jejuni* and *C. lari* using a commercially available, closed-platform real-time PCR. All enrichments were plated onto selective and differential media and up to three colonies with morphological characteristics of *Campylobacter* were confirmed by agglutination. *Campylobacter* isolates were collected and subjected to micro-broth dilution assays to determine minimum-inhibitory concentrations to a panel of antimicrobial drugs, based on clinical breakpoints. Resistant isolates were subjected to speciation using a commercially available, closed-platform real-time PCR.
RESULTS
Campylobacter was isolated from 30.54% (n=54) of 178 raw ground beef samples collected at retail. A total of 162 isolates from 54 positive samples were preserved for further characterization, and 54.34% (n=88) were successfully recovered from frozen stocks. *Campylobacter* isolates showed resistance to specific antibiotics as follows: 4.54% (n=4), ciprofloxacin; 77.3% (n=68), erythromycin; 14.7% (n=13), gentamicin; and 4.54% (n=4), tetracycline. Out of the 88 isolates recovered, 4 were speciated as *C. coli*. The remaining isolates were undetermined species of *Campylobacter*.
CONCLUSION
A high prevalence of antibiotic resistant *Campylobacter* was observed in raw ground beef. Although the *Campylobacter* that appeared here may not contribute to public health burden, there is potential for transfer of erythromycin resistance transfer to *Campylobacter* that cause disease.
RELEVANCE
Campylobacter is considered the most common cause of gastroenteritis attributed to bacteria worldwide. *Campylobacter jejuni* is responsible for the 90% of illness, while *C. coli* causes 5% to 14% of illness. Studies have shown that antibiotic resistance in *Campylobacter* is becoming more common. It is important to consider the amount of antibiotic resistant pathogens are present at the retail level.

P061

Antibiotic resistant Escherichia coli O157 isolated from cattle

Alexandra Calle, Alejandra Ramirez, Mindy Brashears, Texas Tech University, Lubbock, TX, Contact: alexandra.calle@ttu.edu

BACKGROUND
E. coli O157 is a foodborne pathogen responsible for causing illness with symptoms such as diarrhea, hemorrhagic colitis, and life-threatening Hemolytic Uremic Syndrome. Much focus has been put into mechanisms of detection; however, more understanding about the nature of the pathogen is required. Antibiotic resistant strains have been increasingly reported, which creates a public health concern particularly for the treatment of the illness at early stage.
OBJECTIVE
To identify the prevalence of antibiotic resistant strains of *E. coli* O157 isolated from cattle.
METHODS
Detection and isolation of *E. coli* O157 was conducted on hide swabs samples collected from cattle. A total of about 1,428 isolates were recovered and out of those, 100 were randomly selected for minimum inhibitory concentration analysis of antimicrobials (Sensititre^{TM} automated system). The statistical software R was used to establish proportions and to determine statistical differences among antibiotics.
RESULTS
Results of 47 isolates indicate that 13% of the *E. coli* O157 strains expressed resistance to 6 of the 14 antibiotics analyzed (50% to chloramphenicol, 50% to tetracycline, 17% to cefoxitin, 33% to amoxicillin, 67% to sulfisoxazole, and 33% to ampicillin). From the resistant strains 67% were multidrug resistant as follows: 2 strains resistant to 4 antibiotics, 1 strain resistant to 3 antibiotics, and 1 strain resistant to 2 antibiotics. Significant difference ($P \leq 0.05$) among antibiotics was found.
CONCLUSIONS
Findings of this study reveal the prevalence of multidrug resistance *E. coli* O157 strains isolated from cattle, which raises food safety concern.
RELEVANCE
Little attention has been given to research antibiotic susceptibility for *E. coli* O157. Identifying the prevalence of resistant foodborne pathogens to antimicrobials provides better insights into cautiously selecting antibiotics for animal health.

P062

Contribution to quality of health surveillance service in foodborne diseases outbreaks in Mato Grosso do Sul state, Brazil

Natalia Trindade Azevedo-Marques[1], Rani Kleine Farias Baleroni[1], Jane Soila Domingues[2], Vitória Machado Neres[1], Gabriela Tjhio César Pestana Barros[1], **Juliana Arena Galhardo**[1], [1]Universidade Federal de Mato Grosso do Sul, Campo Grande-MS, Brazil; [2]Secretaria de Estado de Saúde de Mato Grosso do Sul, Campo Grande-MS, Brazil. Contact: juliana.galhardo@ufms.br

Purpose: To contribute to the study of the foodborne diseases in Mato Grosso do Sul state and the quality of health surveillance service, were analyzed the reports resulting from foodborne outbreaks investigations carried out by the State Health Surveillance / State Secretariat of Health of Mato Grosso do Sul.
Methods: All the reports recorded from January 2009 to October 2012 were analyzed and the main variables considered were the place of preparation or ingestion, the food type, the microorganism isolated and the municipalities involved.
Results: During this period 74 outbreaks have been reported and the resolution of most outbreaks occurred through epidemiological criteria, without success in the determination of food involved or etiology. It was not possible to determine the number of exposed and affected people in outbreaks. The households presented 31.08% of the places, followed by restaurants (22.97%). From the outbreaks it was collected 204 samples of food for microbiological analysis and the main categories of food were red meat and ready-to-eat dish, collected in 37 outbreaks each, and cereals, collected in 30. About the microorganisms, there were 44 isolates, *Escherichia coli* and thermotolerant coliforms in 56.8%, *Staphylococcus aureus* in 29.5% and *Salmonella* spp. in 13.6%. Of the 79 existent municipalities in the state, only 24 had outbreaks notifications, 43.24% in Campo Grande, the state capital, followed by Três Lagoas city (9.45%).
Conclusions: Foodborne outbreaks in Mato Grosso do Sul might be undernotified. It is necessary to improve the investigation methodology, including the size of the outbreaks, analysis of patients samples and searching for toxins. Information on food handling practices is critical, including the correct hand washing, whereas microorganisms are likely to have the handler as the source of infection. The notification must be popularized, because as a cultural habit people seek medical care when presenting persistent gastroenteritis symptoms.
Relevance: In Mato Grosso do Sul aspects related to foodborne diseases are largely unexplored, requiring studies regarding factors involved in outbreaks and the quality of the health service.

P063

Salmonella numbers, serotypes, and antimicrobial resistance on raw poultry in emerging market countries (China, Colombia, Guatemala, Russia, and Vietnam)

WALID ALALI[1], Bowei Yang[2], Pilar Donado[3], Yen Ta[4], Roman Gaidashov[5], Claudia Jarquin[6], Isabel Walls[7], Michael P. Doyle[1], [1]University of Georgia, Griffin, GA, [2]Northwest A&F University, Yangling, China; [3]Colombian Corporation of Agricultural Research, Bogota, Colombia; [4]National Institute for Food Control, Ha Noi, Viet Nam; [5]Consumer Rights Protection Society, Moscow, Russian Federation; [6]Universidad del Valle de Guatemala, Guatemala City, Guatemala; [7]National Institution of Food and Agriculture, Washington, DC, Contact: walali@uga.edu

Introduction: Data collection on *Salmonella* levels on raw poultry in developing countries will increase the knowledge on how to protect the global food supply and enhance food safety data collection, surveillance programs, and risk assessment at the local level.
Objective: The project goal was to determine the numbers, serotypes, and antimicrobial resistance profiles of *Salmonella* isolates on raw poultry in various emerging market countries (China, Colombia, Guatemala, Russia and Vietnam).
Methods: Whole chicken carcasses (n=300/country) were collected from retail markets (large, small, and wet markets), over a wide geographical range in these countries. *Salmonella* presence and numbers were assessed following United States Department of Agriculture- Food Safety Inspection Service (USDA-FSIS) protocols. Subsets of *Salmonella* isolates were serotyped and tested for antimicrobial susceptibility for a number of medical and veterinary important drugs.
Results: The prevalence and numbers (mean $\log_{10}$/carcass) of *Salmonella* in China, Colombia, Guatemala, Russia and Vietnam were (43%, 0.74), (37%, 0.78), (34%, 2.3), (51%, 1.2), and (49%, 0.98), respectively. Most frequently detected serotypes were *S*. Enteritidis (19%) in China, *S*. Paratyphi B (45%) in Colombia and (35%) in Guatemala, and *S*. Infantis (72%) in Russia. Multi-drug resistant (≥3 drugs) *Salmonella* were detected in 89% (n=671) of isolates in China, 79% (n=378) in Colombia, 74% (n=73) in Guatemala, 94% (n=153) in Russia, and 43% (n=457) in Vietnam. In general, chickens produced by non-integrated poultry company (vs. integrated) and stored at ambient temperature (vs. refrigerated or frozen) had significantly higher levels of *Salmonella*.
Conclusion and significance: Although most of *Salmonella* numbers do not appear to be high compared to USDA-FSIS 2008 data (mean $\log_{10}$ MPN=1.8), small percentages of chicken samples carried high numbers (3-4 logs). Moreover, *Salmonella* prevalence in these countries was relatively high (compared to 6% in U.S.-FSIS 2012 data). These data may be helpful in developing risk assessment models and preventing the transmission of foodborne *Salmonella* from poultry to humans.

P064

Risk assessment modeling of seven major serogroups of Shiga toxin-producing Escherichia coli (STEC) in the beef production chain.

Pius S. Ekong[1], Michael Sanderson[1], Samson Zhilyaev[2], Daniel L. Gallagher[2], [1]Kansas State University, Manhattan, KS, [2]Virginia Polytechnic Institute and State University, Blacksburg, VA, Contact: sandersn@vet.k-state.edu

Purpose

Shiga-toxin producing E. coli are foodborne pathogens with an important reservoir in cattle. They are responsible for an estimated 175,000 illnesses, 20 deaths and more than $1 billion in direct and indirect illness costs each year in the U.S. The aim of this study is to develop a farm-to-fork risk assessment of the public health threat of seven serogroups of STEC - O26, O45, O103, O111, O121, O145, and O157 - (known as STEC-7) in the beef production chain.

Methods

This application is programmed in R 3.1 as a second order Monte Carlo model that simultaneously simulates variability and uncertainty for STEC-7 prevalence and concentrations through a series of steps: pre-harvest, post-harvest, retail, and consumption. The model is parameterized from ongoing targeted research and from systematic review and meta-analysis of published literature. The model accounts for cattle types, seasonal variation in levels of STEC-7, and on-farm control strategies such as vaccination and direct-fed microbials. Furthermore, the model simulates different processing plant sizes and interventions employed at various stages in the slaughtering process, consumer handling, including STEC-7 growth during storage, reductions through cooking and serving size effects. Intact, ground and mechanically tenderized product risk is estimated.

Results

Final model output is an uncertainty distribution of the risk of illness per serving for each STEC-7 strain and beef product simulated. Intermediate results include carcass contamination levels which can be simulated specific to pre-harvest and harvest interventions.

Conclusions, Relevance

Expected outcomes from the model include: (1) A valid, flexible farm-to-fork probabilistic STEC-7 quantitative risk assessment that integrates prevalence and concentration changes from live cattle to consumer consumption to inform policy implementation. (2) An epidemiologically informed intervention strategy for diverse sized plants that minimizes public health risk across all STEC-7 simultaneously. (3) Identification of STEC-7 data gaps and uncertainties to guide future needed research.

P065

A Stochastic Assessment of the Public Health Risks of Fluoroquinolone Resistance Campylobacter and the Use of the Drug in Broiler Production in Japan

Hajime Toyofuku[1], **Kohei Makita**[2], Yuko Osada[3], Takeo Oohashi[4], Michiru Kakinuma[4], Daihi Oushiki[3], [1]Yamaguchi University, Yamaguchi, Japan; [2]Rakuno Gakuen University, Ebetsu, Japan; [3]MRI Research Associates, Inc., Tokyo, Japan; [4]Mitsubishi Research Institute, Inc., Tokyo, Japan. Contact: kmakita@rakuno.ac.jp

Purpose:
Antimicrobial resistance (AMR) is a major global public health and a food safety issue. Risk analysis is an essential tool in assessing the risk to human health from foodborne AMR microorganisms and determining appropriate risk management strategies to control those risks. Although quantitative risk assessments are encouraged and have been performed in some EU countries and the US, so far only qualitative risk assessments are performed in Japan. This project was commissioned by the Japan Food Safety Commission in the context of its programme to develop a quantitative risk assessment, with Campylobacter in broiler and use of fluoroquinolone (FQ) for broiler production as an example.
Methods:
The risk assessment model was subdivided into the release, exposure, and consequence assessment sections. In the release section, FQ resistance mechanism and data from Japanese Veterinary Antimicrobial Resistance Monitoring Program were utilized for the model development.
The model output was percentage of FQ resistance Campylobacter (FRC) among broiler borne human campylobacteriosis. In order to take uncertainties in the data into account, the model was built, and simulations were performed using @Risk 4.5 (Palisade Corp.) .
Results:
The average percentage of broilers infected with FRC was estimated to be 34.0%. Among FRC strains, 10.4% carried a mutation at Thr86Ile of gyrA with overexpression producing strains of efflux pump, 20.8% carried a same mutation of gyrA with low expression producing strains of efflux pump, and 2.8% carried a mutation of GyrA other places than Thr86Ile. The estimated that an average and the maximum annual number of Campylobacter infections per person were 1.02, and 88 times, respectively.
Conclusions:
In the maximum (88 infections per year) scenario, the patient is estimated to be infected with FRC 30 times, and 28 times out of 30 times, he or she is estimated to be infected with Campylobacter with a mutation of Thr86Ile of GyrA.
Relevance:
By using this model, use of FQ in the farm and the effect on the percentage of FRC in broilers was not identified. We couldn't find any adverse human health effects associated with FRC strains.

P066

Risk categorization in the context of a porcine reproductive and respiratory syndrome (PRRS) regional control program: preliminary results

Alberto Allepuz[1], Gerard Martin[2], Gabriel Quero[3], Jordi Casal[1], Enric Mateu[1], [1]CReSA / UAB, Barcelona, Spain; [2]CReSA, Barcelona, Spain; [3]UAB, Barcelona, Spain. Contact: alberto.allepuz@uab.cat

Purpose:
A pilot program of voluntary zonal control of PRRS is being initiated in selected areas of Spain. Within this context a semi-quantitative risk analysis was done in order to estimate the risk of having an external introduction or an internal re-circulation of PRRS virus.
Methods:
Depending on the characteristics of a farm, the risk of introduction or re-circulation of PRRS virus varies. This initial risk would be reduced by the application of external and internal biosecurity measures. Within the frame of a pilot control program a 139-question survey was performed in farms (n=80) in order to obtain data related with the different biosecurity measures applied. These measures included those related to purchase of animals and semen, location, transport vehicles and visits (i.e. external biosecurity) and to management practices, facilities cleaning and disinfection and employees routines (i.e. internal biosecurity). In order to estimate the initial risk posed by the purchase of animals and semen, neighborhood, vehicles and visits along with the importance of the different biosecurity measures, the 'expert opinion' methodology was applied. For this purpose different veterinarians and researchers actively involved in PRRS control activities were asked to quantify the different factors both for assessing the initial risk and the potential risk reduction.
Results:
According to the experts, exclusive personnel for the quarantine, a fence around the farm, delimited clean and dirty areas in the animal loading dock and the use of clothes and boots provided by the farm were the most relevant external biosecurity measures. All-in-all out management in weaning units, adequate disinfection practices and biosecurity training of new workers were considered the most relevant internal biosecurity measures.
Conclusions and relevance
The next step will be to estimate the final risk, taking into account the uncertainty associated with the expert opinion procedure by Monte Carlo simulations. By using this methodology we will be able to rank farms in relation to their risk of introduction or recirculation. This information might be useful for PRRS control.

P067

Identification of risk factors for human brucellosis in smallholder farms in Pakistan

Shumaila Arif[1], Marta Hernandez Jover[1], David McGill[1], Peter C. Thomson[2], Hassan Mahmood Warriach[3], Khizar Hayat[3], Mudassir Ahmad[3], Jane Heller[1], [1]Charles Sturt University, WAGGA WAGGA NSW 2678, Australia; [2]The University of Sydney, 425 Werombi Road, Camden NSW 2570 Australia, Australia; [3]University of Veterinary & Animal Sciences, Lahore Pakistan, 54000 Lahore Pakistan, Pakistan. Contact: sarif@csu.edu.au

Brucellosis is considered by the Food and Agriculture Organization, the World Health Organization and the OIE as one of the most widespread zoonoses in the world, and is still endemic in many developing countries including Pakistan. In Pakistan brucellosis is a neglected disease and is still prevalent at a very high rate due to lack of public awareness and preventive measures.
The aim of this study was to investigate current practice in terms of herd management and household practices that may act as risk factors for brucellosis transmission from cattle to humans in smallholder dairy farms. A cross-sectional study among smallholder farms (n=240) was conducted in the four districts of Punjab province. A questionnaire to measure the risk factors presence was designed and used during face-to-face interviews. A combination of purposive and random sampling was used to select the participant smallholder farms.

Regarding potential risk factors, results from the questionnaire to date indicate that 14% of farms had cattle abortions in the last year, with 9% being in the last trimester, almost a third of farmers reported retained foetal membranes, and 17% reported having animals on the farm with a history of retained placenta. In relation to herd management practices, most participants reported calving space being shared with other animals, half reported introducing new animals and over 60% slaughtering animals at the farm. Only 35% of farmers properly dispose placental membranes by burring, with most disposing them in dung piles or feeding them to other animals. In addition animals are being sampled to estimate the prevalence and result are in processing.

To assess zoonoses the following household practices were addressed: farmers who think they can get disease from animals (32%), farmer families using raw milk (53%) and its products (63%), living in shared place with animals (43%) and farmers that do not cover hand cuts during contact with animals (80%).
In conclusion, results from this study suggest there is a need to estimate the true prevalence of disease in the area and educate the farmer via participatory epidemiology about the risky farm practices and their preventive measures.

P068

Development and implementation of a biosecurity framework plan for the shrimp industry of Honduras

Alejandro Echeverry, Mark F. Miller, Leslie Thompson, Mindy M. Brashears, Texas Tech University, Lubbock, TX, Contact: alejandro.echeverry@ttu.edu

Purpose: The implementation of practical approaches and biosecurity measures to prevent, control, and eradicate disease is of critical importance for economies to protect farms from diseases that could have a devastating consequences on an aquatic agricultural system, all while complying with all the sanitary and phytosanitary (SPS) measures. An emerging disease in shrimp, first identified is Southwest Asia in 2009, and described under the name early mortality syndrome (EMS) (later known as acute hepatopancreatic necrosis syndrome (AHPNS)) caused by a strain of Vibrio parahaemolyticus) created concerns for the shrimp production farms in Latin America when a significant decrease in shrimp production occurred in Mexico due to an outbreak of EMS/AHPNS, leading producers, and government agencies in Honduras to request assistance to improve biosecurity. The purpose of this study was to develop an effective control program that served as a framework to educate personnel and to implement changes in management systems to reduce the risk of introduction and spread of EMS/AHPNS to shrimp farms and processing facilities.
Methods: To develop an appropriate, targeted biosecurity plan, separate visits and audits were conducted to one of the major shrimp farms in the western hemisphere located in Honduras. Recommendations based on the World Organization for Animal Health (OIE) were included in this comprehensive plan.
Results: General plans at the farm, local, and national level were developed that included sections in management, engineering, plant design, health assurance, monitoring and contingency approaches to prevent introduction of diseases.
Conclusions: A biosecurity plan to prevent the introduction and spread of disease causing organisms in an environment usually has to be disease-specific; however, due to the novelty of EMS/AHPNS, diagnostics weren't available at the time of development and were not included in the plan.
Relevance: Follow up visits demonstrated commitment from governmental agencies and quick implementation of control measures in the farms and processing facilities located in Honduras, with no problems with EMS/AHPNS in the facilities reported to date.

P069

Surveillance of milk delivery data for detecting outbreaks of bovine coronavirus - a case study

Nils Fall[1], Caroline Carlström[2], Anna Ohlson[3], Ulf Emanuelson[1], [1]Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]Swedish University of Agricultural Sciences, Uppsala, Sweden; [3]Växa AB, Stockholm, Sweden. Contact: nils.fall@slu.se

Purpose

Infections with bovine coronavirus (BoCV) are endemic to the cattle populations in most countries, causing respiratory and/or enteric disease. In affected dairy cattle herds, milk production has been reported to be affected with significant economic losses.

The infection is highly contagious, but spread between herds can be handled through biosecurity. In order to implement necessary biosecurity measures as early as possible in an affected region, an early warning system would be useful. Our aim was to investigate if milk volume and concentration of bulk tank milk components from regular herd milk deliveries could be used to identify an outbreak of BoCV.

Methods

Seroprevalence of BoCV was monitored in a dairy herd by annual testing of primiparous cows for BoCV serology in milk. Four primiparous dairy cows were sampled each year as an indicator of a recent infection in the herd. After infection animals will remain seropositive for several years. When primiparous, homebred, cows are sampled the results will thus give an accurate description of the recent BoCV history of the herd, corresponding to the life-span of the tested cows.

Results

We observed that sero-conversion had occurred during the period from June 2012 and May 2013. Data on all herd milk deliveries to the dairy plant was received from a national database. Patterns in absolute numbers, moving averages and an exponential moving average were compared to elucidate the best way to identify the outbreak in the variables studied.

Conclusions

The variation in milk delivery data was not negligible why moving average or the exponential moving average were preferable to show the outbreak. The delivered milk volume was the best indicator and gave good indication of when the infection occurred.

Relevance

From both the animal welfare perspective and the economy of the dairy industry, an early warning system for BoCV would be useful to decrease the spread of the disease through early measures of biosecurity.

P070

The effect of farm biosecurity on the seroprevalence of BoCV and BRSV

Nils E. W. Fall[1], Anna Ohlson[2], Karin Alvåsen[1], Cecilia Wolff[3], [1]Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]Växa AB, Stockholm, Sweden; [3]Swedish University of Agricultural Sciences, Uppsala, Sweden. Contact: nils.fall@slu.se

Purpose:
Infections with Bovine Respiratory Syncytial Virus (BRSV) and Bovine Corona Virus (BoCV) are endemic to the cattle populations in most countries, causing respiratory and/or enteric disease. It has been demonstrated that herds can remain free from one of or both infections for several years also in high prevalence areas. Hence, we intended to study herd level factors that could influence BoCV and BRSV seroprevalence.
Methods:
We enrolled 144 dairy herds in a prospective longitudinal study. Milk from four home bred primiparous cows was sampled in each herd in November 2011, May 2012, and May 2013. A herd was defined as negative if all four samples were antibody-negative as determined by an indirect ELISA to BRSV or BCoV, respectively. A questionnaire was distributed in 2011 and was supplemented at the subsequent samplings. We tested whether parameters of biosecurity, health, and herd management was different between herds that were antibody negative to both BRSV and BoCV and other herds by the Wilcoxon rank-sum test and the Fisher exact test.
Results:
Antibody-negative herds had a longer distance ($p < 0.05$) to the nearest farm with a median of 2.5 km (interquartile range 2.0, 4.6) compared to 1.5 km for antibody-positive herds (0.65, 2.5). The median number of monthly visits from others than veterinarians or artificial insemination technicians was 0.5 (0, 0.75) for negative and 1.0 (0.5, 2.0) for positive herds. The number of monthly visits from AI technician differed in 2013, with 1.0 (0, 1.0) for negative and 1.0 (1.0, 3.75) for positive herds.
Conclusions:
Although only a few herd characteristics were associated with herd seroprevalence, further studies are needed to elucidate the importance of biosecurity measures in bovine viral infections.
Relevance:
BRSV and BoCV are endemic in cattle populations causing both unnecessary suffering and economic loss. Knowledge on biosecurity is vital to future control of the diseases.

P071

Risk of animal diseases introduction by passengers intercepted with live animals or animal products in the main border controls in Chile during 2008, 2009 and 2010.

Santiago Urcelay, Hamilton-West Christopher, Luis Ibarra, Pedro Abalos, Fabian Lucero, Faculty of Veterinary Medicine and Animal Sciences, University of Chile, Santiago, Chile. Contact: surcelay@uchile.cl

Purpose: The international movement of animals and animal products threat largely the health status of each country, so that the health safeguard to prevent the entry of animal diseases is the basis for the maintenance of animal health at the national level, process which is handled in Chile by the Agriculture and Livestock Service (SAG). Border control of passengers is a wide used strategy to detect any legal or illegal introduction materials which could carry agents producing exotic or endemic diseases. The aim of this work was to determine high-risk border controls in relation to products intercepted from passengers.

Methods: Data recording the interception of animals or animal's products carried by passengers at four main border control complexes in Chile during 2008, 2009 and 2010, were analysed. Border control facilities selected were: Arturo Merino Benítez International Airport (SCL) in Santiago the capital city; Chacalluta Complex (ChC) at the very north of the country and national border with Perú; Libertadores Complex (LiC) at the central Andean region of the country, national border with Argentina; and the Port of Valparaíso (ValP), at the coastal central region. Each border control was characterized according with products intercepted and a five level risk index (IR) for each product was created depending of the kind, quantity, origin, etc., determined by an expert panel. To estimate the risk for each control border facility, four calculations were made: risk units (products measured in units or weight); interception risk (nº of units per interception); cumulated risk units (total of risk interception in a period of time); risk units per passenger.

Results: The method used determined that the SCL airport and the LiC, presented the higher risks, because of the number of passengers and the characteristics of products intersected, respectively.

Conclusions: These results are useful for responsible authorities in order to improve and make better decisions in the border control strategies.

Relevance: The studies should be make continuously to adjust the control border policies.

P072

The development of a web-based data collection and learning platform dealing with biosecurity in Danish dairy cattle

Mikkel B. Svendsen, Liza R. Nielsen, University of Copenhagen, Frederiksberg C, Denmark. Contact: mikkel.svendsen@sund.ku.dk

In Europe there is an increasing demand for improved prevention of infectious diseases in cattle farms, and recently, livestock disease outbreaks and zoonotic infections have been identified as major threats to the Danish society. This requires research into the effect of different on-farm biosecurity measures, which again calls for an evidence-based system for collection of appropriate information on farm-specific biosecurity measures.
A project was recently started up to develop an online data collection and learning platform. The first objective of this study is to investigate biosecurity factors and practices relevant for the evaluation of biosecurity in Danish dairy cattle.
This will be approached by a thorough study of the current knowledge of biosecurity including a systematic literature review combined with synthesis of current knowledge of and experience with biosecurity in dairy cattle farms. Practicing cattle veterinarians, members of The Danish Agriculture & Food Council and other research and administrative institutions both in Denmark and abroad will be consulted and their expertise incorporated in the research. This will, in October this year, result in formulation of a prioritised list of topics, which will be the starting point of a web-based platform (BioSecure). The above-mentioned work will be available for presentation at the conference.
Subsequently, based on the prioritised topics, a questionnaire will be developed that constitutes the data collection part of BioSecure. In order to disseminate knowledge about biosecurity, the material gathered in the first objective will make up an information section in BioSecure that is accessible to anyone. The questionnaire will be applicable to farmers and their responses will be utilized for quantification of on-farm applied biosecurity practices, and analysed against animal health parameters to evaluate the effect of different biosecurity practices and factors.
This evaluation can help in improving the biosecurity level in the Danish dairy cattle sector along with making knowledge about biosecurity easily available for the farmer and for educational purposes in the veterinary curriculum and farming schools.

P073

Farm animal practitioners' thoughts on clinical audit

Katie Waine, Rachel Dean, Chris Hudson, Jon Huxley, Marnie Brennan, University of Nottingham, Loughborough, United Kingdom. Contact: svxkw@nottingham.ac.uk

Purpose

Evaluating the quality of veterinary care provided in practice is important to ensure that high standards are monitored and maintained. Clinical audit has been shown by the medical profession to be a useful tool for assessing and improving clinical standards. The Royal College of Veterinary Surgeons, the governing body of the veterinary profession in the United Kingdom (UK), encourage veterinary surgeons to carry out clinical audit as part of their clinical governance. However, clinical audit is still a relatively new concept and its use remains very varied between businesses in the UK.

Methods

The Centre for Evidence-based Veterinary Medicine at the University of Nottingham approached three farm animal veterinary practices to undertake a clinical audit and to determine some of the challenges and advantages to doing so. Priority setting meetings (PSMs) were held at the individual practices to discuss conducting audit and to choose topics to audit. Twenty-three farm animal veterinary surgeons within the practices were asked to complete a questionnaire asking for their views on the process.

Results

Eighty-three percent (19/23) of the practitioners fully completed the questionnaire. Overall, opinions about clinical audit were very positive. One hundred percent (19/19) of the clinicians agreed that clinical audit could improve standards in farm animal practice while 89% (17/19) thought it could enhance job satisfaction. The main concerns cited were the accuracy of information that may be collected, the time taken to complete the audit and the difficulty of collecting follow up data. The discussions held during the PSMs raised many questions on the logistics of audit, and highlighted potential difficulties and benefits of the audit process for individuals and the practice as a whole.

Conclusion

The veterinary surgeons involved in this study appeared to have a positive view of clinical audit, but there were some concerns about possible barriers that may potentially affect its success in practice.

Relevance

It is vital that the concerns of veterinary surgeons are taken into consideration when trying to determine the most effective way of completing clinical audit in veterinary practice.

P074

MRSA outbreak investigation in pig workers in a pig farm in NSW Australia

Sahibzada Shafiullah, Jane Heller, Marta Hernandez-Jover, Charles Sturt University, Wagga Wagga, Australia. Contact: sshafiullah@csu.edu.au

Methicillin-resistant *Staphylococcus aureus* (MRSA) strain of porcine origin has been well established as potential zoonotic pathogen in Europe and some other parts of the world. However, limited studies to date have assessed carriage of these bacteria among pigs and pig workers in Australia. A recurrent MRSA outbreak in workers in a piggery in NSW affecting a large proportion of employees over a two years period has been reported.

The main focus of this study was to conduct an investigation of this outbreak and to determine potential risk factors for MRSA carriage in piggery workers.

Nasal swabs were collected from all volunteer pig workers at the outbreak sites after completion of a questionnaire that gathered information on their background, work and health history, antibiotic treatment, hygiene, and perception towards development of antibiotic resistance. At the same time samples were collected from pigs at all piggery sites. The piggery included three different sites and each site had five to six sheds, including dry sows, farrowing, weaners, growers and finishers. At each site a total of 240 samples were taken and pooled in pools of 10, which allowed detecting MRSA at a prevalence of 2%, with assumed test sensitivity of 90%. In addition, environmental samples were also collected from all sheds and other shared areas including kitchen, bathrooms and offices.

Samples were pre-enriched in Mueller-Hinton broth containing 6.5% sodium chloride followed by selective-enrichment in Tryptone Soya Broth containing 3.5 mg/L cefoxitin and 75 mg/L aztreonam. Later on a loop full of the selective enriched cultured were inoculated onto chromogenic agar and blood agar respectively. All isolates were cultured and screened for various antibiotic resistances in the laboratory using Clinical and Laboratory Standards Institute methods. Confirmed MRSA isolates were further characterized by staphylococcal protein A (spa) typing, followed by multi-locus sequence typing.

The outcomes of this study will not only help to investigate the current identified MRSA outbreak but also determine associations between farm-level and farmer-level factors of MRSA carriage and infection in piggery workers.

P075

Factors associated with inter-farm spread of porcine epidemic diarrhea (PED) in Kagoshima and Miyazaki Prefectures, Japan

Kohei Makita[1], Haruya Toyomaki[1], Satoshi Sekiguchi[2], Yosuke Sasaki[2], Masuo Sueyoshi[2], [1]Rakuno Gakuen University, Ebetsu, Japan; [2]University of Miyazaki, Miyazaki, Japan. Contact: kmakita@rakuno.ac.jp

Purpose: In October 2013, an outbreak of porcine epidemic diarrhea (PED) was confirmed in Japan. The disease spread countrywide, and more than 400,000 pigs died in total as of March 22, 2015. The present study was conducted to understand the factors having caused such a wide inter-farm spread.
Methods: Kagoshima and Miyazaki Prefectures, the main pig production areas of Japan, were selected as study sites. A spatio-temporal analysis was conducted to detect disease clustering using SaTScan version 9.3.1, selecting week as time unit and Bernoulli model, with anonymized data on farm size, farm types, administrative units, and date of onset provided by both prefectures (709 and 506 farms in Kagoshima and Miyazaki). Univariate and multivariable survival analyses were performed using the data in R version 3.0.2. Separately, a case-control postal survey was conducted on 78 infected (infection confirmed between Dec 2013 and Aug 2014) and 91 non-infected pig farms in Kagoshima and Miyazaki Prefectures for detailed biosecurity measures, and univariate analysis was performed.
Results: Accumulated incidence rate at farm level was 23.6% in Kagoshima and 15.6% in Miyazaki as of July 24, 2014. SaTScan found three disease clusters: Kanoya (16.9km, Dec 3rd 2013 to Feb 13th 2014, Kagoshima), Miyakonojo (one city, radius not calculated, Jan 10th to 30th), and northern Miyazaki (32.4km, Mar 14th to Apr 3rd, Miyazaki). In survival analysis, survivorship was significantly lower (7.5) in integrated farms which have susceptible suckling pigs and visit slaughterhouses, than grow-finisher farms (8.2, $p < 0.01$). In all farm types, there were significant negative associations between survivorship, and farm size and farm density (both $p < 0.01$). Use of two specific abattoirs, use of communal compost depots, and not disinfecting a floor mat of track transporting pig excrement/compost were significant risk factors for PED.
Conclusions: Our study identified two modes of transmission: slaughterhouses (common source infection), and compost management. Cleaning and disinfection associated with these pathways would reduce the chance of PED transmission.
Relevance: This is relevant to infection control.

P076

The effect of calf gender and age of dam on the risk for calves to develop bovine respiratory disease prior to weaning

David R. Smith[1], Ashley Reeves[2], [1]Mississippi State University, Mississippi State, MS, [2]Mississippi State University, Mississippi State, MS, Contact: david.smith@msstate.edu

Purpose:
The objective of this study was to test the relationship between the gender of the calf and odds for developing bovine respiratory disease (BRD) prior to weaning.
Methods:
Health records representing 5,312 calves from 21 cattle management groups within 5 Nebraska beef cattle ranches were analyzed using multilevel multivariable logistic regression in a generalized linear mixed model. Diagnosis of BRD was modeled with explanatory variables of calf gender, birth weight, and age of the dam, with a correlation structure defining clustering of management groups within ranch. The model was built using manual forward selection with significance set at alpha ≤ 0.05. The gender of the calf was recorded for 5,273 calves: 379 bulls, 2568 heifers, and 2326 steers. The age of the dam was recorded for 5,124 calves. Median dam age was 4 years (range 2 to 16, mean 4.3 years).
Results:
Bovine respiratory disease was diagnosed in 910 of 5,281 calves (17.2%). Calf gender and age of the dam were significant explanatory variables in the final model using 5,078 calf records from 4 ranches and 20 management groups (one ranch lacked data on dam age). Adjusting for age of the dam, heifer calves were less likely (OR = 0.83) and bull calves more likely (OR = 1.46) than steers to develop BRD prior to weaning (p=0.01). Adjusting for gender, compared to calves born to cows 4 years or older, calves with two year old dams and 3 year old dams had 1.67 and 1.11 times greater odds for BRD (p=0.0004).
Conclusions:
We concluded that the gender of calves affects their risk for BRD and calves born to dams younger than 4 years of age had greater risk for BRD than older cattle.
Relevance:
The results of this study suggest that there are sex related differences in the risk for calves to develop BRD prior to weaning. The age of the dam is also an important factor explaining calf risk for BRD. This may mean that management strategies to minimize BRD risk should consider factors of calf gender and dam age.

P077

Salmonella Serotype Discrimination of Beef carcasses, lymph nodes and fecal isolates through Pulsed-Field Electrophoresis

Diana I. Ayala[1], Kendra Nightingale[1], Mark Miller[1], Alejandro Echeverry[1], Rosa Ramirez-Porras[2], Gilberto Ordaz[2], Mindy Brashears[1], [1]Texas Tech University, Lubbock, TX, [2]Universidad Autonoma de Yucatan, Merida, Mexico. Contact: diana.ayala@ttu.edu

Salmonella is one of the leading causes of foodborne illnesses worldwide; however, in Latin America, few surveillance programs exist leading to limited information about the prevalence and discrimination of this pathogen in all production steps including pre-harvest, and on final products. Traditional serotyping has been widely used for Salmonella identification; however, its limited discriminatory ability has led to the development of different genotypic-based techniques. Pulsed-field gel electrophoresis (PFGE) is the "gold standard" Salmonella subtyping method and plays a key role in the determination of clonal relatedness among isolates. The aims of this study were to (i) analyze the relationship among serotypes and PFGE banding patterns from beef carcasses, lymph nodes and feedlot fecal isolates collected from abattoirs in Mexico to assess genetic diversity and (ii) determine the transmission dynamics of Salmonella subtypes among carcasses, in an attempt to improve interventions at different points in the food chain. A total of 94 Salmonella isolates from samples collected in one slaughter facility in Mexico were analyzed. In addition, 33 confirmed Salmonella isolates from mandibular, mediastinal, and mesenteric lymph nodes and fecal samples from cattle were molecularly characterized by PFGE. Samples were collected in one slaughter facility in Merida (Yucatan), Mexico at three times (November 2010, March 2012, and June 2012) over a two year period. High concordance (88.4%) was found between PFGE banding subtype and conventional serotype; Salmonella Kentucky was found to be the most clonal subtype, while Salmonella Muenster was the most diverse with 11 banding patterns identified. For the second part of the study, six serotypes were identified, Salmonella Poona was found to be the most common and high diversity was observed among serotypes from lymph nodes and fecal isolates from the same animal. The findings of this study suggest PFGE is a suitable method for serotyping discrimination among Salmonella isolates and reflect the need of improving interventions at different points in the food chain to avoid further Salmonella spread among carcasses.

P078

Population-level effects of risk factors for bovine respiratory disease in Australian beef feedlot cattle.

K. E. Hay[1], J. M. Morton[2], A. C. A. Clements[3], T. J. Mahony[1], T. S. Barnes[4], [1]University of Queensland, St Lucia, Australia; [2]Jemora Pty Ltd, Geelong, Australia; [3]The Australian National University, Canberra, Australia; [4]University of Queensland, Gatton, Australia. Contact: k.hay1@uq.edu.au

Purpose:
Bovine respiratory disease (BRD) is the major cause of clinical disease and mortality in feedlot cattle populations. Numerous risk factors have been associated with BRD. Population attributable fractions (PAFs) for BRD quantify the effects of risk factors on population BRD incidence. The study aimed to identify risk factors with moderate to large population-level effects in Australian feedlots and to quantify the population-level effects of management-related risk factors.

Methods:
The study population comprised 35,131 animals enrolled at induction when animals were identified and data were recorded before being placed into 170 cohorts (feedlot pens) within 14 Australian feedlots over a three year period. PAFs were calculated for risk factors previously determined to be significantly associated with BRD occurrence. Composite variables were created from the covariate patterns of 'background' (animal and environment) and management-related risk factors. The expected effect of removing exposure to these management-related risk factors while leaving exposure to background risk factors unchanged was estimated using a partial PAF.

Results:
The management-related risk factors for BRD with highest PAFs were shared pen water, history of mixing with other cattle, feedlot move timing, bovine viral diarrhoea virus 1 in the cohort, and the number of study animals in the animal's group 13 days before induction. Breed, induction weight, feedlot region and season of induction were the most important background risk factors. The estimated partial PAF for changing animals to the lowest-risk categories of at least four of the five management-related risk factors was 82%.

Conclusions:
Interventions that remove exposure to at least four of the five main management-related risk factors should dramatically reduce the incidence of BRD in Australia's beef feedlot cattle population.

Relevance:
These population-level effect estimates identified highest priority risk factors for research, development and extension programs to reduce BRD incidence in the Australian beef feedlot industry.

P079

Seroprevalence of abortive and chronic wasting diseases in cattle in the Mexican Tropics: I. State of Chiapas.

Juan H. Hernandez-Medrano, Ana D. Rodrigez-Cortez, Hector D. Najera-Rivero, Carlos G. Gutierrez, Faculty of Veterinary Medicine, Mexico City, Mexico. Contact: jheberth@unam.mx

Purpose:
In tropical production systems (TPS) in Mexico, subclinical infectious diseases are thought to be the main cause of low productivity and infertility in cattle1. These systems show low pregnancy rates (~40%) and extended calving intervals (~17 months; Gutierrez et al. unpublished data). Cattle in TPS represent 55% of the national herd2, yet health information is scarce. The aim of this project is to develop a national seroprevalence map for the most important infectious diseases that affect cattle production efficiency. Here we report seroprevalence data, for the southern state of Chiapas.

Methods:
We set out to sample non-vaccinated cattle in farms in all states of the Mexican Tropics that will serve as disease sentinels (n=10-12 animals/farm) and collected nearly 30-thousand individual samples (n= 29,459). ELISA assays (IDEXX) were used to discriminate between seropositive (s+) and seronegative (s-) animals for abortive and chronic wasting diseases, i.e. Bovine Viral Diarrhea BVD), Bovine Herpes Virus-1 (IBR), Bovine Enzootic Leukaemia (BEL) Parainfluenza-3 (PI3) and Neospora caninum (NC).

Results:
For Chiapas, we obtained samples from individual animals (n=2,413) from103 farms throughout the state. Nearly all farms studied had BVD-s+ and IBR-s+ animals (n=93/103 and n=96/103, respectively), with less than 50% of the farms having BEL s+ animals. All farms had PI3-s+ animals; therefore farms were split into 3 groups (high, moderate and low prevalence) depending on absorbance. Most farms (n=78/103) showed moderate presence seropositive animals, while a low number of farms had high (n=1/103) or low (n=9/103) s+ animals. In the case of NC, all but one (n=1/103) farm were s-.

Conclusions:
This is the first report of seroprevalence of several infectious diseases covering an entire estate. The presence of BVD and IBR in almost all farms supports our hypothesis that these diseases directly impact on productive performance in TPS cattle in Mexico.

Relevance:
An epidemiological map will help to set the basis for a targeted disease control strategies in the Mexican TPS to improve reproductive performance.

P080

Exploring the epidemiology of bovine viral diarrhea virus (BVDV) infection in beef suckler herds in two regions of Argentina: genetic variability and diagnostic implications

Maria S. Perez Aguirreburualde[1], Andrea Pecora[2], Alejandra Ferella[2], Florencia Tassara[3], Adriana Torres[3], Maria J. Dus Santos[2], Emilio Leon[1], [1]INTA, Buenos Aires, Argentina; [2]INTA, Buenos Aires, Argentina; [3]Ministry of Agrarian Affairs, Buenos Aires, Argentina. Contact: solperezburu@gmail.com

Bovine Viral Diarrhoea Virus (BVDV) is highly prevalent worldwide and has a detrimental effect on the performance of beef herds. In Argentina a few reports done in the past showed prevalences between 25-90%, also, the presence of genotype 1 and 2 has been reported. In the recent decades, bovine livestock production in Argentina has undergone a remodeling process due to the expansion of land use for crop. This had an impact in marginal territories like Patagonia, where livestock existence had a significant growth, and also in traditional livestock production areas like Humid Pampa, where extensive holdings have been replaced by more intensive ones. This kind of process can have a great effect on the infectious disease dynamic. Purpose: Considering this context and the lack of up to date information, the aim of this study was to assess the prevalence of BVDV in these two regions, and to evaluate the limitations of the techniques available in the country for serological diagnostic. In addition, a survey was completed on each farm to collect information that could be associated as herd-level risk factors for the disease, analyzed by a logistic regression. Methods: Two cross-sectional studies were performed. Samples were gathered from 83(region I) and 100(region II) herds, collecting 15 and 25 samples per herd respectively, making a total of 4575 samples. The samples were evaluated by serum neutralization (SN) for the presence of antibodies against the 3 different genotypes (1a, 1b, and 2). Results: The results obtained show a prevalence of 96.34% (IC: 92.51% - 100.00%) of positive herds. The independent seropositivity against different genotypes tested was analyzed in both regions (1a, 1b,2:64-47-56.5% and 13.4-76.6-10%, respectively). Conclusions: Preliminary results when analyzing the proportions of serologically positive animals against each strain would show a different frequency distribution of genotypes between the two regions. Relevance: These results would reinforce how essential is to have current and robust epidemiological information as a starting point to design rationally control plans for BVDV for any particular region.

P081

Preliminary assessment of acaricide resistance in cattle tick (Rhipicephalus (Boophilus) microplus) populations from the Caribbean island of Martinique

Stéphanie Depraz[1], Manon Hamon[1], Philippe Pelonde[2], Léonore Lovis[3], Lionel Felixine[2], Marie-Claire Timir[2], Christophe Dalibard[4], Robert Miller[5], Adalberto A Pérez de León[6], Linroy Christian[7], Rupert Pegram[8], Vicki Aimey[9], Bethany Bradford[10], Perlinda Dupre-Ryfer[11], Reginald Thomas[12], Brigitte Marie[13], Eva De Clercq[1], Nathalie Vachiery[1], Jennifer Pradel[1], [1]CIRAD, Petit Bourg, Guadeloupe; [2]Groupement de Défense Sanitaire, Lamentin, Martinique; [3]Novartis Centre de Recherche en Santé Animale SA, St-Aubin, Switzerland; [4]Direction de l'Agriculture, de l'Alimentation et de la Forêt, Fort de France, Martinique; [5]USDA-ARS Cattle Fever Tick Research Laboratory, Edinburg, TX, [6]USDA-ARS Knipling–Bushland US Livestock Insects Research Laboratory, and Veterinary Pest Genomics Center, Kerrville, TX, [7]Microbiology laboratory Antigua, St. John's, Antigua and Barbuda; [8]Retired consultant in acarology, St. John's, Antigua and Barbuda; [9]Veterinary Services, Ministry of Agriculture, St. Michael, Barbados; [10]Department of Agriculture, St. Croix, Virgin Islands, U.S.; [11]Veterinary Services, Ministry of Agriculture, Castries, Saint Lucia; [12]Veterinary Services, Ministry of Agriculture, Roseau, Dominica; [13]Direction de l'Agriculture, de l'Alimentation et de la Forêt, Basse terre, Guadeloupe. Contact: stephanie.depraz@cirad.fr

Context: Ticks and Tick-borne diseases (T&TBD) remain major constraints to livestock development in the Caribbean. The continuous use of acaricides to control ticks is costly for livestock producers. Chemicals were used extensively in the Caribbean during Tropical Bont Tick programs between 1995 and 2005. The Cattle Fever Tick (CFT), *Rhipicephalus (Boophilus) microplus*, is known to develop multiresistance to acaricides. However little is known about acaricide resistance epidemiology in the Caribbean, where CFT is endemic. Recently, several countries reported to the T&TBD working group of the Caribbean Animal Health Network (CaribVET) increasing cases of lack of acaracide efficacy on ruminants, especially in Martinique.

Purpose: A 2-year project "ResisT" involving researchers, tick experts, veterinary services and farmer associations has been established to address resistance in CFT Caribbean populations. Results of a pilot study conducted in Martinique are reported here.

Methods: The Larval Tarsal Test, an innovative test developed by Novartis, was implemented at CIRAD laboratory in Guadeloupe. An exploratory survey was conducted in early 2015 to collect engorged female ticks from cattle, and to study tick control practices of 50 volunteer farmers. Five acaricides from 3 major classes commonly used in the French West Indies were tested: synthetic pyrethroids, amidines and organophosphates. A susceptible strain maintained at the USDA-ARS CFTRL in Texas was used as reference to calculate resistance ratios.

Results: Preliminary results will be reported during this presentation.

Conclusions: Study results and other epidemiological data on acaricide resistance and information on control practices will be integrated to develop tools and awareness materials for Caribbean farmers.

Relevance: Studies like the one reported are needed to formulate strategies to prevent acaricide resistance development by adopting integrated tick control strategies. Knowledge gaps identified during the study enabled CaribVET to prioritize relevant avenues of research and to build collaborations in support of the veterinary services in the region to improve T&TBD surveillance and control.

P082

Intervention with a standardized footbath protocol - impact on dynamics of digital dermatitis

Karin Orsel[1], Herman Barkema[1], Laura Solano[1], Charlotte PIckel[1], Dorte Dopfer[2], [1]University of Calgary, Calgary, AB, Canada; [2]University of Wisconsin, Madison, WI, Contact: karin.orsel@ucalgary.ca

Background: Digital dermatitis (DD), a contagious bacterial disease that can rapidly spread and persist for a long time in dairy herds, is the most prevalent foot lesion in Alberta and Canada. The most common on-farm prevention strategy for DD is the use of footbaths. However, based on a lameness study we have conducted in 81 Alberta dairy farms, there is a wide variability in footbath practices regarding frequency of use, products and concentration, refreshing of solutions and footbath dimensions. Despite a wealth of information in scientific literature regarding the most effective practices, there seems to be a knowledge translation gap between research and on-farm application.
Objectives: The study's objective was to evaluate the effectiveness of a science-based standardized footbath protocol in the field as a preventive measure for digital dermatitis.
Methods: A longitudinal trial was performed on 9 Alberta dairy farms for 7 months. Each farm served as its own historical control with data collection before and after the intervention. The intervention consisted of the implementation of a computerized automated footbath on all farms with a standardized protocol based on literature recommendations. DD scoring using the M0-M4.1 scoring system (Berry et al., 2012) was done every 2 weeks in the milking parlor and confirmed with the gold standard observation in the trimming chute during 3 sessions.
Results: Controlled concentration and programmed refreshing of footbath solutions resulted in changed dynamics of DD on farms. All farms had a significant increase of M0 scores (no lesions; increase from 31% to 40%), whereas cows diagnosed with DD lesions transferred from active M2 to more chronic stages of the infection (M3-M4). Cows affected with M2 lesions reduced from 41% to 25% overall, and M3-M4 from 28 to 35% overall).
Conclusion: Computerized footbaths programmed with a standardized protocol are effective under field conditions to control the dynamics of DD on farm into a steady state with limited new cases and controllable chronic lesions.
Relevance: Controlled and standardized footbath management can result in significant reduction of the prevalence of DD.

P083

The occurrence, associated factors and impact of liver fluke, rumen fluke and abomasal pathology associated with Ostertagia spp. in slaughter cattle in the UK.

Camille Bellet[1], Martin J. Green[1], Andrew Forbes[2], Mary Vickers[3], Elizabeth Berry[4], Jasmeet Kaler[1], [1]The University of Nottingham, Sutton Bonington, United Kingdom; [2]The University of Glasgow, Glasgow, United Kingdom; [3]EBLEX, Kenilworth, United Kingdom; [4]BCVA, Quedgeley, United Kingdom. Contact: camille.bellet@nottingham.ac.uk

Purpose:
Helminth infections are a major obstacle for livestock production efficiency, particularly considering the difficulty of clearly identifying the relationships between infected animals' parasite burdens and insidious subclinical production losses. The study aim was to determine the occurrence of 3 important parasites infections in slaughter cattle in the UK, along with their associated factors and impact.
Methods:
Specific viscera from slaughter cattle were examined quarterly at post-mortem on 4 occasions within a year in an abattoir in England. Lesions due to Ostertagia spp. (scores 0-3), presence of rumen fluke (0-4) and ruminal surface colonisation (0-3), as well as presence of liver fluke and its associated lesions (0-2) were examined and scored. The scoring was done by the same operators and abattoir records were collected. Factors and carcass impact associated with parasites occurrences were investigated by multinomial and linear mixed models respectively, with herd as a random effect.
Results:
Eighty-nine per cent (830/935) of abomasa presented signs of ostertagiasis, among which 40% had more than 1000 related lesions. Twenty-five (232/938) and 29% (274/953) of the carcasses had rumen and liver fluke, respectively. Thirty-nine per cent of the total cattle carcasses (353/974) were co-infected with at least 2 parasites. After controlling for other factors, there were significant differences in the distribution of helminth specific gross lesions among cattle by type of breed, animal category, age, weight and season. Presence of only rumen fluke was significantly associated with a decrease in cold carcass weight. Both abomasal lesions and presence of rumen fluke were significantly associated with decrease in the conformation grade. There were no significant associations between parasite presence/lesions and carcass fat coverage.
Conclusions:
This is the first UK study with evidence and prevalence of cattle polyparasitism infections and their associated negative impact on carcass performances.
Relevance:
Study results emphasize the importance of developing sustainable parasite control strategies on cattle farms.

P084

Risk for transmission of E. coli O157:H7 through cattle manure

Lena-Mari Tamminen[1], Maria Torsein[2], Elöd Szanto[2], Ulf Emanuelson[1], [1]Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]Swedish Animal Health Service, Skara, Sweden. Contact: lena.mari.tamminen@slu.se

Purpose
Shigatoxin producing Escherishia coli O157:H7 (STEC), a zoonotic pathogen shed in the feces of asymptomatic cattle, poses a serious threat to public health. A rising concern is transmission through crops fertilized with contaminated manure. The aim of this study was to investigate the prevalence and the risk of spread of the pathogen through manure.
Method
28 Swedish dairy farms located in an area with high prevalence of STEC were visited and sampled in December (n=27) 2014 and March (n=28) 2015. Environmental samples (over-shoe and fresh fecal samples) and samples from manure storage pits were taken at each farm. Analysis of STEC was done by immunomagnetic separation after pre-enrichment.
Results
In 2014, 14 of the 27 farms were positive for STEC and on 6 of the positive farms the pathogen was found in the manure storage pits. In 2015, after the winter and just before the fertilization period began, 4 farms were positive on environmental sampling. One of the positive farms had a positive manure sample and the remaining 27 were negative. Odds ratios for positive farms having positive manure samples (using a fudge factor of 0.5) were 21 on both sampling occasions while population attributable risk was 0.13 in December and 0.04 in March.
Conclusion
These results indicate that the risk of a positive farm also having a positive manure sample was similar on both sampling occasions. However, due to a reduction in the number of positive farms during winter, the risk for transmission to the environment at the time of fertilization decreased. Thus, screening of positive farms before fertilization could be an alternative in high prevalence areas. Factors causing the reduction of positive farms during winter and if they can be used for decreasing the prevalence of STEC needs further investigation.
Relevance
Different, often costly, ways to manage manure have been suggested to decrease the risk of transmission of STEC. However, previous studies show that survival of STEC in manure decreases over time and depends on several factors (e.g. temperature and season). In order to analyse the need and cost-benefit of manure management, the risk of transmission through manure in real farm situations has to be established.

P085

Salmonella Prevalence on Hides, Carcasses, and in Lymph Nodes of Cattle Administered a Sustainable Diet Derived from Agricultural By-Products in Honduras.

Jessie L. Vipham, Mark F. Miller, Sara Trojan, Ricardo J. Gomez, Maria Bueso, Kari Spivey, Tosha Opheim, Skarleth Chinchilla, Mindy M. Brashears, Texas Tech University, Lubbock, TX, Contact: jessie.vipham@ttu.edu

Purpose:
Protein is a limiting nutrient in human diets in many developing countries. Due to limited feed resources, cattle numbers in Honduras have declined steadily over the past several years. A sustainable cattle diet was developed, with poultry litter as the primary protein source. Because poultry litter may contain *Salmonella*, the purpose of this study was to determine if *Salmonella* was present in beef carcass samples collected from cattle fed a sustainable diet.

Methods:
A beef cattle ration was formulated using African palm meal, sugar cane, and poultry litter, all sustainable by-products in Honduras, and were fed during the dry season. Samples (n = 136) were collected from a Honduran beef slaughter facility (34 samples were taken for hides, pre-evisceration, final carcass, and lymph nodes) and shipped to Texas Tech University for microbial analysis. *Salmonella* presence was determined using Polymerase Chain Reaction (PCR) analysis and subsequent culture-confirmation. *Salmonella* in lymph nodes were determined by direct culture and enumeration methods.

Results:
Results indicated a low presence of *Salmonella* in beef cattle presented for slaughter. Out of 34 swabs samples from carcasses, only three were positive; one hide (2.94%), one pre-evisceration (2.94%) and two final carcass swabs (5.88%). A total of seven lymph nodes were positive (20.59%).

Conclusion:
Results from this study indicate that Salmonella was not excessively present in the cattle fed diets containing poultry litter. *Salmonella* was present on two of the final carcasses, which is indicative of cross-contamination during harvest. *Salmonella* prevalence in lymph nodes mimics previous U.S. and Honduran lymph node prevalence results. Further research is necessary in order to determine if this trend is stable.

Relevance:
Food insecurity is a serious issue facing the world's food industry. Many efforts have been made in the past decade to reduce extreme poverty and hunger, yet 805 million people in the world remain chronically undernourished. This research is an effort to monitor potential food safety risks associated with designing sustainable feed programs for Honduras.

P086

Endemicity of Chlamydia-like organisms in Dairy farms: A cross-sectional study in Great Britain.

Bhagyalakshmi Chengat Prakashbabu[1], Nicholas Wheelhouse[2], Skye Storrie[2], Martina Velasova[1], David Longbottom[2], Javier Guitian[1], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]Moredun Research Institute, Edinburgh, United Kingdom. Contact: bchengat2@rvc.ac.uk

Purpose: Reproductive failure in cattle is a major concern for the UK dairy industry. Approximately 80% of foetal losses remain undiagnosed in the UK which in part could be due to the presence of previously unidentified pathogens. *Chlamydia*-like organisms have been demonstrated in bovine abortions and is an emerging respiratory tract pathogen in humans. Several recent reports from across Europe and North Africa have identified the presence *Chlamydia*–like organisms in aborted bovine foetuses and bovine placental samples. The aim of this cross-sectional study was to determine current status of *Chlamydia* and *Chlamydia*-like organisms in dairy farms in Great Britain (GB).

Methods: The study population consisted of a sample of randomly selected dairy farms in GB stratified by geographic location and herd size. Bulk milk samples were used to test for *Chlamydia* and *Chlamydia*–like organisms. DNA was extracted from bulk milk prior to analysis using a 16S Chlamydiales real-time PCR protocol.

Results: Out of 208 farms studied, bulk milk from 46 (22.1%) farms were weakly positive (CT>35) and 24 (11.5%) farms were demonstrated to be positive (CT <35) for Chlamydiales. Samples which were confirmed as strongly positive were further analysed by sequencing to identify specific species. Among the positive samples 11 (45.8%) were positive for *Parachlamydia acanthamoebae (P. acanthamoebae)*, 6 (25%) were positive for *Chlamydia pecorum* (*C. pecorum*) and 3 (12.5%) positive for *C. abortus*.

Conclusions and relevance: Farms positive for *P. acanthamoebae* were distributed all over GB indicating possible endemicity of the pathogen. Even though the proportion of farms positive for *C abortus* is low, zoonotic potential of the pathogen should not be ignored. *C pecorum* is known to be endemic and can be associated with conditions such as conjunctivitis, endometritis, arthritis and pneumonia in cattle. The findings of this study are compatible with endemic status of *Chlamydia* and *Chlamydia*-like organisms in dairy farms of GB; analytical observational studies should be conducted to assess whether exposure to these agents is associated with reproductive inefficiency.

P087

Prevalence of Salmonella found in lymph nodes of sheep and goats within the United States

Keelyn E. Hanlon, Markus F. Miller, Lacey M. Guillen, Alejandro Echeverry, Kari S. Spivey, Mindy M. Brashears, Texas Tech University, Lubbock, TX, Contact: keelyn.hanlon@ttu.edu

Purpose: *Salmonella* is a potentially serious food safety concern with a known presence in ruminants. *Salmonella* recovery from cattle lymph nodes has been shown to be as high as 91%, but less research has been published about the prevalence in small-ruminants. With this in mind, the objective of this study was to determine the prevalence of *Salmonella* harbored within lymph nodes of sheep and goats from the United States.

Methods: Mandibular, mesenteric and subiliac lymph nodes (N=485) were trimmed from their respective locations during harvest, from 162 small-ruminants. Sampling was done at small abattoir facilities in New Mexico and Texas during the span of one calendar year.

Lymph nodes were trimmed, boiled, pulverized and enriched in Tryptone Soya Broth (TSB). Samples were then analyzed with standard immunomagnetic separation (IMS) procedures for *Salmonella*, enriched in Rappaport-Vassiliadis (RV) broth and plated to two selective agars (Xylose Lysine Desoxycholate (XLD) and Brilliant Green Sulfa (BGS)). Typical colonies from either XLD or BGS were agglutinated using a latex agglutination test for confirmation. A chi-square (PROC FREQ) test was performed using SAS.

Results: *Salmonella* was detected in 4.35% (n=161) of mandibular lymph nodes, 8.02 % (n=162) of mesenteric lymph nodes and 10.49% (n=162) of subiliac lymph nodes.

Conclusions: Previous literature has found *Salmonella* prevalence in mesenteric lymph node samples to be between 3.84% and 9.80% in goats. The results from this study are consistent with this, but the additional evidence of *Salmonella* found in the mandibular and subiliac lymph nodes can contribute to a better understanding of the prevalence of the organism harbored within the different lymphatic areas.

Relevance: These results indicate that *Salmonella* can be found in the lymph nodes of small-ruminants and demonstrate a need for further studies to be done to determine if organism prevalence could fluctuate by season, region or production practices in order to ensure food safety.

P088

Sheep and farm level factors associated with contagious ovine digital dermatitis: a longitudinal repeat cross-sectional study of sheep on six farms.

Joseph W. Angell, Jennifer S. Duncan, Dai H. Grove-White, The University of Liverpool, Wirral, United Kingdom. Contact: jwa@liv.ac.uk

Purpose
Contagious ovine digital dermatitis (CODD) is a cause of severe lameness in sheep in the UK currently affecting approximately 50% of farms. The epidemiology is poorly characterised and there have been no on farm studies investigating risk factors for CODD.
Methods
Six farms were studied to investigate 1) the prevalence dynamics of CODD; 2) the association between sheep with CODD and potential risk factors; 3) the impact of CODD on lameness in sheep. The farms were visited at two-month intervals between June 2012 and October 2013 and 6,515 sheep were examined.
Results
The prevalence of CODD varied between farms (2.5-11.9%). Within farms, prevalence may increase in the early autumn and after housing. Environmental risk factors included larger flocks, lowland pasture, lush pasture and poached pasture. Co-infection with footrot (FR) was strongly associated with CODD (OR: 7.7 95%CI: 3.8-15.5 P<0.001) but negatively associated with co-infection with interdigital dermatitis (ID) (OR: 0.05 95%CI: 0.02-0.1 P<0.001). Reinfection with CODD was observed in 78 individuals but there was no re-infection at foot level.
Lameness on all farms reduced during the study and seasonal changes in lameness followed similar patterns to those for CODD. Infection with CODD leads to a greater increase in locomotion score compared to FR or ID and CODD lesion grade was strongly associated with being lame. Sheep with CODD in more than one foot were more likely to be lame (OR: 25.0 9%%CI: 12.5-49.9 P<0.001) than those with just one foot affected (OR:10.0 95%CI: 8.6-11.6 P<0.001).
Conclusions
The biggest risk factor for CODD is co-infection with FR and therefore control of FR may help reduce the risk of CODD on affected farms. Environmental risk factors for CODD are similar to those for FR adding weight for control strategies that target both diseases in tandem. Effective systemic immunity to CODD in sheep appears to be lacking however there is epidemiological evidence that there may be local immunity within the foot.
Relevance
This disease whilst currently identified only in the UK causes severe welfare implications for affected sheep. This paper highlights key risk factors which may assist in developing control strategies.

P089

Clinical and radiographic features of contagious ovine digital dermatitis, and a novel lesion grading system.

Joseph W. Angell[1], Richard Blundell[2], Dai H. Grove-White[1], Jennifer S. Duncan[1], [1]The University of Liverpool, Wirral, United Kingdom; [2]The University of Liverpool, Wirral, United Kingdom. Contact: jwa@liv.ac.uk

Purpose
Contagious ovine digital dermatitis (CODD) is an infectious foot disease of sheep and causes severe lameness. Currently a diagnosis is made on the basis of broad anecdotal descriptions. The aim of this study was to systematically and formally describe the clinical presentation of the disease in terms of 1) a lesion grading system; 2) associated radiographic changes.
Methods
A five-point lesion grading system was developed and applied to 908 sheep affected by CODD from six farms. Sheep with lesions typical of each grade were euthanased and their feet radiographed.
Results
The five-point grading system may be used to clinically describe stages of CODD lesions. Lesions commenced at the coronary band leading to under-running of the hoof horn capsule dorsally and abaxially resulting in sloughing of the hoof horn capsule. Horn regrowth and recovery is possible. Radiographic abnormalities including soft tissue and bony changes were evident in feet with lesions graded 2-5.
Conclusions
Contagious ovine digital dermatitis has a range of clinical signs, causing severe damage to the soft tissues of the ovine foot and can lead to bony changes in the distal phalanx.
Relevance
Contagious ovine digital dermatitis is a severe and debilitating disease of sheep that has a range of clinical signs. The five-point grading system may be useful as a clinical and research tool.

P090

Non-fatal Injury Occurrence in Southern California Thoroughbred Racehorses 2009-2010

Ashley Hill[1], J. A. Blea[1], R. M. Arthur[2], C. W. McIlwraith[3], [1]University of California, Davis, CA, [2]Southern California Equine Foundation, Inc., Arcadia, CA, [3]Equine Orthopaedic Research Center, Fort Collins, CO, Contact: aehill@ucdavis.edu

Among racing and training Thoroughbreds, musculoskeletal injuries are the most common cause of death or euthanasia, the most common cause of exiting training, and are also a leading cause of wastage. The primary objective of the current study was to describe the incidence, anatomic distribution and characteristics of non-fatal injuries in Thoroughbred racehorses as diagnosed by private practice veterinarians in Southern California. Participating veterinarians recorded non-fatal injuries (definitive diagnosis of a musculoskeletal condition resulting in lameness, injury or loss of training > five days) incurred by Thoroughbred racehorses in their care. Secondary objectives were comparison of this private-practice recording system with an existing regulatory system, and comparison of fatal and non-fatal injury rates. Between May 1st 2009 and April 30th 2010, non-fatal injuries were recorded by seven veterinarians in four practices. Non-fatal injuries were diagnosed in 2-4% of horses in race training per month. The majority of injuries were acute rather than chronic. Stress fractures, superficial digital flexor tendonitis, and suspensory ligament desmitis were common. Agreement between non-fatal injuries recorded in the current study and those recorded via an existing regulatory system was poor, with neither system capturing all injuries. Non-fatal injuries occurred much more often than fatal injuries. Non-fatal musculoskeletal injury remains an ongoing issue for Thoroughbred racehorses, and an accurate, comprehensive system for recording these injuries is needed.

P091

Health of riding school horses - frequency of clinical disease and associations with management

Jens Frederik Agger[1], Louise H. Christensen[1], Rikke Buhl[2], Christian B. Pipper[3], Maj H. Thomsen[2],
[1]University of Copenhagen, Frederiksberg, Denmark; [2]University of Copenhagen, Taastrup, Denmark;
[3]University of Copenhagen, Copenhagen, Denmark. Contact: jfa@sund.ku.dk

The public often perceives the life of riding school horses to be less attractive than the life of privately owned horses. Therefore a study was undertaken to investigate riding school management and associations with frequency of clinical diseases, and disease time horses were absent from work.
The study was based on two types of data. A) A cross sectional survey of management and frequency of disease and culling procedures based on telephone interviews with 100 randomly selected riding schools with 1298 horses. The interview focused on physical facilities, daily management, staff responsibilities and education, riding programs and riding equipment, the general horse day cycle and disease occurrence. B) A prospective study during 4 months in 17 volunteering riding schools with 227 horses with daily recordings for each horse of working hours, free time and hours on pasture, absence due to disease, and recording of clinical disease. Age, gender and years as a riding school horse were also recorded. Descriptive statistical and epidemiological analyses using chi square and Fischer's exact test in cross tabulations and t-test and classical univariable and multivariable linear regression were performed.
Telephone interviews showed that lameness (69%) and behavioral problems (80%) was the single most frequent cause of disease absence and culling, respectively.
Daily records showed an average daily disease prevalence of 2.9%. The incidence rate per horse year at risk was 0.82 cases equivalent to an annual incidence risk of 56%. On average horses were absent 5 days per year due to disease. Lameness caused 54% of disease days and wounds and bruises 15%. An extra hour per week on pasture reduced disease time with 0.11 days per year (P=0.006). Disease time increased with 0.85 days per year of horse age (P=0.05).
It is concluded that lameness is the main health problem and behavior is the main culling problem. Health of riding school horses was associated significantly with several management factors, e.g. number of hours on pasture per week.
Perspectives are many, e.g. that simple changes in the routine management can improve health of riding school horses significantly.

P092

Prevalences of obesity and Equine Metabolic Syndrome in Andalusian horses

Tamara Martin-Gimenez[1], Carla N. Aguirre-Pascasio[2], **Ignacio de Blas**[1], [1]Universidad de Zaragoza, Zaragoza, Spain; [2]University of Murcia, Murcia, Spain. Contact: deblas@unizar.es

Purpose: Equine metabolic syndrome (EMS) is associated with an increased risk of laminitis as the main clinical consequence. The identifiable signs suggesting the presence of EMS comprise several phenotypic characteristics. However despite its clinical importance, there is no established a standard to define its main components and subsequently its prevalence. The aims of this study were to determine prevalence of EMS and their components in Andalusian horses.

Methods: A random sample of 164 Andalusians was used. Obesity was evaluated using a classic subjective method based on body condition score (BCS, scale 1-9) and through the ultrasonographic measurement of subcutaneous fat thickness (SFT) over seven anatomical areas. Hyperinsulinemia was defined as basal insulin ≥ 20µIU/mL and risk for laminitis was determined for values of basal leptin ≥ 7.3ng/ml and/or mid-neck circumference to withers height ratio > 0.71.

Results: According to BCS, 7.9% of horses were classified as undercondition (<4.5), 64.0% as optimal (5-6.5), 23.2% as overcondition (7-7.5) and 4.9% as obese (8-9). Likewise, 8.5, 75.6, 11.6 and 4.3% using STF were classified as undercondition, optimal, overcondition and obese respectively. To determine prevalence of EMS, overcondition and obese were grouped resulting in an overall obesity prevalence of 28.1% (CI95%: 21.7, 35.4) with BCS, and 15.9% (CI95%: 11.1, 22.2) with SFT. The concordance between both methods was low (Cohen's Kappa weighted = 0.254). Prevalence of hyperinsulinemia was 1.8% (CI95%: 0.6, 5.2) and risk of laminitis was 69.5% (CI95%: 62.1, 76.0). Finally, prevalence of EMS was 0.6% (CI95%: 0.1, 3.4) for both scoring obesity methods.

Conclusions: The objetive assessment of body condition through measurement of SFT showed that BCS underestimated the optimal condition and overestimated the overcondition in Andalusians. In addition, prevalence of EMS in Andalusians was much lower than expected.

Relevance: Despite Andalusian horses have been suggested as a breed predisposed to EMS phenotype due to their tendency towards obesity, these results highlight the need to define accurately the main components of EMS to calculate its prevalence unambiguously.

P093

Could the acute abdominal pain in horses be related with moon phase?

Tamara Martin-Gimenez, **Ignacio de Blas**, Universidad de Zaragoza, Zaragoza, Spain. Contact: deblas@unizar.es

Purpose: In human medicine, associations of seizure frequency, anxiety disorders, suicidal thoughts, bite injuries and emergency room admissions with lunar cycle have been studied. Although, in veterinary medicine the references are scarce, and only a significant increase in emergencies for dogs and cats on full moon days has been reported. The aim was to determine the relationship between lunar cycle and frequency of acute abdominal pain (AAP) presentation.
Methods: According to the presumptive diagnosis, AAP were classified as obstructive, motility alterations and other abdominal pains in a case series (n=60) recorded during one year. Moon phases and duration were calculated depending on the degree of illumination as: new moon (0-3%, 2 days), waxing moon (12 days), full moon (97-100%, 2 days) and waning moon (12 days). To evaluate the association between AAP and moon phases and to compare observed cases in each moon phase with expected cases depending on duration of moon period, Chi-square test was used.
Results: Most of cases were classified as obstructive (56.67%) and 13.3% as motility alterations. Neither presumptive diagnosis (p=0.365) nor overall survival (85%, p=0.828) were associated with moon phase. The majority of cases were recorded during waning moon (56.67%), followed by cases occurred during full moon (18.33%), waxing moon (13.33%) and new moon (11.67%). Once daily probability of AAP in each phase was calculated, significant differences between observed and expected probabilities were observed ($p<0.001$). The probability of AAP presentation in a day of full moon was 9.17%, while they were lower for new moon (5.83%), waning moon (4.72%) and waxing moon (1.11%). Regarding to the diagnostic classification, daily probabilities were also significantly greater during full moon and lower during waxing moon.
Conclusions: In this study (with a limited number of cases), the probability of attending a horse due to AAP was greater during a day of full moon.
Relevance: The duration of each moon phase should be adjusted when assessing the probability of a disease outcome. Further studies with more cases are needed to confirm the effect of lunar cycle on equine clinical practice.

P094

Equine atypical myopathy in the United Kingdom: epidemiological characteristics of 2014 outbreak

Sonia Gonzalez Medina[1], Joanne Ireland[1], Dominique Votion[2], [1]Animal Health Trust, Newmarket, United Kingdom; [2]Faculty of veterinary medicine, Liege University, Liege, Belgium. Contact: sonia.gonzalez-medina@aht.org.uk

Purpose: Equine Atypical Myopathy (EAM) is an acute and severe rhabdomyolysis caused by the ingestion of Hypoglycin A from sycamore seeds and seedlings. This highly fatal disease affects mainly postural, respiratory and cardiac muscles. Compare to previous years, a threefold increase in number of cases was reported in autumn 2014. The aim of this study is to describe the largest outbreak of EAM reported in the UK and compare epidemiological characteristics with published data from other European outbreaks.
Methods: Detailed information of 158 cases was collected through the Atypical Myopathy Alert Group in a multicentre collaborative study. Ninety-eight horse owner and 60 veterinary questionnaires were reviewed and descriptive statistics were produced.
Results: The mortality rate (62%) of this outbreak was lower than described in previous studies (70-90%). Breeds most commonly affected were cob (29%), native pony breeds (22%) and Thoroughbred (11%). Like in other European outbreaks, affected animals were predominately young adults (mean= 7 years). The South East of England reported the highest number of cases (36%). Sycamore seeds were identified in 76% and sycamore seedlings in 22 % of pastures where affected horses were grazing. 94 % reported in 2014 occurred in autumn with a peak between mid-October and mid -November (78% of all cases).
Conclusions: Highersurvival rate of EAM in the UK may be explained by the fact that the condition is better recognised and treated by veterinary surgeons. The most commonly affected breeds were “thrifty” breeds, which are frequently kept on sparse pasture all year around and therefore access to sycamore seeds may be more likely.Relevance: These results further support sycamore seeds as a main source of Hypoglycin A intoxication in horses suffering from EAM. These data provide valuable insights into previously unknown epidemiological attributes of the condition in the UK and set up the groundwork for a national prevention strategy.

P095

Feasibility study to inform the design of a randomised, placebo-controlled field trial of a *Clostridium botulinum* type C vaccine against Equine Grass Sickness

Jo L. Ireland[1], Bruce C. McGorum[2], Chris J. Proudman[3], J. Richard Newton[1], [1]Animal Health Trust, Newmarket, United Kingdom; [2]The Royal (Dick) School of Veterinary Studies, Edinburgh, United Kingdom; [3]University of Surrey, Guildford, United Kingdom. Contact: jo.ireland@aht.org.uk

Equine grass sickness (EGS) is a highly fatal polyneuropathy affecting equids, hypothesised to involve toxico-infection with *Clostridium botulinum* type C. As EGS cannot be induced experimentally, a field trial represents the only way to evaluate efficacy of vaccination in preventing naturally occurring disease. Identifying barriers and facilitators for recruitment is vital in assessing the feasibility of undertaking a randomised controlled trial (RCT).

Purpose:
To explore horse owner attitudes towards a RCT of a *C. botulinum* vaccine for EGS prevention and to identify potential issues with participant recruitment.

Methods: 229 owners reporting cases to the authors' EGS surveillance scheme (EGSSS) since 2008 were invited to participate. Owners were mailed questionnaires containing a synopsis of the proposed EGS vaccine RCT, together with questions regarding their horses, experience of EGS and potential participation in the RCT.

Results: Useable response rate was 51%. Since reporting a case to the EGSSS, 79% of owners kept their horses on the same EGS-affected premises, and 31% indicated that ≥1 EGS case had occurred on the premises within the past 2 years. 74% of owners indicated that they would be willing to participate in the RCT. Reasons stated by owners not wishing to participate included concerns regarding vaccine safety (76%); time commitment too great (14%); moving premises imminently (11%), and 'needle shy' animals (7%). 19% of owners reported knowing it was a placebo-controlled trial would influence their decision-making about participating. For insured animals, 18% of owners reported that insurance implications would influence their decision about participating. 46% of owners indicated that they would be prepared to enrol all their horses, and a further 25% indicated that they would enrol some of their horses in the RCT.

Conclusions: There was substantial owner support for an EGS vaccine trial, with 71% reporting that they would consider enrolling their horses. **Relevance:** This study provided an estimated proportion of eligible premises and vital information about barriers to recruitment, informing the design of the RCT protocol and owner information documents.

P096

Site selection survey to assess the feasibility of a randomised, placebo-controlled field trial of a *Clostridium botulinum* type C vaccine against Equine Grass Sickness

Jo L. Ireland[1], Bruce C. McGorum[2], Chris J. Proudman[3], J. Richard Newton[1], [1]Animal Health Trust, Newmarket, United Kingdom; [2]The Royal (Dick) School of Veterinary Studies, Edinburgh, United Kingdom; [3]University of Surrey, Guildford, United Kingdom. Contact: jo.ireland@aht.org.uk

Equine grass sickness (EGS) is a frequently fatal neurodegenerative disease, hypothesised to involve toxico-infection with *Clostridium botulinum* type C. Prevention by vaccination should theoretically be possible, and a randomised clinical trial (RCT) would be required to evaluate the protective effect of vaccination. Site selection questionnaires are an important element of clinical trial feasibility.

Purpose:

To explore veterinary opinions regarding a *C. botulinum* vaccine RCT for EGS prevention and to identify practices attending premises with high EGS incidence.

Methods:

284 practices registered with the authors' EGS surveillance scheme or AHT diagnostic laboratories were sent postal questionnaires containing a synopsis of the proposed RCT and questions on practice caseload, experience of EGS and potential participation in the RCT.

Results:

Useable response rate was 42%. 73% of practices had attended ≥1 EGS case in the previous 2 years (median 4 cases; median period prevalence 0.12%). 91% of responders indicated willingness to recruit owners for the RCT and 51% of practices regularly attended premises affected by recurrent cases of EGS. 93% of responders indicated willingness to participate in the RCT, and 99% would participate if a client registered with their practice wished to enrol. Reasons given by responders not wishing to participate (n=8) included low EGS incidence (50%), did not believe clients would wish to participate (38%), too much paperwork (25%), and time commitment too great (13%). If an effective vaccine for EGS prevention was available, 49% of responders would recommend its use to all equine clients registered with their practice and a further 38% would recommend vaccination to all clients keeping horses on EGS-affected premises.

Conclusions: Site selection questionnaires successfully identified practices meeting site investigator inclusion criteria for the EGS RCT.

Relevance:

The majority of participating practices could readily identify eligible premises and would be prepared to consider entering animals under their care into an RCT investigating the efficacy of *C. botulinum* type C vaccination in the prevention of naturally occurring EGS.

P097

The aid of magnetic resonance imaging in determining long term prognosis for soundness following palmar/plantar digital neurectomy in horses.

CLAIRE E. WYLIE, Richard J. Payne, Andrew P. Bathe, Tim R. C. Greet, Marcus J. Head, Sarah J. Boys-Smith, Sarah E. Powell, ROSSDALES EQUINE HOSPITAL, EXNING, United Kingdom. Contact: claire.wylie@rossdales.com

Purpose: Accurate diagnosis of chronic foot pain in horses by magnetic resonance imaging (MRI) allows appropriate case selection for palmar/plantar digital neurectomy (PDN). The aim of this study was to report long-term follow-up of horses and ponies that had chronic foot pain treated by PDN, either with or without MRI as a diagnostic procedure.
Methods: The electronic patient records of all horses that underwent PDN were reviewed. Follow-up was obtained from owners using a structured questionnaire. Comparisons were made using Chi-squared/Fisher's exact tests or 2-sample t-tests, with statistical significance set as $P<0.05$.
Results: In total, 109 PDN cases were undertaken between 14/08/2003 and 19/09/2013. Response rate for follow-up was 72.5%. From these 79 cases, 52 had MRI (MRI+) and 27 did not (MRI-). There was no significant difference in case distribution: predominantly horses (MRI+ 86.5%, MRI- 96.3%), Warmblood breeds (MRI+ 40.4%, MRI- 44.4%), geldings (MRI+ 71.2%, MRI- 84.6%), used for full competitions (MRI+ 38.5%, MRI- 31.4%). However, MRI+ were significantly younger than MRI- (median 9.99 and 11.71 years respectively, $P=0.004$). Median follow-up time for MRI+ was 31.4 months, and for MRI- was 36.8 months. There was no statistically significant difference in outcome between MRI+ and MRI-. In total, 78.9% MRI+ achieved their intended use, compared to 73.1% MRI-. For those that were intended for exercise, 83.7% MRI+ reached a level of exercise, compared to 87.5% MRI-, and in those that returned to exercise, median length of maintenance was 25.2 months for MRI+ and 24.0 months for MRI-. In total, 82.7% of owners of MRI+ animals considered them safe to ride compared to 88.5% of MRI- owners. There were two complications in the MRI- group necessitating euthanasia.
Conclusions: Although it was hypothesised that prior MRI would reduce the risk of catastrophic complications, no statistically significant difference was found. However, the two catastrophic complications were in the MRI- group.
Relevance: Magnetic Resonance Imaging is increasingly used as a pre-surgical diagnostic procedure but may not aid prognostic advice for palmar/plantar digital neurectomy in horses and ponies.

P098

Findings from an equine ophthalmology survey in Great Britain

Sonia Gonzalez Medina[1], Richard Newton[1], David Donaldson[2], [1]Animal Health Trust, Newmarket, United Kingdom; [2]SASH Veterinary Hospital, North Ryde, Australia. Contact: sonia.gonzalez-medina@aht.org.uk

Purpose: Equine ophthalmology interest has considerably increased among British equine practitioners (EP) and ophthalmology specialists (OS) in recent years. However, a formal survey to determine the most frequent ocular conditions in the British horse population has never been conducted.
Methods: A questionnaire was posted and/or e-mailed to EP and OS between January 2014 - February 2015. A purposive sample of practices was selected based on overall equine caseload (EP >50% equine; OS >4horses/month), to maximise the chance of enrolling participants that diagnosed higher numbers of equine ophthalmic conditions. Data collected included details on overall equine caseload, number of ocular examinations performed per month, whether husbandry practices were included in history taking when dealing with cases and rank scoring of frequency seen (1=most frequent, 10=least frequent) for a defined list ocular conditions**.**
Results: A response rate of 50% (45/90) was achieved. The median
equine caseload was 50 horses/month, with OS seeing significantly fewer equine cases overall; (P=0.02). However, OS examined more equine ophthalmology cases/month (median=6 cases/month) than EP (median=2 cases/month). The most frequently diagnosed ocular condition was corneal ulcer/traumatic ulceration (ranked 1 or 2 by 33/44 respondents), followed by conjunctivitis (ranked 1 or 2 by 29/45 respondents). When assessing ocular conditions, only 15% of respondents always enquired about fly control, 16% about antihelmintic schedule and 7% about control of ectoparasites.
Conclusions: Corneal ulcer/traumatic corneal ulceration and conjunctivitis are the most commonly veterinary diagnosed ocular conditions in the British horse population. Assessment of preventive health-care measures does not appear to be perceived by clinicians as an important part of clinical assessment examination of ocular conditions.
Relevance: This is the first study investigating the relative frequency of veterinary diagnosed ocular conditions in Britain. Description of the most prevalent conditions will facilitate improvements in veterinary care and further identification of risk factors.

P099

Unraveling the causes of respiratory disease in the working equids of Ethiopia.

Gabrielle Laing[1], Rob Christley[1], Andrew Stringer[1], Alan Radford[1], Nigatu Aklilu[2], Richard Newton[3], Gina Pinchbeck[1], [1]University of Liverpool, Liverpool, United Kingdom; [2]Society for the Protection of Animals Abroad (SPANA), Debre Zeit, Ethiopia; [3]Animal Health Trust, Newmarket, United Kingdom. Contact: gabrielle.laing@liverpool.ac.uk

Respiratory signs, particularly coughing and nasal discharge, are consistently ranked amongst the top three health problems by owners of working equids in Ethiopia. Despite this, these syndromes are poorly defined.

Purpose: The studies aimed to unravel the possible contributing factors.

Methods 1: An initial participatory appraisal gained local understanding of experience of respiratory disease using semi-structured interviews, matrices and preference ranking.

Results & Conclusions 1: Forty-four recognised respiratory syndromes were documented by horse owners and cart drivers, described using a combination of twenty-one signs. The most common signs being coughing, altered respiration, bilateral mucopurulent nasal discharge, serous nasal discharge and epistaxis. The top three identified syndromes across all towns were epistaxis, serous nasal discharge and jointly a non-specific cough and a cough with serous nasal discharge. Major themes that emerged as possible causes of disease were temperature & climate, overworking & poor husbandry, environmental factors, dust, feeding practices and infectious disease spread.

Methods 2: Subsequently a cross-sectional study across 19 sites was conducted to determine the frequency of respiratory signs and exposure to major respiratory pathogens.

Results & Concludions 2: Majority of horses examined were driven as “gharri” (cart) horses, with 85% of participants citing their cart as their main source of income. Owners reported 38% animals examined had a recent history of coughing (last 30 days), 8% history of nasal discharge and 3% had suffered other breathing problems. In addition 11% horses examined had a clinically significant nasal discharge. Serology results for 350 horses analysed suggested recent exposure to *Streptococcus equi subsp. equi* in 23%, equine arteritis virus 3.4%, but exposure to influenza virus was very rare. Low antibody titres to equine herpesvirus-1/4 and equine rhinitis virus-A/B were also detected.

Relevance: This approach, combining participatory with classical epidemiological studies, should allow development of appropriate co-operative strategies for communication of interventions in the future.

P100

Epidemiology of a significant outbreak of equine herpesvirus myeloencephalopathy

Andy M. J. McFadden[1], Dave Hanlon[2], Rabecca McKenzie[2], Joe Mayhew[3], [1]Ministry for Primary Industries, Lower Hutt, New Zealand; [2]Matamata Veterinary Services Ltd, 26 Tainui Street, Matamata 3400, New Zealand; [3]Institute of Veterinary, Animal and Biomedical Sciences, Massey University,, Palmerston North, New Zealand. Contact: andrew.mcfadden@mpi.govt.nz

PURPOSE: To describe the epidemiology, biosecurity measures and post-outbreak protocols associated with a significant outbreak of equine herpesvirus myeloencephalopathy (EHM).

METHODS: Equine herpesvirus myeloencephalopathy was confirmed in a suspected outbreak based on detection of EHV-1 virus from various tissues collected after euthanasia from a mare with neurological signs. The epidemiology of the outbreak was investigated by testing approximately 50 mares by PCR and serology, over several periods from those mares associated with affected mares by space and time.

RESULTS: Seven of the 15 clinically affected mares (47%) euthanased. Laboratory testing (serological testing of paired sera and PCR on whole blood and nasal swabs) indicated that of the four paddocks in a "high risk" area where a cluster of cases had occurred, 20 of 21 (95%) horses were likely to have been infected with EHV-1. Of these, 9 mares exhibited clinical signs of EHM including 7 confirmed and 2 unconfirmed cases based on the case definitions utilised. A further 11 mares were considered to have been sub-clinically infected with EHV-1 including 2 confirmed and 9 suspected cases based on detection of EHV-1 in nasal secretions and/or blood by PCR, or based on VNT titres. One of the affected mares was still shedding viable EHV-1 25 days after development of EHM; a period greater than previously reported.Subsequent to the outbreak two mares aborted, one at 9 months and one at 10 months of gestation. The cause of abortion was confirmed as the outbreak strain of EHV-1 with the neuropathogenic genotype, indicating that the farm was still being impacted.

RELEVANCE: The outbreak described shows the considerable impact that can occur in outbreaks of EHM. Strategic testing provided elucidation of the epidemiology of an unfolding farm outbreak. Early biosecurity controls not only reduced the impact on the farm but mitigated the potential for spread to other horse enterprises.

P101

Development and evaluation of a molecular diagnostic method to rapidly detect *Histoplasma capsulatum var. farciminosum* (causing Epizootic Lymphangitis)

Claire Scantlebury[1], Gina Pinchbeck[1], Paul Loughnane[2], Nigatu Aklilu[3], Tibebu Ashine[3], Andrew Stringer[4], Robert Christley[1], Lauren Gordon[2], Alan McCarthy[2], [1]University of Liverpool, Institute of Infection and Global Health, United Kingdom; [2]University of Liverpool, Institute of Integrative Biology, United Kingdom; [3]SPANA Ethiopia, Addis Ababa University, Ethiopia; [4]One Health Consulting, London, United Kingdom. Contact: claire.scantlebury@liverpool.ac.uk

Purpose: *Histoplasma capsulatum var. farciminosum* (HCF), causing Epizootic Lymphangitis (EZL), is endemic in parts of Africa including, Ethiopia, Senegal and Gambia. Despite its high prevalence, impact on animal welfare and socio-economic importance, there is little evidence upon which to build practical and sustainable disease control strategies. The performance and current availability of diagnostic tests in endemic regions is problematic. Methods such as pattern recognition of clinical signs and microscopy lack specificity and other reported methods are either not commercially available or not often feasible (e.g. microbiological culture). This is a significant barrier to further understanding this disease within endemic countries.
Objectives: To validate a nested PCR method to confirm the presence of HCF directly from equine clinical samples.
Methods: This pilot study included 29 horses with suspected EZL from topographically varied regions of Ethiopia. Clinical data, lesion location drawn onto equine silhouettes, blood samples and aspirates of pus from cutaneous nodules were obtained before treatment was provided by SPANA veterinary clinics. Blood and clinical data were collected from a further 20 horses with no cutaneous EZL lesions. Giemsa stained impression smears of pus were examined microscopically. Aliquots of heat-inactivated pus and blood were inoculated onto Whatman FTA cards and imported to the UK with Defra approved licensing. A nested PCR targeting the ITS region, was used to identify samples containing HCF and PCR products were sequenced.
Results: HCF was confirmed in heat-inactivated FTA card pus samples from 24 horses, additionally, 23 blood samples were positive from EZL suspected cases.
Conclusions: This study confirms that HCF can be detected directly from clinical samples furthermore; the identification of HCF DNA in blood raises questions about the pathogenesis of HCF in horses and warrants further investigation.
Relevance: These methods provide a basis for larger population based studies to examine risk factors for EZL aimed at developing practical disease prevention strategies.

P102

The burden of disease in northeast Kenya

Johanna F. Lindahl[1,2], Bernard Bett[1], Francis Wanyoike[1], Delia Grace[1], [1]International Livestock Research Institute, Nairobi, Kenya; [2]Swedish University of Agricultural Sciences, Uppsala, Sweden. Contact: J.Lindahl@cgiar.org

Diseases are often studied singly but occur jointly, with multiple diseases circulating at the same time. In the tropical world, the pressure of multiple diseases may be higher due to higher number of vector-borne and other diseases. In developing countries the burden may be further increased by poverty, under-nutrition, and inadequate health care systems. The dynamic drivers of disease in Africa consortium is looking at how diseases are affected by land use changes, and the case study in Kenya regards irrigation systems. Serologic surveys in both humans and livestock in north-eastern Kenya showed multiple diseases circulating at the same time; Dengue, West Nile fever, Rift Valley fever, Brucella spp, Leptospira spp, and Q-fever. In order to assess the costs for farmers, a short questionnaire was used in 221 households to collect recall data on animal and human disease incidence and costs for preventions and treatments. Data was collected on disease incidence, common symptoms, economic costs, and how work and school was affected. The results show that disease prevention costs were low. No one paid for insurance for animals, and only one family had health insurance for humans, for which they paid 200 Kenyan shillings (KES) the previous year. The most common livestock kept were small ruminants. 197 households had a mean of 34 animals (range0-309). Mean cost of treatment per animal treated in the previous year was 64 KES, with a maximum cost of 1000 KES.Family members reported being sick between 0-6 times during the last two weeks, mean 2.3 times. Although correlated to the reported number of times family members were sick during the last 6 months, the latter number was relatively lower, with a mean of 5.4 and a maximum of 13. Few people could name the diseases, but 18 people mentioned brucellosis as being one of the three last diseases and 64 mentioned typhoid fever. A sick person spent up to 2500 KES on medication, and up to 3000 KES to travel to health facilities.Overall, the study showed high incidence of disease, with households spending little on prevention, and sometimes much on treatment and associated travels. Infectious diseases have both direct and indirect costs and cause a high burden on poor communities.

P103

Efficacy and Synergism of Nitazoxanide and Azithromycin in Calves Experimentally Infected with Cryptosporidium parvum

Jennifer A. Zambriski[1], Nina Isoherranen[2], Rafael Portillo-Gonzalez[1], Kasey Rivas[2], Tracy Sy[1], Wesley Van Voorhis[2], [1]Washington State University, Pullman, WA, [2]University of Washington, Seattle, WA, Contact: jzambriski@vetmed.wsu.edu

Purpose: *Cryptosporidium* spp. are zoonotic protozoal parasites that cause severe diarrhea in animals and people. In dairy production settings infection is an important component of calf-hood diarrhea and contributes to substantial economic losses. Globally, *Cryptosporidium* is the second leading cause of diarrhea in children and is associated with an increased risk of stunting, cognitive impairment, and death. Despite the negative consequences of infection, no consistently effective chemotherapeutic agents exist to treat cryptosporidiosis. Nitazoxanide (NTZ) and azithromycin (AZ) have shown efficacy in reducing severity of clinical illness in calves and people, but are not able to eliminate infection. When tested concurrently in vitro, NTZ and AZ have additive effects in reducing *C. parvum* proliferation, but this has not been tested in vivo. The objective of this study was to determine the efficacy and synergism of AZ and NTZ against cryptosporidiosis in calves experimentally infected with C*ryptosporidium parvum*.
Methods: 105 calves were experimentally challenged with *C. parvum* and randomized to control or 3 treatment groups: NTZ, AZ, or NTZ and AZ. Fecal samples were collected daily and evaluated for consistency and fecal oocyst quantity.
Results: A positive dose-response relationship was observed in infected calves treated with NTZ and AZ. This effect was greater in calves concurrently dosed with both drugs. Complete parasite eradication was not achieved, but there was a significant reduction in fecal oocyst shedding and in severity of diarrhea. This effect was greater in calves concurrently treated with NTZ and AZ.
Conclusions: NTZ and AZ are efficacious in the treatment of cryptosporidiosis in experimentally challenged calves, and this effect is synergistic when they are dosed concurrently.
Relevance: Until new drugs are brought to market, treatment of cryptosporidiosis with NTZ and AZ in calves and people may improve clinical outcomes and reduce the risk of long-term negative sequellae.

P104

The joint risk score for vector-borne diseases used for early detection

Egil A. J. Fischer[1], Mats G. Andersson[2], Céline Faverjon[3], Agnès Leblond[4], Maya Gussmann[5], Jörn Gethmann[5], René Boedker[6], [1]Universiteit Utrecht, Utrecht, Netherlands; [2]National Veterinary Institute, Uppsala, Sweden; [3]INRA-EpiA, Marcy l'Etiole, France; [4]INRA-EpiA, Marcy L'etoile, France; [5]Friedrich-Loeffler-Institute, Riems, Germany; [6]DTU-National Veterinary Institute, Copenhagen, Denmark. Contact: e.a.j.fischer@uu.nl

Purpose:
Risk-based surveillance for vector-borne animal diseases (VBD) and zoonoses aiming for early detection should benefit from continuously gathered data. Passive surveillance does not allow a quick detection of VBD and zoonoses causing few, mild or nonspecific symptoms. E.g. detection of bluetongue virus (BTV) took several weeks and Schmallenberg virus even months. In this paper we present a method for early detection by combining models for risk of release and potential spread of VBD using information from animal health data or syndromic surveillance.

Methods:
The methodology presented combines predicted prior probabilities for an ongoing outbreak with additional evidence from reporting of syndromes in a region and time frame using a Bayesian framework. The prior probabilities of an on-going outbreak in a region and time-frame are based on introduction risks and models for establishment and spread. These prior probabilities are combined with data on animal health into a posterior probability. The resulting posterior probability for an ongoing outbreak of different pathogens, regions ad time windows can be compared to determine which could be prioritized for active surveillance.

Results:
The method was internally validated by using simulated data, where we show that the method can theoretically improve early detection. In two real life examples, we show that it can detect a difference in risk of an ongoing outbreak of West Nile versus Equine Encephalosis in France, allowing to prioritize surveillance activities, but we also showed the limitations in absence of adequate data for BTV outbreaks in Germany.

Conclusions:
The combination of predicted probabilities of release and spread combined with evidence from animal health data, such as syndromic data, in a Bayesian framework is a promising method for risk-based surveillance of vector-borne diseases.

Relevance:
Early detection of outbreaks can reduce economic and environmental damage, as well as reduce public health risks and reduced animal wellfare.

P105

Morphometric discrimination of two sympatric sibling species, Culicoides obsoletus and C. scoticus (Diptera: Ceratopogonidae), vectors of bluetongue and Schmallenberg

Georgette Kluiters[1], Nonito Pages[2], Simon Carpenter[3], Laetitia Gardes[4], Helene Guis[4], Matthew Baylis[1], Claire Garros[4], [1]University of Liverpool, Neston, United Kingdom; [2]CReSA, Barcelona, Spain; [3]The Pirbright Institute, Woking, United Kingdom; [4]CIRAD, Montpellier, France. Contact: g.kluiters@liverpool.ac.uk

Purpose: Certain Palaearctic biting midges have been implicated as vectors of bluetongue virus in northern Europe. Separation of two species (*Culicoides obsoletus* and *C. scoticus*) is considered difficult morphologically, with females often grouped together in entomological studies. Species specific identification is desirable to assess their roles in disease transmission or measure abundance during arboviral outbreaks. Our aim is to investigate whether morphometric identification techniques can be applied to female *C. obsoletus* and *C. scoticus* individuals trapped in different geographical regions and time periods during the year.
Methods: Using light-suction traps, female *C. obsoletus* and *C. scoticus* were sampled from two locations in the UK, France and Spain. A total of 759 individuals were identified with a molecular assay using the cytochrome oxidase I gene. Fifteen morphometric measurements were then taken from the head, wings and abdomen of slide-mounted specimens. Multivariate analyses investigated whether a combination of these could lead to accurate species identification.
Results: Principal component analyses revealed that the length and width of the smaller and larger spermathecae, and the length of, and width between, the chitinous plates can differentiate the species. These are all abdominal characteristics. Seasonal and geographic variation was observed for head and wing measurements, but not for those from the abdomen.
Conclusions: Our results suggest that female *C. obsoletus* and *C. scoticus* individuals can be separated under a stereomicroscope using abdominal measurements. Although we show that morphometrics can be used to differentiate the species, this can be time-consuming and we recommend undertaking this using standardized subsampling of large catches.
Relevance: This work highlights a new morphometric method of discriminating two of the main vector species of bluetongue virus. Such separations generally rely on molecular techniques, which can be expensive. Morphometric identifications may prove useful in outbreak situations when they can be quickly undertaken on a subsample of individuals to determine the proportions of each species present.

P106

Local dispersal of Palaearctic Culicoides biting midges estimated by mark-release-recapture

Georgette Kluiters, Harry Swales, Matthew Baylis, University of Liverpool, Neston, United Kingdom.
Contact: g.kluiters@liverpool.ac.uk

Purpose: As a key component in bluetongue (BT) modelling is farm to farm transmission via *Culicoides* midge movement, there is a need to determine dispersal patterns, in particular the distance over which midges fly during a set period. Yet, dispersal studies have not been undertaken successfully on northern European BT vectors. Our aim is to investigate the flight distances of these vectors between farms over set periods of time.
Methods: The dispersal of *Culicoides* Obsoletus Group members was studied on 19 farms in north Wales. Field-collected midges were trapped in light suction traps and self-marked with micronized fluorescent dust in the trap's collecting vessel. Release was made at a central farm and traps set on 18 surrounding farms ranging from 0.5 to 4 km. The study was repeated using six fluorescent dust colours over 18 days.
Results: An estimated 61,000 marked *Culicoides* were released and 12 (0.02%) *Culicoides* were recaptured. Of the females recaptured, six were *C. obsoletus/scoticus*, two *C. dewulfi*, two *C. pulicaris* and one *C. festivipennis*. The male was *C. obsoletus*. Recaptures occurred 1- 2.5 km from the release site, with the greatest number at 2.5 km. Most recaptures were 2 nights post-release; none were more than 3 nights later. The mean distance travelled for all *Culicoides* was 2.15 km, while for males it was 1 km and for females 2.21 km. Recaptures were made both downwind and upwind during the trapping periods, highlighting passive and active dispersal of *Culicoides* between farms.
Conclusions: This is the first study to demonstrate farm to farm movement of the main Palaearctic BT vectors, the Obsoletus Group. Such movement has disease control implications in terms of the vectorial movement of disease between farms. The results suggest that control measures applied at an infected farm will reduce the risk of spread to neighbouring farms, as well as reduce transmission at the source farm itself.
Relevance: This work highlights novel data on the dispersal of the main northern European BT vectors. This knowledge of flight distances can be implemented in disease transmission models and provides policy makers with an understanding of how fast disease may spread when transmitted by these vectors.

P107

The global transportation of Culicoides midges from flower-packing plants in Africa

Georgette Kluiters[1], Jessica Stokes[1], Eric Fevre[2], Karien Labuschagne[3], Matthew Baylis[1], [1]University of Liverpool, Neston, United Kingdom; [2]International Livestock Research Institute, Nairobi, Kenya; [3]ARC - Onderstepoort Veterinary Institute, Onderstepoort, South Africa. Contact: g.kluiters@liverpool.ac.uk

Purpose: In recent years there has been an increase in the export of flowers from Africa to European flower markets. Coincidentally, a significant outbreak of bluetongue (BT) started near a major Dutch import area for flowers in 2006. Outbreak investigations suggest a risk that the virus arrived in Europe by *Culicoides* BT vectors in cut flowers exported from Africa. Our aim is to determine whether these midges are present in flower-packaging plants in east Africa, and therefore whether *Culicoides* can be unknowingly exported to other countries during flower shipments.
Methods: Field sampling was undertaken at a flower-packaging plant in Kenya. Trapping was done at each stage of production (rootstock, propagation, growing greenhouses, packhouse, cold storage rooms, and transportation to the airport) using light-suction traps. Pooters were used to obtain insects directly from flowers and at composting sites, while emergence traps studied insect emergence from compost, leaf-litter and discarded.
Results: Located just 20 m from the nearest greenhouse, outside the curtilage of the plant, a mean of 95 *Culicoides* per trap per night were identified on a half-acre smallholding. Within the facility, greatest numbers of *Culicoides* were trapped at a pond (25) and leaf-litter compost site (24). Of the seven greenhouses sampled, only three had *Culicoides* trapped overnight (mean = 4, range: 2-8), and none were trapped in the propagation units. No *Culicoides* were trapped in the pack house, cold-store, or during transportation of the flowers to the airport. No *Culicoides* emerged from emergence traps or were trapped when pootering directly from flowers, although other small insects were collected.
Conclusions: This is the first study to investigate whether *Culicoides* are present within flower packaging plants in Africa. The results highlight that although present in small numbers both outside and within a number of greenhouses, the number of *Culicoides* trapped reduces with each stage between production and export.
Relevance: The results suggest that there is a negligible risk of exporting *Culicoides* with packaged flowers, so other possible routes of virus movement into Europe should be explored further.

P108

Validation of fluorescent dust marking of Culicoides biting midges and the design of a self-marking technique

Georgette Kluiters, Kristina Hunter, Matthew Baylis, University of Liverpool, Neston, United Kingdom.
Contact: g.kluiters@liverpool.ac.uk

Purpose: Investigation of insect flight patterns frequently involves dispersal studies. A common method for studying insect dispersal is mark-release-recapture (MRR) using wild-caught insects; however, this requires a suitable marker. At present, no studies have identified markers suitable for use in northern European bluetongue vectors, visible by eye or down a light microscope. Our aim is to determine whether micronized fluorescent dusts are suitable markers for *Culicoides* Obsoletus Group members.
Methods: A series of 11 experiments were undertaken to determine the effectiveness of three colours of Brilliant General Purpose (BGP) fluorescent dusts in marking *Culicoides* midges. Three areas were focused on: 1) dust properties, 2) the effect on *Culicoides*, and 3) dust application in the field.
Results: Each dust was insoluble in water, 10% washing-up liquid and 70% ethanol. They were visible down a microscope, with and without the use of a black light, and two were highly visible without a microscope. The dusts remained adherent to the insects for the duration of the experiments, did not transfer between marked and unmarked individuals or the environment, and remained adherent when the midges were stored in ethanol or water. The dusts had no effect on mortality rate over the 48 hrs of the experiment. There were no significant differences between behaviours undertaken by undusted controls and the BGP dusted insects. Field-based marking of the insects was achieved using a 'self-marking' technique, whereby the trapping vessel was pre-dusted with fluorescent dust prior to trapping the individuals to be marked.
Conclusions: This is the first study to identify BGP fluorescent dusts as markers for use with *Culicoides*. BGP fluorescent dusts provide a quick and effective method of marking and identifying *Culicoides* for both field and laboratory studies. The self-marking technique minimises the time needed to handle specimens prior to release.
Relevance: The results suggest a suitable marker for mark-release-recapture studies that may be of use in other insects. Such a marker can be used to identify insect flight patterns to inform epidemiological parameters in disease control models.

P109

Review of the 2012 epizootic hemorrhagic disease outbreak in domestic ruminants in the United States.

Gary E. Stevens[1], Brian J. McCluskey[2], Alison O. King[3], Emily S. O'Hearn[4], Gregory A. Mayr[4], [1]United States Department of Agriculture, Lincoln, NE, [2]United States Department of Agriculture, Ft Collins, CO, [3]United States Department of Agriculture, Jefferson City, MO, [4]United States Department of Agriculture, Plum Island, NY, Contact: Gary.E.Stevens@aphis.usda.gov

Purpose:
An unusually large number of cases of Epizootic hemorrhagic disease (EHD) were observed in United States cattle and white-tailed deer in the summer and fall of 2012. The purpose of this study was to report the findings of foreign animal disease investigations, state veterinary diagnostic laboratory submissions, and other sources which resulted in a diagnosis of EHD in domestic ruminants.
Methods:
Data on EHD diagnoses made between June 1 and December 31, 2012 were analyzed from foreign animal disease investigation reports, state diagnostic laboratory submissions, and clinical reports from veterinarians.
Results:
EHD was reported in the following species: cattle (129 herds), captive white-tailed deer (65 herds), bison (8 herds), yak (6 herds), elk (1 herd), and sheep (1 flock). A majority of the cases in cattle and bison were found in Nebraska, South Dakota, and Iowa. The majority of cases in captive white-tailed deer were found in Ohio, Iowa, Michigan, and Missouri. The most common clinical sign observed in the cattle and bison herd was oral lesions. The most common clinical sign observed in captive white-tailed deer herds was death. Average morbidity was 7% in cattle and bison herds, and 46% in captive white-tailed deer herds. The average mortality in captive white-tailed deer herds was 42%. EHDV-2 was the most common serotype identified in both cattle and captive white-tailed deer. EHD-1 and EHD-6 were also identified in cattle and captive white-tailed deer.
Conclusions:
This study confirmed that the clinical signs observed in cattle during an EHD outbreak are similar to those of some foreign animal diseases. In some cases, vesicular conditions seen during an EHD outbreak are often attributed to EHD and not reported as a possible foreign animal disease.
Relevance:
EHD symptoms can be similar to some foreign animal diseases such as Foot and Mouth Disease and Vesicular Stomatitis. Detection of these foreign animal diseases could be delayed in the midst of an EHD outbreak if the clinical signs are attributed to EHD and are not investigated as a possible foreign animal disease.

P110

MINTRISK, a Method for INTegrated RISK assessment of vector-borne livestock infections.

Aline A. De Koeijer[1], Wil Hennen[2], Sofie Dhollander[3], Clazien De Vos[1], [1]Central Veterinary Institute (CVI), Lelystad, Netherlands; [2]LEI, The Hague, Netherlands; [3]EFSA, Parma, Italy. Contact: aline.dekoeijer@wur.nl

Purpose:
Increasing occurrence of vector-borne livestock infections (VBADs) in Europe bring about the need for tools to evaluate and compare the risk of exotic VBAD. Although several methods exist for risk assessment, they do not take into account the specific needs of VBADs. Therefore, we developed a tool for risk assessment of VBADs allowing for comparison of the risk for different diseases. The tool can integrate various aspects of risk but still distinguish uncertainty, probability and impact.
Methods: An integral calculation method was developed in Excel and Visual Basic to assess the risk of VBADs based on the structure provided by FEVER, a recently developed Framework to assess Emerging VEctor-borne disease Risks for livestock. Knowledge and information about VBADs is summarized using an extensive questionnaire. An underlying quantitative model combines the answers to the questions, while taking account of the indicated uncertainty for each answer using Monte Carlo simulation. Results are presented for the overall risk, but also separately for the different steps in the model. Furthermore, the model indicates which answers and uncertainties contributed most to the risk.
Results:
The method was developed and tested on several infections. Adjustments were made, resulting in an effective tool for rapid assessment and comparison of disease risks. By separating probabilities, impact and uncertainty in a summarizing graph of the result for each infection, insight in the relevant risk aspects is gained and visualised. The evaluation for the most influential answers and the main sources of uncertainty can guide towards effective control and influential data gaps to be resolved.
Conclusions:
MINTRISK is a useful tool to prioritise in VBAD management. Results of MINTRISK can be used to support management decisions and prioritise resource allocations for research or disease risk preparedness.
Relevance:
Recent incursions of vector-borne pathogens in Europe such as Schmallenberg virus demonstrate the importance of knowledge of and preparedness for VBADs. MINTRISK has already been used to deal with recent requests from both national and international policy makers.

P111

DocNomo: the App to add evidence to your diagnosis

Charles Caraguel[1], Robin Wohlers-Reichel[1], Raphael Vanderstichel[2], [1]The University of Adelaide, Roseworthy, Australia; [2]The University of Prince Edward Island, Charlottetown, PE, Canada. Contact: charles.caraguel@adelaide.edu.au

Purpose: Fagan's Nomogram was invented by Dr. Terrence J. Fagan in 1975 to graphically calculate the probability of a patient having a target disorder given a test result (post-test probability) by entering the likelihood ratio of the test result and the probability of the individual having the disorder before running the test (pre-test probability). A secondary purpose of this nomogram is to explore the impact of the pre-test probability and the likelihood ratio on the post-test probability. If the likelihood ratio of the test result is not available, it needs to be calculated beforehand making Fagan's Nomogram less convenient for routine use.

Methods: Recently, we updated Fagan's Nomogram to integrate an initial step to compute the likelihood ratio directly from the diagnostic sensitivity and specificity. This resulted in a two-step nomogram which allows the user to quickly interpret and explore the outcome of a test. We adapted the new Two-Step Fagan Nomogram to the mobile operating system iOS 8 to facilitate and popularize its use with any Apple Inc. device.

Results: The new Two-Step Fagan Nomogram was digitized in an application called *DocNomo*. Test parameters and the pre-test probability can be entered using exact values or tactile sliders. The sliders allow the user to see how the output parameters change as the diagnostic characteristics and pre-test probability are modified.

Conclusions: *DocNomo* is freely available for download at the Mac App Store and allows the user to quickly and conveniently estimate the probability of a patient having a target disorder given a test result.

Relevance: Diagnostic test user, be it a clinician, student, researcher or regulator, can accesses an alternative option to quantify the evidence provided by a given test result. We hope this extension tool will support daily evidence-based medicine and informed decision making, regardless of the subject species.

P112

Development of an e-learning module for official veterinarians in Switzerland

Sabine Wanda[1], Uli Muellner[2], Katharina Stärk[3], Gertraud Schuepbach - Regula[1], [1]Institute of Veterinary Public Health, Liebefeld, Switzerland; [2]Epi - intercative, Rosenheim, Germany; [3]SAFOSO AG, Liebefeld, Switzerland. Contact: Sabine.Wanda@vetsuisse.unibe.ch

Purpose: In Switzerland, veterinarians, who undergo the training to become an official veterinarian, are trained in four main areas: Animal Health, Animal Welfare, Law and Communication and Food Safety and Drug Usage. Each discipline is taught as a single module of 5-9 days. Risk analysis, Monitoring and Surveillance and Outbreak Investigations (RAMSOI) is taught as part of Animal Health for 2 days. The training for official veterinarians takes place centrally, and is organized by the Federal Food Safety and Veterinary Office (FSVO). In times of budgetary cuts, awareness rose to offer an alternative to travelling, so veterinarians can participate and prepare for the modules from work or home and study at their time and pace and language (Switzerland has 4 official languages).
Th objective of the study was to develop an e-learning tool which should lower costs (travelling, time) and mandatory attendance in the classroom.

Methods:
A didactic concept was developed as the basis for the new learning room. A pilot module was developed for blended learning which involves one day as e-learning (substitute for one day on site) and one day on site. The module should offer practically relevant and easy to understand information in six e-learning units. The content is provided in form of podcasts, quiz, case examples and calculations, as well as relevant reading material on a learning platform. The theory provided in the 6 e-learning units will be applied to solve the tasks and exercises in discussion rounds and working groups on site on day2.

Results:

Conclusions:

Relevance: The e-learning pilot “RAMSOI” was used in 2015 for the first time. In case of positive feedback by the course participants, future e-learning modules will be developed for other parts of the course to ensure an optimal learning for official veterinarians.

P113

Scenario Planning: the future of the cattle and sheep industries in Scotland and their resiliency to disease.

Lisa A. Boden[1], Harriet Auty[2], Paul Bessell[3], Dominic Duckett[4], Jiayi Liu[5], Carol Kyle[4], Annie McKee[4], Lee-Ann Sutherland[4], John Reynolds[6], Mark Bronsvoort[3], Iain J. McKendrick[5], [1]University of Glasgow, Glasgow, United Kingdom; [2]SRUC Epidemiology Research Unit, Inverness, United Kingdom; [3]The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom; [4]The James Hutton Institute, Aberdeen, United Kingdom; [5]Biomathematics and Statistics Scotland, Edinburgh, United Kingdom; [6]SAMI consulting, Newbury, United Kingdom. Contact: lisa.boden@glasgow.ac.uk

Purpose: The future is highly uncertain. Important drivers of change (e.g. consumer preferences, politics, land-use and commerce) interact to compound risks over long time periods. These determinants influence the nature and structure of livestock industries including their resilience to disease. Although statistical or probabilistic models are utilised to identify risk factors for disease in the near future, these types of studies cannot ascertain the magnitude or importance of determinants or account for immeasurable uncertainties inherent in any predictions of the long-term future.

Methods: EPIC, Scotland's Centre of Expertise on Animal Disease Outbreaks, has used scenario planning as a technique to explore plausible but provocative long-term futures that capture dynamics underpinning the resilience of Scottish sheep and cattle sectors to animal disease.

Results: These future scenarios highlighted a number of important drivers that influence disease resilience including: industry demographics, the role of government support and regulation and the capacity for technological innovation to support the industry to meet local and global market demand. Participants in the scenario planning exercises proposed creative, robust strategies that policy makers could consider implementing now to enhance disease control and industry resilience in multiple, uncertain futures. These have resulted in ten key questions proposed for policy makers to provoke further discussion about improving resiliency and disease preparedness.

Conclusions and Relevance: The participatory methods described in this study are a novel application of scenario planning in animal health. The scenarios created are being used to test existing and new models of disease transmission, proposed control strategies, and risk assessments which currently underpin Scotland's animal disease contingency plans. The exercise is a good example of successful participatory epidemiology that has enabled stakeholders to build strategic partnerships with both government and scientists by sharing experiences, exchanging knowledge and finding common ground through understanding one another's constraints.

P114

A network for evaluation of One Health to enhance the evidence base on the added value of interdisciplinary collaboration

Ann Lindberg[1], Simon Ruegg[2], Richard Kock[3], Jonathan Rushton[3], Martijn Bouwknegt[4], Chinwe Ifejika Speranza[5], Maurizio Aragrande[6], Peter Bogner[7], Anthony Staines[8], Anthony Staines[8], Sara Babo Martins[3], Laura Cornelsen[9], Marie McIntyre[10], Helmut Saatkamp[11], Massimo Canali[6], Barry J. McMahon[12], Paulo Roriz[13], Laura C. Falzon[14], Kevin Bardosh[15], Sonja Hartnack-Wilhelm[2], Houda Bennani[3], Barbara Häsler[3], Jakob Zinsstag[16], [1]Swedish National Veterinary Institute, Uppsala, Sweden; [2]Vetsuisse Faculty, Zürich, Switzerland; [3]Royal Veterinary College, Hatfield, United Kingdom; [4]National Institute for Public Health and the Environment, Bilthoven, Netherlands; [5]University of Bonn, Bonn, Germany; [6]University of Bologna, Bologna, Italy; [7]Global Initiative on Sharing All Influenza Data, Washington, DC, [8]School of Nursing and Human Sciences, Dublin, Ireland; [9]London School of Hygiene and Tropical Medicine, London, United Kingdom; [10]University of Liverpool, Liverpool, United Kingdom; [11]Wageningen University, Wageningen, Netherlands; [12]UCD School of Agriculture & Food Science, Dublin, Ireland; [13]Faculdade de Ciências, Porto, Portugal; [14]Veterinary Public Health Institute, Liebefeld, Switzerland; [15]University of Edinburgh, Edinburgh, United Kingdom; [16]Swiss Tropical and Public Health Institute, Basel, Switzerland. Contact: ann.lindberg@sva.se

Purpose: Societal impacts of recent infectious disease outbreaks (e.g. Q-fever, Ebola, MERS) could have been reduced by better interaction between health authorities - a reflection of deficiencies in the collaboration between sectors. A One Health (OH) approach implies that the response to societal challenges is interdisciplinary, by applying both natural and social sciences to human and animal health, while sustaining the global environment. This paper describes an evolving EU COST funded project, "Network for Evaluation of One Health" (NEOH), where over 25 countries in and outside Europe collaborate to enable evaluations of OH initiatives and to further the OH evidence base.
Methods: The prime aim of NEOH is to develop a handbook on the evaluation of OH. The handbook includes a critique of the current status of OH evaluations and a review of separate and integrated health approaches, leading to an evaluation framework with associated methods and metrics. The framework will be applied, tested and refined in a set of case studies, to provide input to a meta-analysis of the added value of OH case studies. OH initiatives will be prospectively examined in order to identify costs and benefits. A research agenda will be devised to enhance European health systems with methods addressing cross-sector cooperation, cost-effectiveness, institutional structures and policy development.
Results: The initial evaluation framework with the plan for testing and preliminary results will be presented.
Conclusions: The aim of NEOH is to generate solid scientific evidence on the efficiency and cost-effectiveness of OH activities, and show how they can be quantified. This is needed for decision-makers to develop sensible and sustainable policies, and allocate resources in the best possible way.
Relevance: While OH approaches for integrated surveillance and control of zoonoses and the provision of health services have been validated in Africa and Asia, examples from the developed world are rare. Moreover, standardised OH evaluation methods are absent, which hampers science-based decision making and optimal resource allocation. NEOH provides an opportunity for the scientific community to bridge this gap.

P115

Tumors detected in cattle at a Brazilian abattoir

Jose G. Amoril[1], Ervaldo L. S. Sena[2], [1]Ministry of Agriculture, Livestock and Food Supply, Goiania - GO, Brazil; [2]Goias Federal University School of Zootechnology and Veterinary, Goiania - GO, Brazil. Contact: jgamoril@terra.com.br

Few diseases are so intriguing as cancer. It is the second human deaths most frequent cause in developed countries. Veterinary oncology raises both economic and a public health concerns. Carcasses disposition is not an easy task and we must avoid non-science-based judgment. Beef export in Brazil is a US$7 billion annual business with 136 countries and thereby efficacy of veterinary services is mandatory. We aim to enhance further comparative oncology and cancer epidemiology studies. We proceeded ante and post mortem inspection of 556,127 bovines at an abattoir in Goias, central part of Brazil, from May 1st, 2012 through April 30th, 2014. Samples of affected tissues were sent to LAPAVET Laboratory, Santo Andre, SP, for histological confirmation and tumor classification. Regarding to malignant lymphomas (ML), additional sterile swabs of lesions and blood samples were screened for Bovine Leukemia Virus (BLV) DNA by a real-time PCR assay at the Molecular Biology Laboratory at the Food Research Center of Goias Federal University School of Zootechnology and Veterinary, Goiania, GO. Histopathology confirmed 23 tumors: eleven ML, 02 liver carcinomas, 01 metastatic ocular squamous cell carcinoma, 03 metastatic carcinomas (lymph nodes), 01 kidney carcinoma, 01 metastatic mesothelioma, 01 fibrosarcoma, 01 hemangiosarcoma, 01 liposarcoma, 01 cholangiosarcoma. We found DNA of BLV in 05 out 11 ML. Carcasses and respective parts with ML or other metastatic cancer were condemned according to Brazilian meat inspection regulations, RIISPOA (regulations for industrial and sanitary inspection for products of animal origin). Carcasses not adversely affected by a tumor without metastasis were judged as fit for human consumption.Incidence of cancers might have been influenced by our research short period and age of most animals (ca. 2-3 years old). BLV DNA in bovine tissues with ML might pose public health risk since researchers also found BLV DNA in human breast tissues recently. Probable BLV zoonotic role deserves attention and One-Health approach studies.Our results can help further research in comparative oncology as well as in bovine cancer epidemiology and economics.

P116

OIE Veterinary Education Twinning Programme RVC-JUST

Imadidden I. M. Musallam, Javier Guitian, Royal Veterinary college, Herts, United Kingdom. Contact: Imusallam@RVC.AC.UK

Purpose: To establish a knowledge exchange platform to share best academic practice in the broad field of Veterinary Public Health between Royal Veterinary College (RVC) and Jordan University of Science and Technology (JUST) and to use this platform to complete a series of activities that will facilitate the eventual accreditation of JUST by EAEVE and the long term engagement of RVC and JUST in the provision of state of veterinary public health training in the Middle East (ME) and the Arab region. Here we present the overall strategy to achieve this goal and preliminary outcomes.

Methods: The project began in January 2015 with funding for an initial period of 3 years including three strands of activities: undergraduate, postgraduate and professional education. The undergraduate strand involves the design, implementation and evaluation of a number of interventions in the undergraduate curriculum, the postgraduate strand will be based on paired research projects with joint supervisory arrangements. As part of the professional education strand, staff from the Jordanian Veterinary Services will follow a modular field epidemiology training program.

Results: Specific changes introduced in the undergraduate veterinary curriculum of JUST will strengthen undergraduate VPH teaching and facilitate fulfilment of OIE recommendations on the competencies of graduating veterinarians. Enhanced engagement of stakeholders including Jordanian veterinary and public health services in the undergraduate and postgraduate educational activities at JUST. Establishment of strong educational and research links between JUST and RVC will promote VPH research in Jordan and the region. The establishment of a program for continuous professional development of veterinarians in epidemiology, VPH and bioethics will potentially benefit the veterinary services of the ME countries.

Conclusions and Relevance: This program is one of the first education twinning programmes endorsed by the OIE; as such its design and implementation provides insights that can be useful for future OIE twining projects aimed at strengthening the provision of veterinary epidemiology and public health education worldwide.

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One Health initiatives in the veterinary medicine curriculum at University of Copenhagen

Liza R. Nielsen[1], Anders Dalsgaard[2], Anita Forslund[2], Tine Hald[3], Maria V. Johansen[2], [1]University of Copenhagen, Frederiksberg C, Denmark; [2]University of Copenhagen, Frederiksberg C, Denmark; [3]Technical University of Denmark, Søborg, Denmark. Contact: liza@sund.ku.dk

Denmark is a small country in Europe with 5.3 million inhabitants and one veterinary school with 180 students admitted annually. The curriculum is organized into a 3-year bachelor of 180 ECTS (credit points) and a 2½ year master program (150 ECTS). As part of the master program the veterinary students focus on one area for 17 weeks (26.5 ECTS) in one of six specialization tracks (i.e. One Health, Herd Health, Equine Clinic, Advanced Companion Animals, Biomedicine and 'Alternative track'). The One Health track was initiated in 2015 in response to a growing need for candidates with One Health expertise reaching beyond traditional food hygiene. The intention was to produce candidates with competences aimed at the type of work performed in international and national public health organizations.

The first four weeks of the One Health track is taught together with the Herd Health track to cover the responsibilities and interactions between private herd health veterinarians and state veterinarians, principles of systematic disease control and prevention/biosecurity, legislation and practical performance of contingency planning. The students meet with veterinarians working with these topics, and they use the knowledge gained in the writing of a report with emphasis on the systems, processes and responsibilities in decision making.

One Health track students are then introduced to global preparedness by working with essential topics and methods, e.g. surveillance and outbreak investigation, source attribution, burden assessment, cost-effectiveness analysis, the role of the external environment, use of waste-water, antimicrobial use and resistance in livestock production and companion animals, neglected zoonoses, vector-borne diseases, and translational medicine. Parts of the program are open to students from other tracks, other master programs or from abroad. Furthermore, a 5 ECTS One Health International Summer Course is offered to veterinary students in the alternative track and other national and international participants. In total, 11 students participated in the One Health track in 2015. Experiences with these educational initiatives will be discussed in the presentation.

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Molecular epidemiology an important tool in the prevention and control of animal disease. Cuban experience.

Carmen Laura Perera Gonzalez[1], Ana María Acevedo Beiras[1], Abdulahi Alfonso Morales[1], Nadia Martinez Marrero[1], Liani Coronado Baez[1], Liliam Rios Cordero[1], Orlando Martinez[2], Yoandry Hinojosa Lopez[1], Damaris Relova Vento[1], Armando Vega Redondo[1], **Maria Irian Percedo Abreu**[3], Maria Teresa Frias Lepoureau[1], Heidy Diaz de Arce Landa[1], Lester Josue Perez Rodriguez[1], [1]National Animal and Plant Health Center-CENSA, San Jose de las Lajas, Cuba; [2]University of Informatics Science, La Habana, Cuba; [3]National Animal and Plant Health Center-CENSA, San Jose de las Lajas, Cuba. Contact: percedo@censa.edu.cu

For over 30 years, molecular epidemiology has served as a very important tool for studying the spread of infectious diseases. This work will be focused to summarize the use of the molecular epidemiology supporting characterization of the viral agents with main economical importance in Cuba in the last 10 years.The combination of molecular biology, epidemiology and population genetics in the science of molecular epidemiology is a powerful tool to develop control strategies for infectious disease. This approach is especially significant for viral diseases, due to the rapid changes in the viral genome, regardless of it consists of DNA or RNA, which allows the drawing of conclusions about the origin of the virus lineage, classification, the influence of immunologic and environmental pressures, development of diagnosis tool and spatial tracking of the viral agents. The current work was focuses to provide an overview of phylogenetic analysis applied to molecular epidemiology and characterization analysis supporting the diagnosis, prevention and control of viral diseases in Veterinary Medicine in Cuba. For this purpose the examples bovine coronavirus, and porcine circovirus 2, classical swine fever, avian influenza and Infectious bursal disease viruses will be taken as models.

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Defining requirements and execution of international field trials for next generation foot-and-mouth disease vaccines and diagnostics

Michelle Colby[1], R. Brooks-Motroni[1,2], D. Brake[3], P. Hullinger[4], [1]Department of Homeland Security, Washington, DC, [2]American Association for the Advancement of Science, Washington, DC, [3]BioQuest Associates LLC, East Lyme, CT, [4]Lawrence Livermore National Laboratory, Livermore, CA, Contact: michelle.colby@hq.dhs.gov

Background The agricultural defense mission of the U.S. Department of Homeland Security Science and Technology Directorate is to develop state of the art countermeasures for high priority transboundary animal diseases. This includes funding the development of a human Adenovirus vectored (Ad5) FMD vaccine and a FMD 3B cELISA, which can be used to differentiate infected from vaccinated animals (DIVA). The monovalent Ad5FMD vaccine (serotype A24 Cruzeiro) has completed potency, purity, efficacy and field safety trials in the U.S. and is conditionally licensed for use in cattle in the U.S. Ad5FMD vaccine candidates for other sero/sub-types are currently in development. While vaccine candidates have been through rigorous testing in the U.S., primarily in BSL3 biocontainment, there is a desire to further evaluate their performance/efficacy in a field setting in an endemic environment.
Objective To design a field efficacy study of a multivalent Ad5FMD vaccine and evaluation of FMD 3B cELISA technologies in a FMD endemic country. To build international partnerships to facilitate future testing of other countermeasures in development.
Methods A series of meetings is underway. The first was held in June 2014, with U.S. stakeholders and potentially interested collaborating countries discussing the feasibility and best approach to the design and execution of a field evaluation of an Ad5 FMD vaccine and 3B ELISA assay. Ultimately, the goal is to design a study that will further evaluate the performance and efficacy of the Ad5FMD vaccine and the 3B ELISA in a FMD endemic country, to identify FMD endemic partner countries, and to identify the regulatory pathway to conduct the required study.
Relevance Relationships with FMD endemic countries are necessary to evaluate the efficacy of next generation FMD vaccines and performance of diagnostics in field settings. These research collaborations must be conducted in a well-coordinated, open and transparent manner, with benefit to all parties involved. Such studies are helpful to the FMD endemic countries evaluating their vaccination options and to the U.S. in providing valuable information that can inform vaccination and other outbreak response policy.

P120

Challenges and opportunities when using ontologies in animal health syndromic surveillance

Fernanda C. Dórea[1], Flavie Vial[2], Céline Dupuy[3], Ann Lindberg[1], Crawford Revie[4], [1]National Veterinary Institute, Uppsala, Sweden; [2]University of Bern, Bern, Switzerland; [3]French Ministry of Agriculture, Lyon, France; [4]University of Prince Edward Island, Charlottetown, PE, Canada. Contact: fernanda.dorea@sva.se

Purpose: The variety of animal health data sources explored for veterinary syndromic surveillance (VSS) presents great opportunities for the extraction of information in real-time. However, the lack of data classification standards can impede development and prevent output comparability. Ontologies can be used to formalize the knowledge employed for syndromic classification, by storing concepts and relationships as machine-interpretable definitions. This work aims at developing an ontology for VSS, which will facilitate the development of smart systems for data use which do not rely on standard coding practices at source.

Methods: In order to investigate the potential for developing an ontology for a standardized syndromic classification of animal health data (SSynCAHD - www.sva.se), two workshops were held involving interested experts, and an inventory of existing ontologies was conducted.

Results: Experts provided details regarding the data sources available for VSS in their institutions (a total of 27 data sources from 8 countries). As laboratory data were reported to be in use in 6 of the 8 countries, it was decided to use this as a starting point for the ontology, with an initial focus on "reproductive" and "respiratory" syndromes. Reusable ontologies covering most of the basic biological knowledge to be modelled (e.g. pathogen taxonomy, animal anatomy, disease processes, and clinical signs) already exist. Therefore, in developing an ontology for SSynCAHD, focus is being given to the relationships between these entities. For instance the knowledge that "pathogen: Brucella sp AFFECTS organ system: Reproductive", results in the decision to classify a laboratory test request for detection of brucellosis as "reproductive syndrome".

Conclusions:SSynCAHD is being developed with strong community involvement in all stages of ontology development, maximizing the utility and use of the developed ontology.

Relevance: An ontology of VSS will increase the potential use of animal health data for automated extraction of surveillance information, as well as promote communication between VSS systems across institutions and different countries.

P121

Behind the OIE World Veterinary Day 2013

Noluvuyo R. Magadla, Gauteng Department of Agriculture and Rural Development, Johannesburg, South Africa. Contact: noluvuyo.magadla@gauteng.gov.za

There has been rapid development in the areas of livestock management system and animal identification and traceability systems around the first world countries motivated by food safety, market access and disease control. A number of Southern African countries have established traceability system based on the need to enter lucrative export markets. Gauteng Province started with the traceability system using International Committee for Animal Recording (ICAR) approved tamper evident non-reusable livestock ear-tags in April 2013. The main objective of the project was monitoring of farm production management and disease control in the previously underserviced areas. The initial stage of the project was looking at the census of the area, the herd composition and recording of vaccines used and disease tests. The most prominent breed of animals in the area was Bonsmara (49%) followed by Brahman (26%) and crossbreed (22%). The area herd was composed of 82% females (12% 0-1year of which less than 1% were below 4 months, 7% 1-2years, 48% were 2-5years, 30% were 5-10 years and 4% were above 10 years) and 17% males (27% were 0-1year of which 2.5% were below 4 months, 15% 1-2years, 50% were 2-5years and 6% were 5-10 years). All animals in the area were vaccinated against Bacillus anthracis, Clostridium botulinum types C1 +2 and type D and Clostridium chauvoei. The livestock management and traceability system accommodates the whole production chain from birth to slaughter at the same time it is a disease control tool achieving economical sustainability through international compliance. The recorded proportion of calves and mature cows was a source of concern. From the database, the herd consisted of 17% of calves at the age of 12 months and below whilst the number of replacement heifers was low (7% where a normal herd replacement would be expected to be 20%). The initial information from the database revealed a need for skills development on production systems and a need further veterinary awareness interventions. More could be achieved in advancing livestock production management, through technology as the system uses portable cell phone device and disease control measures using full traceable system.

P122

A survey of the use of veterinary information resources across the global veterinary profession.

Selene J. Huntley, Rachel S. Dean, Andrew Massey, **Marnie L. Brennan**, University of Nottingham, Nottingham, United Kingdom. Contact: marnie.brennan@nottingham.ac.uk

Evidence-based veterinary medicine is the use of best evidence in combination with clinical judgement to make clinical veterinary decisions. The aim of this study was to assess the current breadth of resources used by veterinarians globally. This knowledge is essential to ensure that research findings are appropriately located to reach the intended audience in order to enhance the use of evidence by the profession.

The study population was veterinarians worldwide, with the exception of those in the UK. An online questionnaire was distributed to veterinarians via veterinary organisations, online forums, social media or directly by the researchers. Respondents were asked to list up to ten journals and up to ten electronic resources they commonly use and to nominate which they found most useful.

There were 2137 responses received from veterinarians in 80 countries. The top three most represented countries were USA (34 %), Sweden (11%) and Australia (9%). The majority of respondents (89%) did clinical work. Respondents listed a mode of three journals and one electronic resource. The most frequently listed journal and electronic resource was the Journal of the American Veterinary Medical Association (JAVMA) (11%) and the Veterinary Information Network (VIN) (5%), respectively. The journal resources nominated as the most useful differed between clinicians and non-clinicians. The top three journals nominated as most useful by clinicians were JAVMA (15%), Clinicians' Brief (8%) and Compendium; Continuing Education for Veterinarians (7%) and by non-clinicians were Preventive Veterinary Medicine (16%), Veterinary Pathology (14%) and Veterinary Record (6%). The top three electronic resources nominated as most useful by clinicians were VIN (57%), International Veterinary Information Service (9%) and PubMed (6%) and by non-clinicians were PubMed (16%), VIN (9%) and the website of the Office International des Epizooties (7%).

In conclusion, veterinarians worldwide use a diverse range of resources. The most commonly accessed resources could be utilised to disseminate important principles of evidence-based veterinary medicine and veterinary research to a global audience.

P123

Develop an epidemiological and economic meta-model to assess the impact of an African horse sickness epidemic in a free region, under different environmental scenarios.

Almudena Sánchez-Matamoros[1], Marta Martínez-Avilés[1], Eduardo Fernández-Carrión[1], Beatriz Martínez-López[2], Eva Iglesias[3], **Jose Manuel Sánchez-Vizcaíno**[1], [1]Complutense University of Madrid, Madrid, Spain; [2]Medicine and Epidemiology, UC Davis, California, CA, [3]E.T.S Agronomics Engineering, Technical University of Madrid, Madrid, Spain. Contact: jmvizcaino@ucm.es

Purpose

African horse sickness (AHS) is a lethal vector-borne viral disease of equines classified as OIE notifiable disease, and for which Europe is officially free. Given the serious socio-economic effects of AHS in the equine population, a re-emergence should be controlled through efficient decision-making. Nowadays, there is European legislation on AHS control (92/35/EEC); however, it does not specify under which epidemiological circumstances is the vaccination recommended. The aim of this study is to develop an epidemiologic and economic meta-model to assess the impact of an AHS epidemic in the equine sector in a free region and to evaluate whether vaccination measure would be recommended.

Methods

A transmission and economic meta-model was developed to assess the socio-economic consequences of two different control strategies following an outbreak, control measures with the application or not of vaccination, under different environmental scenarios.

Results

The estimated financial impact varied between €135.5 mln and €584.0 mln. In all scenarios, the highest financial impacts were the cost of production losses and the cost of control measures associated with the large number of dead, immobilized and vaccinated animals. The cost of vaccination was 2 to 3% of the control measures. The implementation of vaccination allowed the reduction of the socio-economic consequences compared with the results of the control measures without vaccination, reducing widely the number of infectious and dead equines, and obtaining a net benefit of between €2 mln and €117 mln. This strategy was efficient in all scenarios due to the overall benefit-cost ratios was higher than one.

Conclusions

This epidemiological and economic meta-model has allowed to estimate, for the first time, the potential socio-economic impact of AHS a free region. The results allow to conclude that the control measures with vaccination is the best strategy for all scenarios.

Relevance

The meta-model developed is important for policy makers to support decision-making, since this methodology allows the selection of the most efficient strategy for AHS control based on estimated epidemiological and economic information.

P124

Implementation and validation of an economic module for the epidemiological model Be-FAST to predict the costs generated by livestock diseases epidemics.

Eduardo Fernández Carrión[1], Benjamín Ivorra[2], Ángel Manuel Ramos[2], **José Manuel Sánchez-Vizcaíno**[1], [1]Universidad Complutense de Madrid, Madrid, Spain; [2]MOMAT grupo de investigación de la Universidad Complutense de Madrid, Madrid, Spain. Contact: jmvizcaino@ucm.es

Purpose:
To develop a computer program to provide a framework for modelling the economic consequences of infectious livestock disease spreads.
Methods:
To integrate a new module into Be-FAST program, a time-spatial stochastic spread mathematical model for studying the transmission of infectious livestock diseases within and between farms. To validate the new extension with historical cases of Classical Swine Fever (CSF) in Spain. To make a deep study of costs involved in CSF epidemics.
Results:
Direct costs associated with control measures are strongly associated with the number of infected farms and indirect costs with the duration of the epidemic. Real information of Spanish epidemic show that payable and calculated costs were around 33% and transferred costs were around 67% of the total costs, with a total amount of 81.52 million of euros. Simulated cases estimated median values around 30% and 70% for both expenses, with a total amount of 85.26 million of euros.
Conclusions:
The economic model allow us to study the behaviour of economic patterns in livestock epidemics spreads depending on the disease, region and control measures features.
Relevance:
Useful tool to decision with high computing speed. Economic parameters integrated in stochastic model for livestock disease for Monte-Carlo simulations.

P125

A conceptual framework for risk stratification to inform the design of risk-based surveillance aimed at early detection of exotic or emerging diseases

Marta Martínez Avilés[1], Lucy Snow[2], Gerdien van Schaik[3], Arianna Comin[4], Birgit Schauer[5], Barbara Haesler[6], Betty Bisdorff[6], Marie-Isabelle Peyre[7], Linda Hoinville[6], Katharina Staerk[8], Dirk U. Pfeiffer[6], **José Manuel Sánchez-Vizcaíno**[1], [1]Universidad Complutense de Madrid, Madrid, Spain; [2]Animal and Plant Health Agency, Addlestone, United Kingdom; [3]GD Animal Health, Deventer, Netherlands; [4]Statens Veterinaermedicinska Anstalt, Uppsala, Sweden; [5]Friedrich Loeffler Institute, Riems Island, Germany; [6]Royal Veterinary College, London, United Kingdom; [7]CIRAD, Montpellier, France; [8]SAFOSO, Geneva, Switzerland. Contact: jmvizcaino@ucm.es

Purpose: The objective is to present a conceptual framework to inform the design of risk-based surveillance aimed at the early detection of exotic or emerging disease. Commonly, free countries consider border areas with infected countries to have the highest probability of exposure. This approach is usually reactive and often does not take into account the epidemiology of an infectious disease, where as a result of trade, hunting or other human behaviours, high risk areas may not lie along these border regions. This means the benefits of a risk-based surveillance approach are not applied effectively. While appropriate tools for estimating this probability of exposure are available, there is a lack of standardization across diseases and countries, and therefore disagreement with respect to the validity of information generated.
Methods: We describe and compare the epidemiological tools that are currently available for performing estimation of the spatial and temporal variation in the probability of exposure expanding on recently published systematic review of surveillance systems (Rodriguez-Prieto et al, 2014), classifying them according to data needs and type of analysis (i.e. quantitative, qualitative or semi-quantitative). Advantages and disadvantages of the tools are discussed, and recommendations made for optimum sets of tools will be tested for different types of infectious diseases.
Results: Based on the OIE risk assessment framework, we present tools to enable the identification of the threat, to assess the entry through the identification of transmission pathways for the introduction, and to assess the risk of exposure to the threat. Many of the tools presented are based on spatial analysis and have been mainly applied to vector-borne diseases.
Conclusions: Not all subpopulations are at equal risk of infection. There are several ways of considering factors to benefit from a risk-based approach to surveillance at each step in the design process.
Relevance: The conceptual framework enhances the setting of guidelines for early detection of emerging diseases through the application to a variety of disease models, data needs and technical requirements.

P126

Needs assessment in small-scale farms and urban animal agriculture in Western States of the US

Alda Pires[1], Amos Peterson[2], Dale Moore[3], Beatriz Martínez-López[4], Lauren Gwin[5], [1]School of Veterinary Medecine, University of California, Davis, CA, [2]College of Veterinary Medicine,Washington State University, Pullman, WA, [3]College of Veterinary Medicine, Washington State University, Pullman, WA, [4]VM: Medicine and Epidemiology, University of California, Davis, CA, [5]Oregon State University, Corvallis, OR, Contact: apires@ucdavis.edu

Purpose: The growing consumer interest in local food production and sustainability, and increased preference for fresh, local and organic products in the last years has been linked to an increase the number of small-scale farms, community supported agriculture and farmer's markets in Western US (CA, OR and WA). This increasing popularity of small-scale farms and urban agriculture has led to a growth of production of livestock animals in urban and peri-urban areas. One of the recognized challenges faced by small-scale farmers is the lack of access to technical information and veterinary oversight. This might create an increased risk of occurrence of zoonotic and emergent diseases, drug or chemical residues and foodborne pathogens in the food chain.
Methods: The objectives of this study were to conduct a needs assessment to determine the needs of farmers, related to management practices, biosecurity, and food safety and of veterinarians who might serve them. We used a mixed mode cross-sectional survey in 3 states (CA, OR and WA). Logistic and spatial methods were used to identify potential risk factors associated with deficient biosecurity, husbandry and food safety and to identify areas where target education efforts should be prioritized.
Results: Preliminary results shows that 73 % of the respondents raised poultry, 35.5 % goats, 27.6% sheep, 24.7% cattle and 16.4% swine. Twenty five percent (43/170) of the respondents did not know of a veterinarian would treat their production animals. Thirty two percent of the respondents were primarily raising their animals for the sale of animals or animal products.
Conclusions and Relevance: Results of this needs assessment will provide information about the needs and trends of small-scale farms and urban animal agriculture and will allow the implementation of risk-based interventions and outreach activities.

P127

Dissemination of antibiotic resistance genes from human and agricultural sources into the environment: a systematic review of the evidence

IRENE BUENO[1], JESSICA WILLIAMS-NGUYEN[2], JAN SARGEANT[3], ANDRE J. NAULT[4], HAEJIN HWANG[5], RANDALL S. SINGER[5], [1]UNIVERSITY OF MINNESOTA, ST.PAUL, MN, [2]UNIVERSITY OF WASHINGTON, SEATTLE, WA, [3]UNIVERSITY OF GUELPH, GUELPH, ON, Canada; [4]UNIVERSITY OF MINNESOTA, ST.PAUL, MN, [5]UNIVERSITY OF MINNESOTA, ST.PAUL, MN, Contact: bueno004@umn.edu

Purpose:
To systematically review the question: Are environmental levels of antibiotic resistance higher in close proximity to point sources compared to areas more distant from these sources?
Methods:
A comprehensive search of PubMed, CABI, and Scopus, was conducted on 10/14/14 to capture all publications of relevance to the question. Citations were exported to EndNote. Titles and abstracts were screened by excluding any study that a) was not primary research, b) did not involve the collection of environmental samples (soil, water, air, or wildlife), or, c) did not measure prevalence or concentration of bacterial antibiotic resistance factors (bacteria or genes). This abstract pertains only to the antibiotic resistance genes (ARG) component. The methods section of these studies was then screened to determine if the study design permitted the collection of evidence on the review question. Studies were excluded if a) proximity to, or direction from, suspected sources were not mentioned, or b) a comparison group was not used. At the time of this submission, these studies are being evaluated for biases that might impact the results. Data consisting of exposure, outcome (ARG), measures of association, and statistical methods, are being extracted and compared from these studies.
Results:
A total of 4,525 citations were identified, and 734 records were relevant.
The number of studies that provided evidence about the dissemination of ARG from a suspected source was 33. Biases and extracted data are being analyzed.
Conclusions:
Preliminary results show there is lack of evidence to demonstrate an association between point sources and an increase in environmental levels of ARG, but the studies need further assessment.
Relevance:
There is a growing concern about the role the environment plays in the dissemination of ARG. However, the overall evidence that potential sources of ARG, such as agricultural facilities, are associated with a measurable increase in these genes in adjacent areas has not been systematically evaluated. The results of this systematic review will be used to summarize the existing evidence to answer the study question, and will highlight data gaps that need to be addressed.

P128

Social factors influencing the eradication of Bovine Tuberculosis in Spain: preliminary results.

Giovanna Ciaravino[1], Sebastian Napp[2], Alberto Pacios[3], Patricia Ibarra Arteaga[4], Josep Espluga Trenc[5], Jordi Casal[1], Lourdes Anaya[3], Ignacio Garcia-Bocanegra[6], Alberto Allepuz[1], [1]Universitat Autònoma de Barcelona, BARCELONA, Spain; [2]Centre de Recerca en Sanitat Animal (CReSA)- Institut de Recerca i Tecnologia Agroalimentàries (IRTA), BARCELONA, Spain; [3]Consejería de Agricultura, Pesca y Desarrollo Rural, Junta de Andalucía, SEVILLA, Spain; [4]Universidad de Sevilla y Asociación Andaluza de Antropología, SEVILLA, Spain; [5]IGOP - GEPS - ARAG-Universitat Autònoma de Barcelona, BARCELONA, Spain; [6]Facultad de Veterinaria, UCO, Campus Universitarios de Rabanales, CORDOBA, Spain. Contact: giovanna.ciaravino@uab.cat

Purpose: In Spain, the intensification of the Bovine Tuberculosis (bTb) eradication program at the end of the 80s, allowed a reduction of the herd prevalence from 11.1% in 1986 to 2.2% in 2000. Despite these efforts, in the last decade this reduction has reached an impasse. The engagement of stakeholders is one of the key factors for the eradication program's success, but the influence of social factors, despite being well known in human medicine, is often ignored in the control of animal diseases. In order to investigate perceptions and attitudes of farmers and veterinarians in relation to the bTb eradication program, and their influence on its efficacy, we are carrying out a sociological study in the south of Spain (high prevalence area).
Methods: The study includes three phases: exploratory interviews, qualitative in-depth interviews and a quantitative survey. In the first phase (i.e. exploratory interviews) key people representative of the different sectors involved in the bTb program were interviewed: three farmers (beef, dairy and bullfighting farmers) and five veterinarians (central and regional veterinary services, diagnostic laboratory and two private veterinarians). Semi-structured exploratory interviews, which lasted between 50 and 120 minutes, were conducted in order to discuss different themes: 1) strong and weak points of the bTb eradication program; 2) Reasons for failing to eradicate bTb; 3) Future perspectives and proposed changes to the program; 4) Benefits of being bTb free.Results:Some topics that arose from the interviews were related to weak communication and confidence among stakeholders, lack of confidence in the eradication program, lack of benefits of being bTb free, lack of training for farmers and pressure faced by veterinarians conducting the tests due to personal relations with farmer. Next steps will be to further investigate these aspects through qualitative in-depth interviews to a sample of different types of stakeholders, and to quantify the importance of the different social factors through a representative quantitative survey. Qualitative in-depth interviews are ongoing, and the most relevant results will be presented at the conference.

P129

One health observatories for emerging zoonotic arboviroses

Marta Martínez Avilés[1], Joaquín Goyache Goñi[1], Eduardo Fernández-Carrión[1], Amaya Sánchez Gómez[2], Carmen Amela[2], **José Manuel Sánchez-Vizcaíno**[1], [1]Universidad Complutense de Madrid, Madrid, Spain; [2]Ministry of Health, Social Services and Equality, Madrid, Spain. Contact: jmvizcaino@ucm.es

Purpose: In the past years, zoonotic arbovirosis such as West Nile disease or Crimean Congo Haemorrhagic fever have been reported in Europe. There are other known arbovirosis that have yet to emerge in Europe, like Rift Valley fever, which keeps spreading with unsufficient control in many African territories. Spain's location between two continents, its annual and increasing presence of potential vectors, its animal hosts characteristics of exposure and also particular socio-cultural factors, offer a unique opportunity to monitor emerging zoonotic arboviroses in Europe.
Methods: a) spatial risk assessments that consider the distribution of host and vector population at risk and the factors involved in their transboundary presence, the distribution of risk factor for exposure of both the animal and human hosts populations, and the distribution of risk factors that favour infection and spread among vector, animal and human host population; b) an assessment of the impact on the results of the gaps in knowledge on the infection behaviour; and c) an assessment of the diagnostic and logistic capacity to face this challenge.
Results: a) risk-based choice of location for "one-health" observatories for zoonotic arbovirosis; b) activities that can reduce the current gaps in knowledge; and c) structure and coordination between animal and human health sectors involved in the observatories.
Conclusions: The development of coordinated surveillance systems offer a solution to complex transmission cycles of zoonotic arbovirosis that can compromise the success and cost-effectiveness of control and eradication plans.
Relevance: The frequency and rapid distribution of new emerging vector-borne diseases or its spread to new territories have increased globally. The last new vector-borne disease that emerged in Europe, Schmallenberg disease, proved today's permeability for the emergence of new vector-borne diseases, independently of their morbimortality impact or zoonotic potential.

P130

Assessment of ecological and anthropogenic drivers of Anthrax outbreaks in the upper Zambezi basin (Kavango-Zambezi Transfrontier Conservation Area - KAZA TFCA)

HARVEY K. KAMBOYI[1], **Michel de Garine-Wichatitsky**[2], MUSSO MUNYEME[1], [1]UNIVERSITY OF ZAMBIA, LUSAKA, Zambia; [2]UNIVERSITY OF ZIMBABWE, HARARE, Zimbabwe. Contact: degarine@cirad.fr

Anthrax is an acute and invariably fatal zoonotic disease affecting multi-species and caused by a bacteria, *Bacillus anthracis*. In Zambia, anthrax has emerged as a serious ecosystem disease resulting in mortalities across humans, livestock and wildlife. The disease has had devastating effects on tourism resulting in socio-economic destabilisation of three pristine wildlife sanctuaries namely the upper Zambezi basin, the Lower Zambezi and the Luangwa valley. Preliminary trend analysis reveals sporadic annual outbreaks in the upper Zambezi basin. Consequently, the thrust of this study was to determine ecological drivers of anthrax recurrence, its maintenance and epidemiological linkage to human activities in the study area. Particular emphasis was given to establish an epidemiological linkage between socio-cultural and economic activities of the inhabitants and the incidence of anthrax at ecosystem level. Environmental and biological samples were collected within the livestock production and conservation areas (*n*=163). Questionnaires (*n*=106) and focused group interviews (*n*=4) were conducted at independently distinct villages in terms of space and time. Samples were analysed through blood agar culture, gram staining and PCR. Analysis of questionnaires and notes from interviews showed that the inhabitants consumed animals that died from anthrax as they in turn mainly suffered from the cutaneous form of anthrax. This was mainly the case as local communities were not aware of the fatal pulmonary and gastrointestinal forms of the disease. Poverty ”hunger for meat” being the main driver of consumption of anthrax carcasses contributed to environmental contamination with anthrax spores through dressing of anthrax carcasses where they lay resulting in environmental contamination, which is a major source of primary infection for livestock and wildlife. These socio-cultural activities together with lack of anthrax knowledge strongly intimate their contribution to anthrax recurrence and maintenance in the upper Zambezi basin.

P131

Systematic review on the relationship between antimicrobial usage and resistance in food-producing animals.

Luís P. Carmo[1], Alejandro Dorado-Garcia[2], Lucie Collineau[3], Laura C. Falzon[1], Gertraud Schüpbach-Regula[1], Katharina Stärk[3], Lis Alban[4], Liza R. Nielsen[5], Cedric Müntener[6], Dick J. J. Heederik[2], Ioannis Magouras[1], [1]University of Bern, Bern, Switzerland; [2]University of Utrecht, Utrecht, Netherlands; [3]Safe Food Solutions Inc., SAFOSO AG, Bern, Switzerland; [4]Danish Agriculture & Food Council, Copenhagen, Denmark; [5]University of Copenhagen, Copenhagen, Denmark; [6]University of Zurich, Zürich, Switzerland.
Contact: luis.gomesdocarmo@vetsuisse.unibe.ch

Purpose: Since the publication of the Swann Report, which warned about the risks associated with veterinary antimicrobial usage (AMU), innumerous alerts about the emergence of resistant bacteria due to animal AMU have been released. There is, however, not clear evidence on the magnitude of the link between AMU and antimicrobial resistance (AMR) in livestock.
Methods: The objective of this systematic review was to consolidate existing knowledge on the relationship between veterinary AMU and emergence of AMR in the main food producing species - cattle, swine and poultry, and to identify knowledge gaps. The outcome of interest was AMR in the most relevant indicator or pathogenic bacteria - Escherichia coli, Enterococcus (E.) faecium, E. faecalis, Salmonella spp., Campylobacter (C.) coli, C. jejuni and Methicillin resistant Staphylococcus aureus (MRSA). To be included, studies had to present a measure of association (Odds Ratio and Risk Ratio) or correlation between AMU and AMR, or sufficient data to estimate one. With the exception of in vitro experiments, all types of primary research studies were considered.
Medline, CAB abstracts, Agricola and EMBASE electronic databases were screened using a combination of free- and thesaurus terms specifically developed for each search engine. Additional publications were identified through expert elicitation and manual search of references. Each abstract was screened by two independent reviewers; selected publications were full-text screened and relevant data extracted.
Results: After removal of duplicates, both through the reference manager and manually, there were 9779 abstracts left. At the moment of submission, the title and abstract screening process was in progress.
Conclusions: Future analysis includes stratification per antimicrobial class, animal and bacterial species. In the presence of sufficient data, a meta-analysis will be conducted.
Relevance: Results obtained through this systematic process will improve our understanding on how animal AMU is driving the emergence of AMR, and inform future recommendations on regulation of animal AMU.

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Creating engagement, empowering communities, and sharing wisdom: dealing with dogs in northern Saskatchewan

Jasmine M. Dhillon, Tasha Epp, University of Saskatchewan, Saskatoon, SK, Canada. Contact: jasmine.dhillon@usask.ca

Purpose:
Dogs in remote, rural First Nations communities are primarily unrestricted and free roaming. Yearly, unrestrained dogs cause 1-2 fatalities and countless non-fatal injuries. Currently numerous methods are implemented to attempt to decrease aggressive dog-human interactions. Two questions are central: How are communities choosing methods? How successful and sustainable are these methods?

Methods:
A multiphase, convergent mixed methods design was used in four communities to assess the perception of dog-related issues, dog demographics and rates of aggressive encounters. Methods of community-driven policy creation and implementation were recorded, management plans and strategies were monitored, and options were evaluated for successful reduction in dog bites and violent encounters. Community-based participatory methods created exchange and discussion with all levels of society, providing in-depth knowledge translation for researchers and community members.

Results:
Remote First Nations communities face significant challenges impacting the priority placed on dog-related issues. Policy development, health initiatives and population control measures for dog ownership and bite prevention vary significantly between regions, and are often dependent on the risk of an aggressive dog-human encounter. No single model can be effective in all situations. Sustainability of interventions requires full community approval and support, and access to resources.

Conclusions:
Participatory community engagement and knowledge translation allows researchers to interact with communities as issues are classified, and long-term interventions and solutions are identified. Involving community members in research collection gives them an opportunity to appreciate the scope and breadth of problems and community opinions. Ensuring communities are enabled, empowered and capable of achieving their goals for dog-human relationships, requires comprehensive communication and education.

Relevance:
Community-initiated education has the potential to dramatically decrease the number of aggressive dog-human encounters that occur in indigenous communities in Canada.

P133

One Health in Action: protecting the safety of veterinary drugs and feed.

Patricia C. El-Hinnawy, U.S. Food and Drug Administration, Rockville, MD, Contact: patricia.elhinnawy@fda.hhs.gov

Purpose: The U.S. Food and Drug Administration (FDA) oversees the U.S. market for animal drugs and feed, among other responsibilities. Unique among Federal regulators, FDA maintains an in-house law enforcement office and law enforcement agents, the Office of Criminal Investigations (OCI). OCI investigators concentrate on signfiicant violations of the law, with a priority on conduct that may present a danger to the public health. Violations of the relevant animal drug or feed statutes may lead to OCI scrutiny.

OCI becomes involved when the threat to the public health is imminent, or when the FDA's regulatory actions have not been sufficient to remove the threat to the health of animals and/or people.

Methods: OCI agents employ customary Federal law enforcement methods and techniques as they investigate suspected criminal violations of the Federal Food, Drug, and Cosmetics Act and related statutes. The office was founded in 1992, in the wake of a generic drug scandal which led to convictions both inside FDA and within the generic drug industry.

OCI, in coordination with FDA's Center for Veterinary Medicine's Office of Compliance, prioritizes cases that involve unapproved animal drugs (compounded animal drugs, foreign-sourced drugs), and animal drug and human food adulterations that arise from tissue residues.

Results: Recent cases that have successfully concluded involved charges of falsifying records to conceal the sale of cattle with drug medication residues, as well as the manufacture and importation of tainted ingredients used to make pet foods.

Conclusions: Criminal violations are investigated by OCI and prosecuted by the U.S. Department of Justice and can lead to fines, restitutions, forfeitures, loss of professional licenses, and Federal prison sentences.

Relevance: Finally, a series of recommendations is made to help guide the veterinary professional through the process of engaging with an OCI agent, should that eventuality ever become a reality.

P134

Continuous education through networking and experiential learning - is it worth it?

Jorge Pinto Ferreira[1], Katharina Staerk[1], Sara Martins[1], Lucie Collineau[1], William Hueston[2], [1]SAFOSO, Liebefeld, Switzerland; [2]University of Minnesota, Minneapolis, MN, Contact: jorge.pinto-ferreira@safoso.ch

Purpose: Continuous education and networking are considered important. However the literature available on the quantification of these ideas is scarce. The University of Minnesota (together with SAFOSO) organized for the past eight years the course “Engaging Intergovernmental Organizations”. Participants of this course visit different intergovernmental organizations (IGOs), during a week, thus engaging in experiential learning. The key elements of the course are visits to the organisations, presentations by staff and engaging in a dialogue around specific challenges.
The objective of this study was to evaluate among the course alumni the usefulness and influence that the course had in their careers, mostly concerning their engagement with IGOs, after the course.
Methods: A 10-questions (SurveyMonkey®) survey was distributed to 123 course alumni.
Results: The response rate was 22.7%. 96.4% of the course participants said that their participation in the course had been worth the investment; Top-3 main obstacles to further engaging in work with IGOs were: i. lack of funding, ii. difficulty in identifying the relevant contact person, iii. lack of understanding of the opportunities IGOs can offer; 93% of the participants worked for academia or government.
Conclusions: Future similar courses should try to provide funding and facilitate the identification of the right contact people (in the IGOs) and opportunities, as these were the main obstacles faced when trying to engage with IGOs. The participation of professionals working in the industry sector is very limited.
Relevance: This study provided results that can be used in the future by those developing training courses, to assure benefits not only for the professional development of the individuals enrolled, but also to the narrowing of the distances between IGOs, governments, academia and industry.

P135

Would the single intradermal tuberculin test (SIT) be effective to screen for bovine Tuberculosis (bTB) in Irish cattle herds?

Anthony Duignan[1], Elizabeth A. Lane[1], **Margaret Good**[1], Feyisa B. Ashenafi[2], Klaas Frankena[3], [1]Department of Agriculture, Food and the Marine, Dublin, Ireland; [2]Addis Ababa Unversity College of Veterinary Medicine and Agriculture, Debre Zeit/Bishoftu, Ethiopia; [3]Wageningen University, Wageningen, Netherlands. Contact: margaret.good@agriculture.gov.ie

Purpose:
The Single Intradermal Comparative Tuberculin Test (SICTT) is used in Ireland to screen for bovine Tuberculosis (bTB). The aim of the study was to determine the effectiveness of utilising a Single Intradermal Test (SIT) for bTB screening.

Methods:
Testing records of herds from 3 separate years were analysed, namely
127 herds Officially TB Free (OTF) for a minimum 5-years prior plus 2 years post 2008;
from 2009 and 2012 respectively 21,007 and 16,832 SICTT negative herds.
A backward-stepwise multivariable logistic regression analysis was utilised to determine the effect of factors including test-type, tester (official or private veterinarian), herd size, mean age, region risk of TB infection and significant interactions on the risk of an animal having a bovine injection site skin thinkness increase of 3 mm or greater (inconclusive/responder) or 4 mm or greater (positive/ responder).

Results:
A herd revisit would have been required to herds with positive or inconclusive reactions i.e. 43%, 42% and 47% of all herds in 2008, 2009 and 2012, respectively, if a SIT had been utilised to screen for bTB.
In 2008, 6.3% of cattle in OTF herds showed positive or inconclusive reactions to the SIT at time of test.
In 2012, 38% of herds that were considered free of bTB based on the SICTT would have been reclassified as having a positive 'reactor' animal if the SIT was utilised. Factors associated ($P<0.001$) with increased risk of responder animals included test-type, tester, herd size and age.

Conclusions:
The use of a SIT to screen for bTB in Irish cattle herds would not be efficient.

Relevance:
The SICTT remains the test of choice for screening purposes in the bTB eradication programme in Ireland.

P136

Badger home ranges are porous and plastic in a medium density population.

Teresa MacWhite[1], **Margaret Good**[2], David J. Kelly,[3], Enda Mullen[4], Peter Maher[2], Nicola M. Marples[5], [1]Department of Agriculture, Food and the Marine, Dublin, Ireland; [2]Department of Agriculture, Food and the Marine, Dublin, Ireland; [3]Trinity College, Dublin, Ireland; [4]Department of Arts, Heritage and the Gaeltacht, Dublin, Ireland; [5]Trinity College, Dublin, Ireland. Contact: margaret.good@agriculture.gov.ie

Purpose:
European badgers, *Meles meles,* are wildlife vectors of TB caused by *Mycobacterium bovis*. The aim of the study is to examine territory use and ranging behaviour of badgers and update previous information, largely based on bait-marking of social groups and radio-telemetry of individuals over relatively short periods of time.

Methods:
During this four-year study the positions of free-ranging badgers were recorded up to eight times a night, using collars fitted with GPS (Global Positioning System) units.
Seasonal, gender and age related gender differences in range size, changing outline of territories within the study area and extra territorial ranging were investigated.

Results:
Analysis of the data revealed a detailed picture of the ranging behaviour of the study animals.
The ranging behaviour of the European badgers in County Wicklow, Ireland, varied enormously throughout the year with seasonal, gender and age related differences in range size identified as significant.
Badgers had very small ranges in winter and much larger ranges in summer.
Generally, males had larger home ranges than females, but there were seasonal and age-related variations to this trend.
Both sexes made excursions outside their “regular” home ranges throughout the year.
While individuals of the same social group shared large parts of their home ranges, they also used considerable areas which other members of their group did not use.
In addition the area used by any one badger changed markedly from year to year.

Conclusions:
The ranging behaviour of the individuals and social groups in our study demonstrated plasticity and porosity in contrast to the classic notion of a territory as an area shared and defended by the social group. Knowledge of the movement patterns of animals is crucial for understanding the epidemiology and potential transmission routes of diseases they carry.Relevance: Badger movement patterns play a key role in the transmission of *M. bovis* both within the species and to other susceptible hosts, especially cattle which can therefore have a significant economic impact on cattle farmers.

P137

Advances in monitoring of tuberculin testing in the Irish bTB eradication programme, 2008 - 2013.

Anthony Duignan[1], Simon More[2], **Margaret Good**[1], [1]Department of Agriculture, Food and the Marine, Dublin, Ireland; [2]University College Dublin,UCD School of Veterinary Medicine, Dublin, Ireland. Contact: margaret.good@agriculture.gov.ie

Purpose The Single Intradermal Comparative Tuberculin Test (SICTT) is the principle means of detection of infection in live animals in the Irish Bovine Tuberculosis (bTB) Eradication Programme. Private Veterinary Practitioners (PVPs) are responsible for the application of 95% of the testing in Ireland, amounting to circa 8 million animal tests per annum. The aim of the study was to develop a specialist report using the Animal Health Computer System to monitor the performance of each PVP in delivery of the SICTT and to enable comparison of PVP performance over time and between peers.
Methods This report captures all data relevant to testing by each PVP and concentrates on measuring key deliverables that affect the quality of both administrative and disease detection performance. The key measures of performance are critical control points which were chosen because they are objective and readily measurable**.**
Results The application of the performance reports and demonstrates improved delivery in the quality and reporting of testing since the introduction of the reports in 2008.
Conclusion It is now possible to give considerable attention to the standard of SICTT application on an objective basis. It is also possible to apply performance based sanctions or rewards based on analysis of the specialist reports.
Relevance The test when carried out correctly is highly reliable and has been assessed under Irish conditions as 90-98% sensitive and 99.95% specific. However, the test is subjective and prone to considerable individual variation in performance in the field. Consistent application of the test in compliance with international requirements is critical to the success of the eradication programme and to providing security to markets.

P138

The role of tuberculin assays on naturally infected cattle in the Irish eradication programme.

Anthony Duignan, **Margaret Good**, Department of Agriculture, Food and the Marine, Dublin, Ireland.
Contact: margaret.good@agriculture.gov.ie

Purpose: The purpose of this presentation is to give an account of the procedures, and outline the role of assays, carried out on naturally infected cattle in the quality control on the Irish Bovine Eradication Programme. OIE recommends that tuberculins are assayed in the population of animals in which the eradication programme is to be carried out, but due to practical difficulties in performing potency assays in cattle they are usually assayed in guinea pigs.
Methods: The potency of a tuberculin is estimated by comparing the size of the reactions, elicited by an intradermal inoculation, to the size of the reactions of a 'standard' tuberculin of known potency in naturally infected (*Mycobacterium bovis*) bovines.
Results: Ireland is perhaps unique in that it is one of the few, if not the only country conducting routine tuberculin assay as part of the quality control of the national bTB eradication programme.
Conclusion: Tuberculin PPD standardisation is necessary in order to ensure sufficient diagnostic strength for eradication and also to guarantee animal status for international trade.
Relevance: The Irish Bovine Tuberculosis (bTB) eradication programme includes annual Single Intradermal Comparative Tuberculin Test (SICTT) screening of all herds. The SICTT is conducted by comparing the separate cell-mediated immune responses to an intra-dermal injection of avian and bovine PPD tuberculins in each animal. However, ever since inadvertently using sub-potent tuberculin many years ago the routine assay of tuberculins in naturally infected cattle is regarded as imperative to the assurance of potency of tuberculins used in the Irish bovine tuberculosis eradication programme.

P139

Landscape context and deer-cattle interactions: a targeted approach to bovine tuberculosis surveillance

João Ribeiro-Lima[1,2], James D. Forester[3], Michelle Carstensen[4], Lou Cornicelli[4], **Scott J. Wells**[2], [1]Faculdade de Medicina Veterinária, Universidade Lusófona de Humanidades e Tecnologias, Lisboa, Portugal; [2]College of Veterinary Medicine, University of Minnesota, St. Paul, MN, [3]College of Food, Agricultural and Natural Resource Sciences, University of Minnesota, St. Paul, MN, [4]Minnesota Department of Natural Resources, St. Paul, MN, Contact: wells023@umn.edu

Purpose: Wildlife that spatially overlap with livestock operations represent an additional source of infection and a susceptible population for infectious disease transmission. The objective of this analysis was to evaluate the impact posed by the landscape surrounding any given cattle farm on the risk for cattle-deer interactions.
Methods: White-tailed deer (*Odocoileus virginianus*) were captured (n=19) and fitted with satellite-linked radio collars. The study area contained 25 private cattle farms and included a mix of state forest and wildlife management areas in addition to private recreational lands. A step selection function (SSF) was estimated using a standard conditional logistic regression (50 controls per deer location). Model selection for data from individual deer, was based on AIC, where models with $\Delta AIC \leq 3$ were considered.
Results: The best fitting model showed that for five of the six cattle farms with deer visits, farm locations overlap with higher resource selection areas. On average, there was a tendency for stronger selection for open areas outside forest in early Spring and Fall. In the Summer months, the selection was stronger for within forest areas, while in the Winter deer preferentially selected for the edge of forest. Broad-scale patterns in the distribution of RSF values show that the eastern portion of the study area had higher values, corresponding to higher densities of forest land.
Conclusion: In this study, we show that the type of landscape surrounding a cattle farm can predict risk of deer-cattle interactions.
Relevance: Understanding factors that drive habitat use by deer will aid in the implementation of targeted approaches for disease surveillance.

P140

Determinants of Bovine tuberculosis in dairy farms covered by the tuberculin screening test: A herd level case control study

Alireza Bahonar[1], Hessam Akbarein[1], Saeed Bokaie[1], Nader Mosavari[2], Alisafar Makenali[3], Hamid Sharifi[4], [1]University of Tehran, Tehran, Iran, Islamic Republic of; [2]Razi Vaccine & Serum Research Institute, Karaj, Iran, Islamic Republic of; [3]Iranian Veterinary Organization, Tehran, Iran, Islamic Republic of; [4]University of Kerman, Kerman, Iran, Islamic Republic of. Contact: abahonar@ut.ac.ir

Purpose: Bovine Tuberculosis (BTB) is one of the most important zoonoses. Mycobacterium bovis is the responsible agent of BTB in the cattle. The current study was conducted to investigate the determination factors of BTB in dairy farms covered by the tuberculin screening test.
Methods: A herd level case- control study was carried out in 124 (62 cases & 62 controls) dairy farms in the provinces of Tehran, Alborz, Hamedan, Isfahan, Qazvin, Qom, Mazandaran and Semnan. The control farms were individually matched with case farms by farm capacity and distance. Statistical analyses were done by Stata 11.2 using conditional logistic regression.
Results: Proper management of manure (OR=0.12; 95% CI: 0.03-0.49), regular flaming of stalls (OR= 0.21; 95% CI: 0.04-0.92) and complete fencing around the farm (OR= 0.17; 95% CI: 0.03-0.81) decreased while the presence of rodents (rat) (OR= 4.90; 95% CI: 1.04-23.01) increased the risk of infection. The interaction among these variables was not statistically significant
Conclusions: This research showed that attention to managerial and environmental factors is necessary for controlling Bovine tuberculosis in dairy farms.
Relevance: According to the results, there is an essential need to pay more attention to rodent control in farms.

P141

How much bovine Tuberculosis surveillance is needed? A quantitative study in low risk areas in England

Liliana C. M. Salvador[1], Michael Deason[1], Paul R. Bessell[2], Jessica Enright[3], Rowland R. Kao[1], [1]University of Glasgow, Glasgow, United Kingdom; [2]The Roslin Institute, The University of Edinburgh, Edinburgh, United Kingdom; [3]University of Stirling, Stirling, United Kingdom. Contact: liliana.salvador@glasgow.ac.uk

Purpose:A key question in disease surveillance is how to design more effective methods to either improve disease detection, make cost savings or do both. Currently, in England, the bovine Tuberculosis (bTB) surveillance system tests all herds at 1 or 4 year intervals, depending on factors including the local disease prevalence and perceived future risk. While opportunities exist to improve this system, any changes must balance the costs due to missed infections against the benefit of cost savings due to reduced testing. Therefore a better understanding of which herds are at risk and how this information can be included into surveillance systems is necessary. This work investigates which risk factors can be used to better predict bTB breakdowns in low risk areas in England (LRA) and evaluates alternative risk based strategies in order to use a more cost-effective method.
Methods: We use statistical methods on both the cattle life history and the bTB disease databases, to identify the determinants of infection at the herd level that are driving the spread of the disease, and to test alternative risk based surveillance strategies to the current 4-year testing regime based on a model of freedom of infection.
Results: In LRA, the risk of breaking down is largely determined by the herd size and by the number of animals bought from high-risk areas. By incorporating these factors in alternative surveillance strategies, our results show that a more intensive testing frequency of herds appears to have little advantage since the probability of picking up additional infections is very low. We estimate, under the most advantageous scheme, a saving of over 260 whole herd tests per year (3086 vs 3346 under the current scheme) and a lower number of missed infections (31 vs 34 under the current scheme).
Conclusions: Incorporating risk-factors into surveillance models improves the efficiency of the testing regime by saving on the number of herds tested and on the number of missed infections, limiting the hidden burden of the disease.
Relevance: This study evaluates the current surveillance regime and has the potential to establish a more cost-effective surveillance strategy to control the spread of bTB in the future.

P142

Use of whole genome sequencing to understand the phylogenetic structure and epidemiology of Mycobacterium bovis in the United States

Kathleen A. Orloski[1], Suelee Robbe-Austerman[2], Tod P. Stuber[2], Charles W. Hench[1], Mark S. Camacho[3], Mark A. Schoenbaum[1], [1]United States Department of Agriculture, Ft. Collins, CO, [2]United States Department of Agriculture, Ames, IA, [3]United States Department of Agriculture, Raleigh, NC, Contact: kathy.a.orloski@aphis.usda.gov

National slaughter inspection is the primary method of detecting bovine tuberculosis (BTB) in cattle in the United States. Skin tests are administered for surveillance and investigation purposes. BTB continues to be sporadically detected in cattle and farmed cervids. It is unknown whether herds are infected by new introductions from animals or humans, or low levels of residual infection. Understanding the infection source is critical for managing program efficiency.

Lower resolution genotyping methods such as spoligotyping have been used for several years. Whole genome sequencing (WGS) was implemented in 2012, and performed on isolates from 1990 to the present. Consensus single nucleotide polymorphisms (SNP) were identified and used to classify strains, along with phylogenetic tree analysis.

875 *Mycobacterium bovis* isolates recovered within the U.S. were sequenced. These isolates separated into 23 major phylogenetic groups, with different strain types within groups. During 1998-2014 there were 129 BTB infected cattle and cervid herds and one feedlot. An isolate was not available for one herd. In addition, 18 cattle cases were found through slaughter surveillance where BTB was not confirmed in the herd of origin, for a total of 147 herds/cases. Of these, 78 strain types occurred in the U.S. prior to 1995, including the Michigan endemic area, (64 herds) and farmed cervid outbreaks (14 herds/cases). The remaining 68 herds/cases and the feedlot were infected with 43 strain types. Of these, 30 herds/cases were within 15 SNP of isolates from imported cattle. An additional 10 herds/cases were more distantly related to imported cattle. The source is not apparent for the remaining 28 herds/cases. Outside of known outbreaks, most cattle herd isolates are unique with limited spread to other herds. Imported cattle appear to be a source of introduction; however, limited imported cattle surveillance may underestimate this relationship. Other possible sources include low level residual infection or new introductions from infected humans. WGS is a powerful new tool in understanding the transmission dynamics of BTB in the United States that assist in prioritizing and directing local investigations.

P143

Livestock disease outbreaks and their impact on the evolution of trade networks

Thomas Selhorst[1], Franz Conraths[2], Christine Mueller-Graf[1], [1]The Federal Institute for Risk Assessment (BfR), Berlin, Germany; [2]Friedrich-Loeffler Institut, Greifswald, Germany. Contact: thomas.selhorst@bfr.bund.de

Purpose
Livestock trade can represent an important route of disease transmission. Veterinary epidemiologists have analyzed the topology of trade networks to identify node and edges relevant for the distribution and the dynamics of livestock epidemics. However, this approach is valid only under the assumption of unchanged trade activity during and before an animal disease outbreak.
In order to validate this assumption, the evolution of the German pig trade network during an outbreak of classical swine fever in North Rhine Westphalia in spring 2006 was analyzed and compared with the topology during periods when relevant livestock diseases did not occur.
Methods
The analysis used the methodology of time varying graphs [1] combined with changepoint detection [2] for the identification of relevant changes in network topology. Additionally, rewiring rates [3] and loyalty indices [4] were calculated.
Results
As expected, the trade volume changed considerably close to the time of the implementation of movement restrictions. In contrast to this finding, substantial rewiring and sustainable changes in the topology of the trade network could not be identified.
Conclusion
With respect to the German pork production chain, considerable industrial specialization is obvious. Each production stage can be attributed to specialized premises or enterprises. This seems to limit the change of trade partners.
Relevance
A new set of methods is proposed in order to characterize changes in trade patterns between animal holdings caused by disease outbreaks. The supposed methodology can be applied to any contact network.

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P144

Using pathogen strain-typing to inform transmission dynamics in social networks of livestock movements

Nelly Marquetoux[1], Cord Heuer[1], Peter Wilson[1], Anne Ridler[1], Mark Stevenson[2], [1]Massey University, Palmerston North, New Zealand; [2]The University of Melbourne, Melbourne, Australia. Contact: nelly.marquetoux@gmail.com

Purpose:
The movement of infected stock is thought to be the primary factor for introducing Mycobacterium avium subsp. paratuberculosis (MAP) to properties, although documented evidence of farm-to-farm transmission of MAP is scarce. The objective of this study was to combine molecular pathogen typing with animal movement data to infer the possible extent of transmission of MAP between farms.
Methods:
The data for this study were provided by Landcorp Farming Limited (LC), farming deer, sheep, beef and dairy cattle on 119 properties throughout New Zealand. Data of livestock movement between LC properties were available from 2006 to 2010. All farms were screened for evidence of MAP infection in a subset of 20 animals per farm and species in 2010. MAP isolates from positive pooled fecal cultures on each farm were typed, resulting in 11 VNTR/SSR strains. We analyzed the probability of two in-contact farms sharing the same strain, depending on different measures of connectedness between farms in the contact network.
Results:
Our analysis supports that farms sharing the same MAP strain were significantly more closely connected ($p<0.05$) in the livestock movement network than farms harboring different strain types.
Conclusions:
Social links between farms are of dyadic nature, in other words the outcome for analysis was at the level of a pair of objects. The purpose was thus to correlate adjacency matrices representing relations between farms. A major obstacle for analyzing dyadic data is the lack of independence between observations, making classical significance tests often inappropriate. However there is a lack of consensus for alternative methods, especially in the case of multivariate analysis.
Relevance:
We show the short-comings of classical significance tests for dyadic observations and present results based on Multiple Regression Quadratic Assignment Procedure, an alternative based on permutation tests for making inferences in social network data and how it applies to our epidemiological data.

P145

A new approach for bovine cysticercosis control

Samuel Carvalho de Aragão[1], Silvana de Cássia Paulan[2], Yuri Tani Utsunomyia[2], Pier Kenji Rauschkolb Katsuda Ito[2], José Henrique Hildebrand Grisi Filho[3], Cáris Maroni Nunes[2], [1]Instituto Federal do Pará, Paragominas, PA, Brazil; [2]São Paulo State University, Araçatuba, SP, Brazil; [3]University of São Paulo, São Paulo, SP, Brazil. Contact: samuel.aragao@hotmail.com

Bovine cysticercosis is a worldwide spread parasitic disease caused by the larval stage of Taenia saginata and responsible for economic losses in the beef cattle industry. It is also a public health issue and the taeniasis-cysticercosis complex occurrence is associated with poor hygiene habits and sanitation problems. The main measure adopted in Brazil to prevent human infection is the sanitary inspection at slaughterhouses. Network properties are increasingly been used in epidemiological studies to manage, control and predict a disease outbreak.

Purpose:

This study aimed at characterize the bovine cysticercosis occurrence and the cattle movement network of a Brazilian state (Mato Grosso do Sul) in order to direct control strategies.

Methods:

Cattle movement data consisted in a summary of all Animal Movement Permits (AMP) issued during 2012. AMPs had information on the origin and destination municipalities, number of animals moved, movement purpose and date. A cattle movement network was constructed with nodes representing the municipalities and edges connecting nodes representing the purpose, date and number of cattle moved between them. Infomap algorithm was used to cluster nodes with narrower relationships. The number of slaughtered animals and the number of carcasses affected by live and calcified T. saginata cysts from each municipality for that year resulted in a choropleth map of the proportion of infected animals.

Results:

The mean cysticercosis incidence was 1.09 and the map evaluation revealed that the southern region of the state is endemic for the disease. The observed network shows greater trade movement between close municipalities.

Conclusions:

The network model associated to the disease geospatial representation suggest that the southern region of the Mato Grosso do Sul state would be a priority target for implementing cysticercosis control measures such as health education programs, massive chemotherapy treatment in bovine population, human diagnosis and chemotherapy.

Relevance:

This study highlighted regional characteristics that provide support information for planning strategies not only for cysticercosis control but for other diseases as well.

P146

Detection of unhealthy cows and actions taken by dairy farmers - differences between high and low mortality herds

Karin Alvåsen[1], Marie Jansson Mörk[2], Ulf Emanuelson[1], [1]Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]Växa Sverige, Stockholm, Sweden. Contact: karin.alvasen@slu.se

Purpose:
On-farm mortality (euthanasia or unassisted death) could in many cases be prevented with better management, especially during the transition period and in early lactation, but also if unhealthy cows were identified at an early stage of disease. The objectives of this study were to evaluate potential differences in how dairy farmers in high mortality (HM) or low mortality (LM) herds: 1) ranked the importance of disease symptoms when detecting unhealthy cows; and 2) acted when unhealthy cows had been detected.
Methods:
A questionnaire was sent to HM and LM herds with >35 cows. HM herds had mortality rates (deaths/100 cow-years) in the highest quartile (>7.7) and LM herds in the lowest quartile (<2.7). The questions: “How do you detect unhealthy cows?” and “What is the first thing you do when you have detected an unhealthy cow?” were followed by statements such as “alterations in milk” and “contact the vet” etc. The answers were recorded on a VAS-scale. Wilcoxon rank-sum tests were used to evaluate if differences between HM and LM herds were statistically significant ($P<0.05$).
Results:
There were no significant differences in how farmers with HM (n=60) or LM (n=85) herds detected or acted when they recognized unhealthy cows. In both groups, the most important factors to detect unhealthy cows were inappetence, poor general condition, fever, changed milk, swollen udder, refused milking, increased lying behaviour, diarrhoea, vaginal discharge and nasal discharge. The most common actions taken by the farmers when noticed unhealthy cows was to measure the cow’s temperature, call the vet, move to an isolation pen, add to a surveillance list and start an own treatment. It was unlikely that the farmers would just wait.
Conclusion:
There was no difference in how farmers in HM and LM herds stated that they detected or how they acted when they noticed unhealthy cows. Still, the HM and LM farmers’ ability to detect unhealthy cows may differ.
Relevance:
High on-farm cow mortality may indicate sub-optimal herd health or welfare and causes financial losses. There is a need to identify herd characteristics and management routines associated with HM and LM herds so that advice for reducing mortality can be given.

P147

A randomised clinical trial on the effect of antibiotic or non-antibiotic topical treatment of digital dermatitis in dairy cattle

Ruurd Jorritsma[1], Amarins Dotinga[1], Gerwen Lammers[2], Mirjam Nielen[1], [1]Utrecht University, Utrecht, Netherlands; [2]Intracare, Veghel, Netherlands. Contact: r.jorritsma@uu.nl

Digital dermatitis (DD) is a superficial, painful, contagious epidermititis of the feet of dairy cattle which frequently results in lameness. A common individual treatment for DD in Europe is a topical administration of antibiotic chlortetracycline (CTC) spray. Given potential induction of antibiotic resistance there is a need for effective treatments without antibiotics. We performed a randomised controlled trial to compare clinical improvement of ulcerative DD lesions following treatment with IR spray versus CTC spray (non-inferiority testing).
We included 9 dairy herds of around 100 cows housed in a freestall system with an estimated DD prevalence of 20-25%.
In total, hind legs of 944 cows from 9 dairy herds were trimmed by professional hoof trimmers and scored using the M1-M4 scoring system. All legs with M2 lesions were included and randomly treated with IR spray or CTC spray according to the instructions of the manufacturers. Clinical improvement was defined as the transition of an ulcerative M2 lesion to any other lesion at treatment evaluation on day 10. At the end of the study 231 cows, of which we included one M2 affected leg each, were eligible for analysis.
After treatment with IR spray, most lesions (71%) transitioned into an M3, while the percentage of M1 and M2 lesions was almost equal (respectively 14% and 13%). After treatment with CTC spray most lesions remained M2 (52%). The percentage of M1 lesions after treatment with CTC spray was a little higher compared to treatment with IR spray (19%). Only 1% and 3% of M2 lesions for respectively IR spray and CTC spray transitioned to M0.
The overall clinical improvement rate of IR spray was higher compared to CTC, respectively 86.8% (range 61.5% - 100.0%) and 47.9% (range 17.7 - 85.2%). In all 7 herds clinical improvement was numerically higher for IR spray and in 3 out of 7 herds significantly higher. The Odds Ratio, adjusted for herd effects, for IR spray versus CTC spray was 8.2 (95% CI 4.2 - 15.7) with an estimated Relative Risk of 1.9.
In conclusion, the non-antibiotic IR spray was at least as effective as the CTC treatment in the reduction of M2 lesions.

P148

Distribution of CNS species in subclinical and clinical mastitis and their impact on somatic cell count

Larissa A. Z. Condas, Jeroen De Buck, Diego B. Nóbrega, Domonique Carson, John P. Kastelic, **Herman W. Barkema**, University of Calgary, Calgary, AB, Canada. Contact: barkema@ucalgary.ca

Background: The role of coagulase-negative staphylococci (CNS) in bovine udder is controversial; some species maybe protective and others pathogenic. Study objectives were to determine distribution of CNS species in cows with intramammary infection (IMI), subclinical and clinical mastitis, and the impact of CNS on udder health.

Methods: Data and isolates were obtained from National Cohort of Dairy Farms (overall, 122,913 quarter-milk samples from 91 herds across Canada). Based on molecular techniques, there were 5518 CNS isolates from 1947 cows and 2872 quarters, plus 67 isolates from clinical mastitis cases. Prevalence was estimated using mixed effects logistic regression models, whereas effect of CNS species (compared to culture-negative quarters) on SCC was estimated by GLM.

Results: Prevalence of CNS IMI in low (<200,000 cells/mL) and high SCC (≥200,000 cells/mL) quarters was 8.8 and 25.7 per 100 quarters, respectively. Prevalence of the 10 most frequently isolated CNS species was higher in high compared to low SCC quarters. The SCC of quarters with *Staphylococcus epidermidis* (geometric mean SCC = 148,000 cells/mL) and *S. simulans* (98,000 cells/mL) was higher than *S. xylosus* (53,000 cells/mL) and *S. haemolyticus* (56,000 cells/mL). Furthermore, SCC of all CNS-infected quarters was higher than culture-negative quarters (18,000 cells/mL). Incidence of CNS clinical mastitis was 1.14 cases/100 cow-years at risk. *S. chromogenes* and *S. xylosus* were isolated less frequently from clinical mastitis cases than from low or high SCC quarters, whereas *S. simulans* and *S. sciuri* were isolated more frequently from clinical mastitis cases than from low or high SCC quarters.

Conclusion: SCC of quarters with CNS IMI of the 10 most common CNS species was higher than SCC of culture-negative quarters. Additionally, *S. epidermis* and *S. simulans* increased SCC the most, along with *S. sciuri* (the latter was more commonly associated with clinical mastitis).
Relevance: The CNS are a large, heterogenous group; therefore, considering them as a group rather than at the species or even genotype level has undoubtedly contributed to apparent discrepancies among studies of their effects on udder health.

P149

Neospora caninum seroprevalence and risk factors in a sample of small dairy farms in central Chile

Luis Pablo Hervé-Claude[1], Alan Lavado[2], Dácil Rivera[3], María José Navarrete-Talloni[4], Christopher Norman Hamilton-West Miranda[2], [1]Universidad de Chile, Santiago, Chile; [2]Universidad de Chile, Santiago, Chile; [3]Universidad de Chile, Santiago, Chile; [4]Universidad Austral de Chile, Valdivia, Chile. Contact: lpherve@u.uchile.cl

Purpose: To determine the *Neospora caninum* seroprevalence and identify risk factors associated with the infection.
Methods: A commercially available ELISA diagnostic kit from IDEXX, the Neospora X2 Test was applied to all catlle within the study farms. This determined which farms and cattle was seropositive for *N. caninum*. A structured questionnaire was applied to all participating farms owners, to provide information on the risk factors associated with the infection.
Results: The seroprevalence found was of 46% of animals within farms in average. 56% of the farms has at least one seropositive animal. Regarding the risk factor analyses and despite the relatively small size of the study, abortion history (Previous abortions recorded), management of abortions and abortions byproducts (No management), dogs feed source (Home made feeding) and cattle water source (Access to open eater sources/ditches management) were found as significant risk factors for *N. caninum* infection.
Conclusions: Small dairy farms in central Chile are largely exposed to *N. caninum* and the parasite is widespread among these, being also a large proportion of the animals affected. Water source, feeding of dogs and management of abortions appera to be significant risk factors, added to the history of previous abortions in the farm.
Relevance: This si the first study since 2000 in reporting *N. caninum* seroprevalence in Chile. This is a serious menace for livestock productions and firther stuides need to be done to asses and control the disease in Chile.

P150

Antimicrobial resistance findings in calves up to 30 days of age between the years 2002 to 2012 analyzed in the Animal Pathology Institute of the Universidad Austral de Chile

Luis Pablo Hervé-Claude[1], Barbara Valenzuela[2], Enrique Paredes[2], Manuel Moroni[2], Christopher Norman Hamilton-West Miranda[3], María José Navarrete-Talloni[2], [1]Universidad de Chile, Santiago, Chile; [2]Universidad Austral de Chile, Valdivia, Chile; [3]Universidad de Chile, Santiago, Chile. Contact: lpherve@u.uchile.cl

Purpose:
To summarize over ten years of antimicrobial resistance findings at the Universidad Austral Anatomy Pathology Laboratory in Valdivia, Chile.
Methods:
All antimicrobial resistance evaluations performed between 2002 and 2012 in samples originated from calves necropsies or submitted samples was included in this retrospective study. All tested antimicrobials and bacterial agents were considered. An Antimicrobial Resistance Score (ARS) was constructed based on each isolate resistance patternb y assigning a score to each antimicrobial tested on every isolate. These results (for exple, six antimicrobials tested on one isolate), were averaged and the score was obtained. An ARS of 1 represents an isolate sensitive to all antimicrobials tested, while an ARS of 3 represents a fully multiresistant isolate.This score was used to describe de antimicrobial resistance trends in the Chilean livestock industry in the last decade.
Results:
One hunderd sixteen calves samples were tested for antimicrobial resistance. Samples came mainly from the Los Ríos, Los Lagos and the Araucanía regions. The isolates that showed higher ARS were *Pseudomona aeruginosa* and *Proteus miriabilis* (ARS>2) followed by *Actynomices pyogenes* and *E. coli*. (ARS=1.75).
Conclusions: By building such a simple score, it is possible to evaluate and compare which bacterial agents represent to date the higher resistance t antimicrobials. The most common pathologic agents *E. coli* and *Salmonella sp*. represented only moderate resistance while other not so relevant agents showed very high resistance scores.
Relevance: To date there is very few information on antimicrobial resistance in livestock in Chile. This study represents an overall sight of the local situation in southern Chile.

P151

Comparative composition, diversity, and quantity of oligosaccharides in early lactation milk from commercial dairy and beef cows.

William M. Sischo[1], Daniela Barille[2], Diana M. Short[1], [1]Washington State University, Pullman, WA, [2]University of California, Davis, CA, Contact: wmsischo@vetmed.wsu.edu

Purpose: Compare prevalence and relative abundance of milk-source oligosaccharides (OS) from early lactation commercial dairy and beef cows.

Methods: 10 commercial dairy and beef herds and 5-8 animals per herd were recruited. Data collected included age, parity, breed, body condition, and calving information. Milk and blood samples were collected once. Milk was assessed for total solids and pH and serum for BHBA. OS were profiled by ToF and nano-liquid chromatography. OS abundance was standardized and transformed using PCA. PCA components were used to create similarity clusters. Cluster membership was used as dependent variable in logistic regression to assess the association between animal production type and age.

Results: Study included 65 cows from 10 herds, 5 beef (n=32 cows) and 5 dairy (n=33 cows). All study cows were multiparous (4-10 yrs), days in milk ranged from 4 to 13 days. Dairy body condition scores ranged from 2.00-3.25 (5 point scale). Beef body condition scores ranged from 3.5-8.0 (9 point scale). Based on serum BHBA, 4 dairy cows from three different herds and no beef cows were classified as ketotic. Milk mean percent solids were similar between dairy and beef cows, 12.9 and 12.8, respectively. Mean milk pH was the same in dairy and beef cows (6.4). A total of 30 OS were detected, the majority in all milk samples regardless of production type, 4 OS were detected in equivalently low prevalence, 3 OS were more prevalent in beef cows. Two clusters, one dominated by dairy cows and the other by beef cows described distribution patterns of OS for our study sample. Comparing median OS abundance between the two clusters found that overall abundance tended to be greater in the cluster dominated by beef cows.

Conclusions: No novel OS were found in beef compared to dairy milk, there were differences in OS prevalence and abundances (beef being higher), and 7 OS explained these differences.

Relevance: The selection of traits for beef and dairy animals is contrasted by high milk production and successful calf crop. While the traits for successful calf rearing are complex, the marked difference between beef and dairy OS content suggests that it may have an important role in supporting calf health.

P152

Revisiting the effect of Johne's disease status on milk production in dairy cows

Rebecca L. Smith[1], Ynte H. Schukken[2], Yrjo T. Grohn[3], [1]University of Illinois, Urbana, IL, [2]GD-Animal Health, Deventer, Netherlands; [3]Cornell University, Ithaca, NY, Contact: rlsdvm@illinois.edu

Purpose: The effect of Johne's disease (JD) status on milk production has been established in multiple studies. However, these studies have all assumed that animals with a given test status will have a similar disease trajectory. New understanding in the biology of mycobacterial disease indicates that only a small proportion of infected animals will ever become clinically affected. The objective of this study was to revisit the question of JD status and milk production while accounting for the dual-path nature of mycobacterial infection.

Methods: Longitudinal data were collected from 3 commercial dairy herds in the northeast United States between 2004 and 2011. Disease status was determined through quarterly ELISA serum testing, biannual fecal culture, and culture of tissues and feces at slaughter. Milk production data were collected from the Dairy Herd Improvement Association. Animals with positive test results were categorized as high path (at least one high-positive culture) and low path. The effect of Johne's disease path and status on milk production were analyzed using a mixed linear model with an autocorrelation random effect structure.

Results: On average, ever-positive animals produced more milk prior to their first positive test than always-negative animals, especially high path animals. While mean production decreased after a first positive test, low path animals were predicted to recover some productivity over time. High path animals, however, continued to exhibit a decrease in milk production, especially after their first high-positive fecal culture.

Conclusions: These results show that not all animals test-positive for Johne's disease will have long-term production losses.

Relevance: This has strong implications for the economic benefit of culling all test-positive animals.

P153

Effect of passive immunity transfer on growth performance of pre-weaned dairy calves

Ibrahim Elsohaby[1], Marguerite Cameron[1], Ahmed Elmoslemany[2], Gregory Keefe[1], [1]Atlantic Veterinary College, Charlottetown, PE, Canada; [2]Faculty of Veterinary Medicine, Kafrelsheikh University, Kafrelsheikh, Egypt. Contact: ielsohaby@upei.ca

Growth rates, disease incidence and mortality are the most important parameters to monitor during the preweaning period as they reflect the overall outcome of farm management practices and husbandry. Two measures of the success of the calf rearing program are body weight (BW) and average daily gain (ADG), which can subsequently be compared to breed averages for a specific age level. A total of 142 Holstein dairy calves from 5 commercial dairy farms were enrolled in this study. Calf BW was determined at birth (n = 142), 21 days (n = 101) and weaning age (n = 59) using an electronic scale. Blood samples (n = 142) were collected at 24 to 48 hours after birth. Serum IgG concentration was then measured using radial immunodiffusion (RID) assay. The mean BW of calves at birth, 21 days and weaning age (42 days) were 40.8 ± 6 Kg, 51.7 ± 7.5 Kg and 66.8 ± 8.2 Kg, respectively. The average daily gain (ADG) for the 1st 21 days, 2nd 21 days and full pre-weaning period (birth to 42 days) of life were 0.54 ± 0.23 Kg, 0.68 ± 0.24 Kg and 0.62 ± 0.16 Kg, respectively. The mean serum IgG concentration at 24 to 48 hours after birth was 17.3 ± 9.1 g/L. The number of calves with IgG concentrations below a cut-off value of 10 g/L for failure of transfer of passive immunity (FTPI) positive cases was 36 out of 142 calves, resulting in a FTPI prevalence of 25%. No significant association was detected between serum IgG concentration at 24 to 48 hours and birth weight, weaning weight and ADG for 2nd 21 days of life. A significant association was detected with BW at 21 days age and ADG for 1st 21 days, with better immune transfer being associated with higher values. Additionally, the ADG for the whole pre-weaning period showed a trend toward improvement (P=0.08). Each 1 g/L increase in serum IgG concentration at 24 to 48 hours after birth was associated with a 219 g, 8 g and 4 g increase in BW at 21 days age, ADG for 1st 21 days and full pre-weaning period, respectively. We conclude that colostral IgG transfer is an important predictor of growth performance of pre-weaned dairy calves.

P154

Culling perspectives from dairy producers, veterinarians, DHI and feed mill advisors: a Q-methodology study

Denis Haine[1], Roger Cue[2], Asheber Sewalem[3], Kevin Wade[2], René Lacroix[4], Daniel Lefebvre[4], Jonathan Rushton[5], Julie Arsenault[1], Émile Bouchard[1], Jocelyn Dubuc[1], [1]Université de Montréal, St-Hyacinthe, QC, Canada; [2]McGill University, Ste-Anne-de-Bellevue, QC, Canada; [3]Agriculture and Agri-Food Canada, Guelph, ON, Canada; [4]Valacta, Ste-Anne-de-Bellevue, QC, Canada; [5]University of London, London, United Kingdom. Contact: denis.haine@gmail.com

Purpose:
If minimizing total losses is most profitable, producers can still decide the timing of the cull and take individual choices (e.g., genetic selection), or have to face certain constraints (e.g., regulations, quotas, etc). Motivational and behavioural aspects of culling expectations and its decision process were not explored yet. Our goal was to describe shared criteria on culling decision among dairy producers and farm advisors, with the help of a Q-methodological study, which allows for the systematic exploration of subjectivity.

Methods:
Forty-one dairy producers and 42 advisors (17 veterinarians, 13 feed mill advisors and 12 DHI advisors) undertook a Q sort with 40 statements that represented a range of viewpoints about cow and herd health, production performances, management issues, and material factors that might impact their culling decision-making process. Sorts were analyzed by-person using factor analysis and oblimin rotation.

Results:
Dairy producers shared a single view on culling, where udder health, milk production performances, milk quota management and producing a healthy, secure milk were key criteria. Farm management parameters (debts, amortization, employees, milking parlour capacity, herd size) were not considered at all. Two profiles were identified among farm advisors. They all used the same key parameters as producers. The first profile - 81% similar to producers - stressed withdrawal period and animal welfare. The second - 56% similar to producers - differed more clearly by considering reproduction status (pregnancy, gestation stage) as key criteria, followed by post-partum diseases and production financial incentives.

Conclusions:
Our findings suggest that dairy producers and their advisors generally hold a common viewpoint. A subgroup of advisors is using recommendations from economic models where reproduction status is central to farm profitability.

Relevance:
Despite outreach programs promoting this approach, it did not reach most of the advisors nor the majority of producers. Understanding and managing these differences is important to assist change management processes required to increase farm profitability.

P155

Risk factors for Mycoplasma bovis associated outbreaks in Danish dairy cattle herds

Lene Jensen[1], **Mette B. Petersen**[2], Mikkel B. Svendsen[2], Kaspar Krogh[3], Liza R. Nielsen[2], [1]Skovbjerg DyrlægeTeam, Varde, Denmark; [2]University of Copenhagen, Frederiksberg, Denmark; [3]Kaspar Krogh - Dairy Herd Heath Specialist, Kolind, Denmark. Contact: mbp@sund.ku.dk

Purpose: *Mycoplasma bovis* is a bacterium associated with severe disease and production losses in cattle herds. Since 2010 Denmark has experienced an apparently increasing number of outbreaks on herd level and an increased severity of clinical signs associated with *Mycoplasma bovis*. Studies of both external and internal risk factors are lacking. Besides from purchase of cattle, herd size and feeding of waste milk to calves, few risk factors for developing an outbreak has been established. The objective of this study was therefore to identify risk factors for developing an outbreak of *Mycoplasma bovis* associated disease in dairy herds.

Methods: The study population (N=504) was selected based on either prior knowledge of *Mycoplasma bovis* associated disease, or a test-positive bulk tank milk sample (PCR-Ct < 40 or ELISA-ODC% >= 55) from national screenings. In total, 324 (64%) farmers were interviewed or answered an online questionnaire concerning management routines and potential explanatory factors for outbreaks of *Mycoplasma bovis.* Of these, 201 farms reported not having had an outbreak and 123 farmers reported having had an outbreak of *Mycoplasma bovis* associated disease in the period 2010-2014.

Results and conclusions: Potential risk factors for an outbreak vs. no outbreak were analysed using logistic regression analysis, including data from the questionnaire along with register data from the Danish Cattle Database and Central Husbandry Register. Biologically important and statistically significant (p<0.01) risk factors that influenced the probability of a clinical outbreak were:
Increasing herd size (> 450 vs. < 300 cattle: OR=5.6, 95% CI[2.7-11.3])
Shared calving pens (> 2 cows calving together vs. single calving pen: OR=2.5, 95% CI[1.4-4.9])
Contact vs. no contact between young calves and other age groups (OR=2.9, 95% CI[1.3-6.3])
Number of movements from calf to calving (>5 vs. < 4: OR=0.3, 95% CI[0.1-0.6])
Lack of the use of sick pens for sick cows (OR=2.3, 95% CI[1.3-4.1])
Increasing amount of milk delivered to the dairy per cow confounded the effect of herd size.

Relevance: The results can be used in *Mycoplasma bovis* disease control and in preparation of biosecurity plans.

P156

Characterisation of outbreaks associated with Mycoplasma bovis in Danish dairy cattle herds

Lene Jensen[1], **Mette B. Petersen**[2], Mikkel B. Svendsen[2], Kaspar Krogh[3], Liza R. Nielsen[2], [1]Skovbjerg DyrlægeTeam, Varde, Denmark; [2]University of Copenhagen, Frederiksberg, Denmark; [3]Kaspar Krogh - Dairy Herd Health Specialist, Kolind, Denmark. Contact: mbp@sund.ku.dk

Purpose: *Mycoplasma bovis* is a bacterium associated with severe disease in both dairy and beef cattle herds. It seems to be an emerging disease around the world. The bacterium is usually associated with mastitis in dairy cows, and pneumonia, arthritis and otitis media in young stock. Since 2011, there have been an increased number of outbreaks in Danish dairy herds, including some with serious and atypical clinical signs. The objective of this study was therefore to characterise the Danish *Mycoplasma bovis* associated outbreaks, with regard to both duration and occurrence of clinical signs.

Methods: The study population consisted of 504 farms, chosen based on either prior knowledge of *Mycoplasma bovis* associated disease, or a test-positive bulk tank milk sample (PCR-Ct < 40 or ELISA-ODC% >= 55). In total, 324 farmers were interviewed or answered an online questionnaire in the fall 2014. Of these, 123 farmers reported having had an outbreak of disease associated with *Mycoplasma bovis* in the period 2010-2014. The questionnaire included questions on how the farmers experienced the outbreak. The characterisation of the outbreak was based on duration, farmers' perception of what constituted an outbreak with *Mycoplasma bovis*, which diagnostic procedures were used and which clinical signs the farmers observed during the outbreak.

Results and conclusions: The duration of the outbreaks was reported to last from a few weeks up to approximately 3 years, on average about 4 months. Outbreaks appeared to start more frequently in late winter or early spring. Farmers most frequently perceived arthritis (87%), mastitis (69%) and otitis media (62%) as clinical signs associated with *Mycoplasma bovis.* When diagnosing *Mycoplasma bovis* in the herd, farmers most frequently relied on blood (50%) and milk (46%) samples from sick cows, and bulk tank milk samples (31%). During the outbreak farmers most frequently noticed an increase in the following clinical signs: other signs (reduced milk yield, fewer, death) (72%), pneumonia in cows (60%) and pneumonia in calves (43%).

Relevance: Improve the understanding of the occurrence of clinical signs and in planning further studies of *Mycoplasma bovis* associated disease.

P157

Molecular variation of Streptococcus agalactiae in dairy herds of Antioquia, Colombia.

Julian Reyes Velez[1], Marcelo Chaffer[1], Natasha Robinson[1], Ruth Zadoks[2], Ximena Cardona[3], Diana Macias[3], Nicolás Ramírez[4], Gregory Keefe[1], [1]University of Prince Edward Island, Charlottetown, PE, Canada; [2]Moredun Research Institute, Penicuik, Scotland, United Kingdom; [3]Cooperativa COLANTA, Medellin, Colombia; [4]Universidad de Antioquia, Medellin, Colombia. Contact: jreyes@upei.ca

Purpose: Group B *Streptococcus agalactiae*, continues to be a challenge for milk quality programs in countries like Colombia, in which management practices create an advantageous environment for contagious pathogen transmission. Strain information is needed to understand the variability of this pathogen for the development of eradication procedures. The aim of this project was to characterize *Streptococcus agalactiae* bovine isolates by two molecular techniques.

Methods: Random Amplified Polymorphic DNA PCR (RAPD PCR) and representative Multi-locus sequence typing (MLST). The isolates represented samples from an epidemiological study of mastitis and a separate study on pathogen eradication in the same region. These strains were collected from 87 cows in 27 different herds from 7 geographical regions of Antioquia, Colombia.

Results: One hundred and sixteen isolates were analysed by RAPD PCR and 40 strains were subsequently selected to perform MLST. A total of 4 clusters were found by the RAPD technique from this population with the following frequencies: Cluster I (85.34%), Cluster II (4.3%), Cluster III (0.86%) and Cluster IV (9.48%). Additionally, MLST showed three different sequence types (ST), distributed in ST 248 (75%), ST22 (10%) and ST1 (15%). These sequence types were also grouped in three different clonal complexes CC314, CC1 and CC1.

Conclusions: From these data, it is apparent that the *Streptococcus agalactiae* population had a low diversity distribution with the majority being in Cluster I and ST 248. The mastitis events on these Colombian herds were mainly caused by ST248, which have previously been reported affecting bovine populations in Europe and China and in occasional human acquired community infections. The low genetic diversity of bacterial strains recovered in the study could be related with contagious transmission of a small number of strain types due to management practices.

Relevance: This study provides important insight into bacterial population structure and the potential for inter-species strain transmission with this pathogen. This knowledge will help to develop more effective control programs in dairy herds of the region.

P158

Effects of threshold levels for milk somatic cell count on ranking of dairy herds within and across European countries.

Karin Sjöström[1], Aurélien Madouasse[2], Julie Duval[2], Ulf Emanuelson[1], [1]SLU, Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]Oniris, Nantes, France. Contact: karin.sjostrom@slu.se

Somatic cell count (SCC) is used worldwide as an indicator of subclinical mastitis. An optimum sensitivity and specificity has been found at a threshold of 200 000 cells/mL, and this is commonly used worldwide, although other thresholds are also used. The objective of this study, a part of the IMPRO-project (www.dairy-impro.eu), was to investigate if the choice of SCC threshold influenced the ranking of farms according to SCC prevalence, between and within European countries. A total of 190 organic dairy farms in Germany (n=60), Spain (n=26), France (n=49) and Sweden (n=57) were selected and data from the milk recording schemes was retrieved. Based on test-day observations from June 2012 until May 2013, herd prevalence's of cows with SCC > 100, > 200 and > 300 thousand cells/mL were calculated. Spearman rank correlations were used to study the effect of different thresholds on the ranking of herds within and across countries. Also, the re-ranking of the 20 herds with highest and lowest prevalence was assessed. The mean herd prevalence, using 200 as the threshold, was 0.28 in Germany, 0.39 in Spain, 0.33 in France and 0.26 in Sweden. The highest rank correlation (0.96) across the countries was found when the thresholds 200 and 300 were compared, and the lowest (0.81) comparing 100 and 300. The same patterns were seen when testing within country, except for Sweden where a high correlation (0.96) also was found between 100 and 200. This could be explained by a higher proportion of cows with SCC below 200 in Sweden than in the other countries. Studying the ranking of top and bottom herds confirmed a picture of relatively little re-ranking across countries, where 16 of the 20 herds with highest prevalence based on the threshold 200 also were among the 20 highest when using 300 as a threshold. Corresponding numbers comparing 200 and 100 as thresholds were 14 out of 20. In this study we found that SCC threshold levels did not have a large impact on the ranking of herds across countries, and any of the chosen thresholds would be useful to pinpoint the herds with most subclinical mastitis. The thresholds did, however, matter for the within country ranking, and was affected by the general SCC-level. www.impro-dairy.eu

P159

Fecal shedding and immune response in calves from an experimental transmission trial after exposure to penmates infected with Mycobacterium avium subsp. paratuberculosis

Caroline S. Corbett, University of Calgary, Calgary, AB, Canada. Contact: c.corbett01@gmail.com

Purpose:
Johne's disease (JD) is a progressive, chronic enteritis in the small intestine of ruminants caused by Mycobacterium avium subspecies paratuberculosis (MAP). Clinical onset of JD is characterized by chronic, non-treatable diarrhea and wasting despite a good appetite. Prior to the onset of clinical symptoms, JD can be present for years before detection without showing any clinical signs; however, MAP can still be shed into the environment, therefore increasing the risk of spreading JD.
There is no vaccine or treatment for JD; therefore, control is primarily based on preventing transmission. One common assumption is that only cows are infectious, and only calves are susceptible. This has lead to the practice of separating calves from dams and placing them in group pens; however, research by our group has confirmed that calves are not only susceptible but can actively shed MAP. Therefore, current practice of separating calves from dams and placing into group pens may not be an effective method to prevent new infections.

Methods:
The objectives of this ongoing experimental trial were to determine the extent of transmission that is occurring between penmates. 32 newborn Holstein bull calves were allocated into pens of 4. In 7 of these pens, 2 calves were inoculated with MAP, and 2 calves acted as sentinels. The 8th pen of 4 was designated as a control group. Calves were group housed for 3 months to allow for any potential transmission to occur. After 3 months, the calves were individually penned for 3 more months until the conclusion of the trial to ensure any new infections could be detected. Blood samples for antibody and interferon-γ detection were collected weekly, and fecal samples for evidence of MAP shedding were collected three times a week for all animals.

Results:
Data is still being collected, and will be analyzed to determine shedding patterns, immune responses, onset of infection, contamination of the pens, and the extent of transmission.

Conclusions:
Results from fecal and blood samples will be ready to present in November 2015.

Relevance:
Understanding the extent to which transmission occurs between penmates will lead to more effective management practices, minimizing the spread of JD.

P160

Assessing Footbath Protocols for the Prevention of Digital Dermatitis in Dairy Cattle: A Systematic Review and Network Meta-Analysis.

Casey Jacobs, Emily Morabito, Karin Orsel, Herman W. Barkema, University of Calgary Faculty of Veterinary Medicine, Calgary, AB, Canada. Contact: jacobs.casey@gmail.com

Digital dermatitis (DD) is an infectious disease causing erosive, ulcerative skin lesions typically found above the heel bulbs or along the coronary band of cattle. As a result, cattle may be reluctant to walk on affected limbs, and resulting lameness leads to decreases in cow comfort, longevity, milk production, and fertility. Footbaths are the most used practice for preventing DD lesions. However, the variability in the field and in the literature makes it difficult to compare protocols and provide recommendations. There is a need to be able to compare protocols available in the literature and rank the efficacy of these protocols to determine the most effective footbath protocol.

Purpose: The objective of this study was to identify footbath protocols available in the literature, and compare and rank these protocols based on their efficacy in prevention of DD using meta-analysis.

Methods: A search of the online databases MEDLINE (PubMed), CAB Abstracts, Agricola, and Web of Science will be conducted to identify articles. The search strategy will not be limited by study design nor footbath product, concentration or frequency in order to capture all relevant comparisons available for a comprehensive network meta-analysis. Criteria for inclusion in the systematic review and network meta-analysis will include the use of original data, a footbath intervention focused on lactating dairy cattle with digital dermatitis lesions as the reported outcome. Included articles will have relevant data abstracted for the network meta-analysis and risk of bias of each study will be assessed. A network meta-analysis will be conducted to determine direct and indirect comparisons between all footbath protocols included to compare and rank protocols on efficacy in preventing DD lesions.

Relevance: This systematic review and network meta-analysis will provide information on the footbath protocols available in the literature and how these protocols compare. Results from this study will be valuable in providing recommendations on the most efficacious footbath protocols and can be used to inform a subsequent economic decision model to determine the cost-benefit of each footbath protocol.

P161

Prevalence of digital dermatitis in Alberta dairy cattle using intensive copper sulphate footbath protocol.

Casey Jacobs, Karin Orsel, Steve Mason, Laura Solano Quesada, Herman W. Barkema, University of Calgary Faculty of Veterinary Medicine, Calgary, AB, Canada. Contact: jacobs.casey@gmail.com

Digital dermatitis (DD) comprises 43% of all hoof lesions associated with lameness in dairy cattle in Alberta, and likely Canada. DD is highly infectious and on-farm management procedures routinely consist of differing footbath protocols.

Purpose: A clinical trial was conducted to determine the effect of an intensive copper sulphate footbath protocol on the prevalence of all DD lesion stages and active DD lesions.

Methods: 10 Alberta dairy farms were recruited to participate; 5 farms were assigned to an intensive copper sulfate protocol (5% solution, once a day, Monday - Friday), and 5 farms continued their previous footbath protocol (non-interference). Lesions of hind feet of all lactating dairy cattle were scored in 3-week intervals for copper sulfate group and 6-week intervals for non-interference group. Scoring was done in the milking parlor using the M-stage scoring system by Dopfer et al. (1997).
Results: Prevalence of all stages of DD lesions and active lesions (M1 and M2 stage) are reported in

Table 1.
Table 1. Prevalence (%) of all and active (M1 and M2) DD lesions during trial.

Treatment	Lesions	Initial	Week 6	Week12
Copper sulfate	All DD	60	51	40
	Active	2.4	2.1	2.2
Non-interference	All DD	57	41	42
	Active	8.4	5.1	11.3

Conclusions: DD lesions are highly prevalent on Alberta dairy farms despite on-farm footbath and treatment protocols. However, the use of an intensive copper sulphate footbath protocol decreased all DD lesion stages and maintained a low prevalence of active lesions compared to farms with less specific protocols.

Relevance: Developing and maintaining specific and consistent footbath strategies will likely decrease and maintain low levels of DD, potentially improving the health status of lactating cows.

P162

Associations between herd somatic cell count level and applied mastitis control measures in Swedish dairy herds

Ulf Emanuelson[1], **Ian Dohoo**[2], Christel Nielsen[3], [1]Swedish University of Agricultural Sciences, Uppsala, Sweden; [2]University of Prince Edward Island, Charlottetown, PE, Canada; [3]FoU-centrum Skåne, Lund, Sweden. Contact: dohoo@upei.ca

Purpose:
The aim of this study was to investigate the association between udder health and preventive measures targeting mastitis implemented in Swedish dairy herds.
Methods:
Data were collected through a self-administered postal questionnaire sent to 898 dairy farmers. The questionnaire contained general questions about the herd and specific questions about the implementation of preventive measures. The response rate was 48%. Questionnaire data were merged with data from the official milk recording scheme. When herds with combined systems had been removed, 395 herds with tie-stalls and pipeline milking, free-stalls and parlor milking, and free-stalls with an automatic milking system (AMS) remained. Bulk milk somatic cell count (BMSCC), calculated from individual test-day information on milk yield and somatic cell counts, was used as indicator of udder health. The BMSCC was categorized as low (200 000 cells/mL). Associations between preventive measures and BMSCC classes were assessed by Chi2 tests.
Results:
Significantly fewer herds with tie-stalls and pipeline milking were in the high BMSCC class. Several of the mastitis preventive measures, e.g. a strict milking order, could not be implemented in herds with AMS. The only statistically significant differences were that “Stalls cleaned and fresh bedding material provided ≥ 2 times daily” and “Dry cows fed a mineral feed that covers their needs” was less frequently applied in herds with high BMSCC than in the other herds.
Conclusions:
Very few of the implemented preventive measures targeting mastitis were associated with the udder health of the herds, but causality cannot be inferred from this cross sectional study.
Relevance:
Mastitis prevention measures are implemented at a cost and should have a significant impact on the udder health status of a herd to be relevant.

P163

Clinical mastitis frequency and economic consequences in dairy herds from Argentina: A pilot study

Melina Richardet[1], Sergio Castro[2], Liliana Tirante[2], **Claudina Vissio**[1], Alejandro Larriestra[1], [1]Universidad Nacional de Río Cuarto, Río Cuarto, Argentina; [2]APROCAL, Buenos Aires, Argentina. Contact: cvissio@ayv.unrc.edu.ar

Clinical mastitis (CM) is an emerging problem under the current transformation of dairy sector in Argentina. A CM survey was conducted to collect data about its magnitude and variation among dairy herds. Prevalence (PR), cumulative incidence (CuI) and incidence density (ID) were estimated, exploring the risk pattern at herd and cow level and the economic consequences of CM cases. A cross sectional convenience sample of 2535 Holstein-Friesian cows from 19 herds was the study population. Cows within herd were selected by a random systematic procedure. Herd PR of CM was estimated the day of the visit. Cows selected without clinical signs were followed during 15 days to get incidence estimates. Mixed logistic models and survival analysis were applied. Using PR data, each CM case was monetized considering milk discharged, treatment costs and estimated milk losses until dry-off. Production data was customized according to farm records. Milk price considered was 0.37 US$/lt. The overall gross PR of CM was 2.5 (95%CI 1.9-3.1) cases/100 milking cows, the CuI was 3.9 (95%CI 4.5-3.8) new cases/100 milking cows and an ID was 2.7 (95%CI 2.2-3.3) new cases/1000 milking cow-days. The medians of PR, CuI and ID were 1.69 (q1=0, q3=4.2), 3.6 (q1=2.0, q3=4.6) and 0.25 (q1=0.14, q3=4.2), respectively. Cows with CM during first third of lactation show higher odds of being a prevalent case (OR: 1.69; 95%CI 1.01-2.85). The CuI was 3 times higher for heifers (OR: 3.36; 95%CI 1.84-6.11). The ID in heifers was 34 % higher compared with cows (HR: 1.34; 95%CI 1.17-1.68) after the adjustment for days in milk and herd. The average cost for case was about US$ 118.97 and US$ 87.78 for cows and heifers, respectively. Adjusting the losses by number of cows, CM represented US$ 3.94 per milking cow (95%CI 2.97 - 4.92 US$). The study provided baseline data for further adjustment in the sampling design and showed CM risk variation and its economic impact. Incidence estimates suggest that a great proportion of cows may experience at least one CM episode within a year. These findings highlighted the opportunity of conducting a nationwide CM survey to estimate the actual distribution and economic impact of the CM among Argentina dairy herds

P164

Situation analysis of the dairy industry in the Punjab, India: Identification and characterisation of hazards

Hannah R. Holt[1], Narinder Sharma[2], Jatinder P. S. Gill[3], Rajesh Kumar[4], Manmeet Kaur[4], Punam Mangtani[5], Javier Guitian[1], [1]The Royal Veterinary College, Hatfield, United Kingdom; [2]Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, India; [3]Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, India; [4]Post Graduate Institute of Medical Education and Research, Chandigarh, India; [5]London School of Hygiene and Tropical Medicine, London, United Kingdom. Contact: hholt@rvc.ac.uk

Purpose:
The Punjab is India's largest State in terms of milk productivity. Although the number of organised dairy farms is increasing, the vast majority of milk is produced by rural smallholders. Producers can market their milk through cooperatives, multi-nationals or informal channels. There is little regulation of dairy production and processing. The aim of this study is to perform preliminary situation and risk analyses of the dairy sector in the Punjab to identify public health risks and production constraints.

Methods:
First steps were identification of actors and generation of product flow diagrams detailing supply chains and processing. This allowed hazard characterisation and risk point identification. Data collection is through a cross-sectional study, focus group discussions, in-depth interviews and available literature.

Results:
Production constraints identified include access to inputs e.g. fodder and disposal of cows which are no longer productive as slaughter is forbidden. Disease constraints include mastitis, Johne's and haemorrhagic septicaemia and zoonoses bovine tuberculosis, brucellosis and leptospirosis. Control is hindered by a lack of secure cold chain for government subsidised vaccines e.g. the S19 vaccine for brucellosis. Risk hotspots are found in informal channels through which 80% of milk still flows, where milk chilling facilities and pasteurisation processes are sometimes absent. Most consumers are aware of food safety risks and raw milk is generally boiled before consumption, although exceptions occur.

Conclusions:
Disease control programs, with appropriate incentives and sanctions, are needed to ensure product safety for consumers whilst enabling producers to maintain their competitiveness.

Relevance:
The dairy industry is intensifying and output is increasing, without addressing food hygiene issues. Results will be used to propose sustainable risk mitigation strategies accounting for socio-cultural, economic and political drivers of behavior and the impact of proposed strategies on all actors. Findings will be disseminated to key stakeholders and policymakers.

P165

Producer attitudes towards mastitis in dairy cattle in the Bogota plateau, Colombia

Efrain Benavides[1], Luis C. Villamil[1], Andrea P. Lizarazo[1], Ruth Rodriguez[1], Liliana Chacon[1], Jaime R. Romero[2], [1]Universidad de La Salle, Bogota, Colombia; [2]Instituto Interamericano de Cooperacion para la Agricultura, Lima, Peru. Contact: efbenavides@unisalle.edu.co

Purpose: Dairy is an important economic activity in the highlands of Colombia, where semi intensive production systems, exists. Area five is an administrative region within the Bogota plateau at 2650 m.a.s.l. including 13 municipalities centered in Zipaquirá. Cattle population in the area is around 140,000 cattle (7,751 farms); however, smallholder producers are the most frequent
Methods: The knowledge and producer attitudes towards bovine mastitis were examined through an exercise of participative epidemiology and a semi structured survey applied to producers. In the workshop participated 55 producers, the reasons for which they considered mastitis as a problem were associated with subjects of: productivity (45 responses), animal health (18), milk quality (18), public health (12) and animal welfare (2). The survey interviewed 85 producers stratified according herd size as: small (101 animals) 14 farms.
Results: They considered mastitis as a major problem in 65%, 79% and 86% of the responders respectively for small, medium and big herds ($P > 0.05$). The declared use of the California Mastitis Test in each of the strata was 62%, 83% and 93% ($P = 0.037$); however cases of rejection of milk due to somatic cells has been respectively of 7%, 24% and 64% ($P < 0.01$).
Conclusions: It was found that the concept of subclinical mastitis (SC) is not clear between producers, and they are oriented to implement treatments rather to establish preventive measures. Despite of the misunderstanding about SC, a cross sectional study (underway) highlighted its relevance, as the frequency of cows with subclinical mastitis ranges between 20-86% in the sampled farms, indicating that the problem in farms is intense, but unnoticed.
Relevance: Understanding producer´s attitudes under an interdisciplinary approach is key for designing any mastitis control program in the region.

P166

Determinants for runt-fish mortality in Rainbow Trout during their marine phase, in Chilean production sites

Gustavo Monti[1], Adriana Mendoza[2], Marilyn Wolter[2], Barbara Etcharren[2], [1]Universidad Austral de Chile, Valdivia, Chile; [2]SGS Chile Ltda., Puerto Varas, Chile. Contact: gustavomonti@uach.cl

Purpose
To assess risk factors associated with mortality cases of runt-fish in Rainbow Trout (Oncorhynchus mykiss) starting their marine phase between 2009 & 2013.
Methods
A retrospective study design was used, with all complete production cycles that started between 01/01/2009 and 31/12/2011. The study was censored at 31/05/2012 for those in production. The unit of analysis was the cage and a case was considered for when exceeded a 3,0% cumulative mortality rate, after veterinary inspection. The study included 5 companies, contributing with 49 sites, totalizing 1,008 cages, located in the X & XI Regions. Information was obtained from the company's databases and by applying a questionnaire to responsible veterinarians or technician, after a training session.
The association between risk factors and the status of the cage was assessed by a mixed-Cox model, and the association between risk factors and the amount of affected fishes was assessed by a mixed-Poisson model, using R.
Results
The overall prevalence during the study was 46.2% of the cages and the median time for the first outbreak was 181 ds IQR (122; 265).
Risk factors associated with an increased risk to -be-a case- cage were:
−Cumulative amount of dead fish
−Average weight of smolts when they were introduced
−Genetic strain; and those associated with a decreased risk were:
−Company
−Neighbourhood
Conclusions
Several risk factors were identified that will allow to adjust management for controlling this productive problem in salmonids aquaculture.
Relevance
Productive efficiency could be improved.

P167

Identification of risk factors for Piscirickettsia salmonis (SRS) mortality on salmonids, Los Lagos and Aysen regions, Chile.

Catalina Flores[1], **Raúl A. Alegría-Morán**[1], Gabriel Arriagada[2], Santiago Urcelay[1], [1]University of Chile, Santiago, Chile; [2]University of Prince Edward Island, Charlottetown, PE, Canada. Contact: ralegria@veterinaria.uchile.cl

Purpose:
The beginning of salmonid commercial production in Chile brought with self the emergence of a group of pathologies that greatly effected this industry, being piscirickettsiosis (SRS) one of the most emblematic at a national level. This study aims to determinate risk factors for SRS outbreaks in Los Lagos and Aysen regions, plus the vaccination efficacy in productive conditions in coho salmon and rainbow trout.

Methods:
To accomplish the risk factor estimation, a retrospective, observational study from 2006 - 2007 period, was realized, describing the relationship between environmental and management factors and the cumulative mortality percentage attributable to SRS, through a multiple linear regression analysis. Risk factors included on this model were cultivated specie, kind of smolt origin facilities, vaccination against SRS, presence of other pathology during the fattening period, cumulative mortality percentage attributable to drop and physical causes, number of antibiotic therapies applied and rest week from cages.

Results:
10.4% of average cumulative mortality attributable to SRS was obtained. Risk factors associated with mayor cumulative mortality percentage attributable to SRS were cultivated specie, where rainbow trout presented an increased risk ($\beta = 1.15$; p-value < 0.0001), kind of smolt origin facilities, where estuary and mixed origin presented an increased risk ($\beta = 2.54$; p-value < 0.0001 and $\beta = 1.62$; p-value < 0.0001 respectively), presence of other pathology, where jaundice syndrome presented an increased risk ($\beta = 1.22$; p-value = 0.0041). A mayor rest period from the cages was associated to a minor cumulative mortality attributable to SRS. The variable vaccination against SRS brought confounding results and was not statistically associated to mortality caused for this pathology.

Conclusions:
Rainbow trout breeding, estuary or mixed smolt origin facilities, presence of jaundice syndrome and short rest periods increase mortality attributable to SRS.

Relevance:
This study provide important background for the development of control strategies for greater impact disease on Chilean salmon industry.

P168

Cleaner fish that controlled sea lice exposed salmon to viral haemorrhagic septicaemia virus, a new route for disease emergence?

Alexander G. Murray, Malcolm Hall, Stuart Wallace, Marine Scotland Science, Aberdeen, United Kingdom. Contact: Sandy.Murray@scotland.gsi.gov.uk

Purpose:Parasitic sea lice are a key limitation on farmed salmon production. One method that is increasingly applied to their control is the use of cleaner fish such as wrasse that eat the lice off cohabiting salmon. Unfortunately, these wrasse can carry infections, some of which they can transmit to salmon. Recently, wrasse held on salmon farms in the Shetland Islands off north Scotland were found to be infected with viral haemorrhagic septicaemia virus (VHSV); VHS disease causes high mortality in trout and other fish, this might lead to emergence of a salmon VHS with consequences similar to VHS in trout.
Methods: The substantial benefits of using wrasse for lice control must be weighed against this risk. Therefore the potential for disease emerging in salmon from wrasse, due to VHSV or other pathogens, has been analysed using a risk modelling framework. Wrasse could be a source of pathogens if: (1) infected on introduction to the salmon farm, (2) they become infected from wild reservoirs on farm, or (3) pathogens evolve virulence in the wrasse under farm conditions. Pathogens in wrasse it must then transmit to salmon. Should such an emergence event occur, the infection would have to spread between farms. Risk associated with wrasse is considered relative to other routes by which infection could reach the salmon farm, such as movements of salmon
Results: The risk associated with emergence of disease from wrasse in salmon was found to be low relative to the benefit of lice control. This risk can be reduced by good practice, notably use of hatchery reared wrasse (not wild caught), surveillance of both wrasse and salmon for clinical disease, and area-management of salmon farms (including synchronised fallowing).In Shetland, VHSV in wrasse originated from a wild reservoir in the region, but no transmission occurred to salmon and the wrasse were culled.
Conclusions: We conclude disease risk from wrasse use is acceptable for salmon farming - provided good biosecurity is in place.
Relevance: Resistance to the medicines that sea lice have traditionally been controlled by is increasing, and so other methods of control are needed. Wrasse are suitable and safe for such lice control in salmon.

P169

Mortality and common diseases during grow-out of red tilapia (Oreochromis spp.) cultured in the Mekong Delta, Vietnam

Annette S. Boerlage[1], Thu T. Dung[2], Tran T. T. Hoa[2], Jeffrey Davidson[1], K. Larry Hammell[1], [1]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada; [2]College of Aquaculture and Fisheries, Can Tho University, Can Tho, Viet Nam. Contact: aboerlage@upei.ca

Purpose: Vietnam is one of the most productive aquaculture countries in the world. Although production of red tilapia (*Oreochromis* sp.) is small compared to production of striped catfish (*Pangasianodon hypophthalmus*), tilapia are important for local consumption and increasingly for export. In the Mekong Delta, red tilapia are cultured in floating cages. Little is known about the frequency of mortality events or the prevalence of major tilapia diseases. The objectives of this pilot study were to describe and quantify mortality and disease occurrence within a crop of red tilapia in floating cages in the Mekong Delta.

Methods: Following a survey of 200 farms to identify management variables contributing to higher pathogen introduction risk, two farms per province in Ben Tre, An Giang, Dong Thap, and Vinh Long agreed to participate in a mortality evaluation study. Five moribund fish per one cage per farm were sampled at four time intervals between June 2014 and March 2015. Daily mortality was recorded continuously throughout the study. Pathogens of primary interest were: *Streptococcus* sp., *Aeromonas* sp., *Flexibacter* sp., and *Trichodina/monogenean* parasites.

Results: Statistical methods were used to investigate 1) the relationship between mortality levels and detection of pathogens, and 2) spatial and temporal variation in mortality and pathogen occurrence.

Relevance: This study provides a quantitative overview of mortality and disease in red tilapia aquaculture that can help to prioritize disease management.

P170

The direction of sampling bias when hooking fish from a sea cage: case study of fluke monitoring in Australian farmed Yellowtail Kingfish (*Seriola lalandi*)

Charles Caraguel[1], James Fensham[1], Matt Landos[2], Erin Bubner[3], Trent D'Antignana[4], [1]The University of Adelaide, Roseworthy, Australia; [2]Future Fisheries Veterinary Service Pty Ltd, Port Lincoln, Australia; [3]Flinders University, Adelaide, Australia; [4]CleanSeas, Port Lincoln, Australia. Contact: charles.caraguel@adelaide.edu.au

Purpose: The Australian Yellowtail Kingfish (*Seriola lalandi*, YTK) farming industry routinely monitors the burden of skin fluke (*Benedenia seriolae*, SF) and gill fluke (*Zeuxapta seriolae*, GF) in fish cages to make treatment decisions. Up to 10 YTK are conveniently captured using hook and line from the edge of the cage and flukes are collected and counted. It is generally believed that hooking caged fish tends to select the fast swimming, dominant, and healthier fish. This approach is expected to result in an under-estimation of parasite prevalence and burden within the population, and ultimately could mislead or delay intervention. However, the presence and direction of a sampling bias when hooking YTK has not been investigated before.
Methods: Individual weight, fork length and fluke counts were compared between 100 hooked and 100 seined YTK, assumed to be a fair representation of the study cage population.
Results: Hooking increased by almost 6 times the probability of sampling YTK of a weight and length in the lowest 5th percentile of the cage (RR=5.75, $p<0.001$). These low end fish had on average an extra 32 juvenile and 6 adult GF per kg of fish and an extra 3 juvenile and 0.4 adult SF per kg of fish, compared to the rest of the population ($p<0.05$).
Conclusions: Hooking biased sampling towards the smallest and most heavily infested fish resulting in an over-estimation of parasite burden in the study cage.
Relevance: In Australia, a short rod is used to hook YTK which mainly access the smaller fish swimming on the edge of the cage. Hooking methods accessing fish from the centre of the cage may select a different category of fish. In the instance where the cage population is very homogenous, sampling bias may be less severe. More cage scenarios with different parasite burdens and fish profiles should be investigated to better predict the presence and direction of the bias.

P171

Mapping exposure risks of wild aquatic animal populations due to aquatic animal processing

Birgit C. Oidtmann, David Ryder, Centre for Environment, Fisheries and Aquaculture Science, Weymouth, United Kingdom. Contact: Birgit.Oidtmann@cefas.co.uk

Purpose:
The purpose of the study was to map locations of potential exposure of wild aquatic animal (AA) populations in England and Wales to exotic notifiable AA pathogens through discharge of liquid waste from AA processing to inform risk based surveillance.

Methods:
Data from 5 Border Inspection Posts in England were analysed for raw AA products imported from third countries for human consumption over a 1 year period (November 2009 - October 2010), covering >60% of all AA products imported into GB during that period.
The data were filtered for imports of susceptible species from countries with a history of the diseases within scope. The destinations were risk scored depending on activity (processing) undertaken, and weight of raw product received. Disease specific heat maps were generated. Case studies were undertaken to assess the level of waste water treatment of liquid waste from processing.

Results:
Large quantities of raw AA product were imported from countries with a history of Infectious Haematopoietic Necrosis (> 15.000 t), White spot syndrome virus (> 24,500 t), Taura Syndrome (> 9,700 t) and Yellow Head Disease (> 12,600 t). Areas of increased risk of exposure were identified in the North East of England and around London. The case studies showed that most processing facilities discharged into municipal sewer, leading to dilution and reduction of viable pathogen. However, some processors appeared not to be connected to the public sewer.

Conclusions:
The data were limited to arrivals from third countries. The heat maps provide a good basis for targeting surveillance for exotic crustacean AA diseases, since countries with a history of these diseases are outside of Europe. Since many imports of fish from infected countries are from the EU, the risk maps are likely to underestimate the exposure of wild fish populations to exotic fish pathogens. However, no detailed records of arrivals of raw AA product from the EU are available.

Relevance:
This is the first time that a spatially explicit assessment of risks associated with commodity trade has been undertaken. The data presented here provide a basis for targeting surveillance in areas of increased likelihood of exposure.

P172

A new framework for aquatic health in Brazil: developments and constraints

Marina K. V. C. Delphino, Eduardo A. P. Cunha, Pedro H. S. Oliveira, Lilian A. Figueiredo, Daniel P. Machado, Luciana A. Santana, Ministry of Fisheries and Aquaculture, Brasília, Brazil. Contact: sanidade@mpa.gov.br

Brazil has favorable conditions to increase its aquaculture production but it still faces animal health and technical and structural constraints. After the creation of the Ministry of Fisheries and Aquaculture, in 2009, there were significant structural and regulatory advances in aquatic animal health to improve the prevention, control and eradication of diseases and contribute to increase productivity. In 2010, Brazil began to carry out import risk analysis of aquatic animal products, following the OIE methodology. Since then, eight IRA were finished and more than 30 are still in progress. Other noteworthy measures were the onset of the national program for monitoring, controlling and mitigating microorganisms and marine biotoxins of bivalve molluscs and the establishment a national network of laboratories (RENAQUA), essential for the implementation of health programs. By mid-2013, the Ministry created a collaboration network in veterinary epidemiology (AQUAEPI), responsible for the technical and scientific support for the formulation and implementation of public aquatic health policies. In 2014, it was launched the national programes for Antimicrobial Resistance Monitoring on Fisheries Resources and for Aquatic Animal Health. These are being implemented with the support of regional agricultural agencies in states and municipalities. So far, 10 states have already concluded an agreement on animal health with the Ministry. Amongst the major hurdles, it stands out the low awareness of the productive sector regarding the need to invest in surveillance and disease control. Moreover, environmental permits still limit the access of farmers to the increased availability of credit. It should also be stressed that states' veterinary services have limited knowledge on aquatic health and have most of their operational capability dedicated to terrestrial animals. In conclusion, Brazil is putting up serious measures to improve aquatic health but there is plenty to be done in order to implement an effective system of epidemiological surveillance of aquatic animals in the country.

P173

Quality of drinking water in Italian turkey farms: chemical-physical and microbiological comparison of well and aqueduct supply

Guido Di Martino[1], Clara Montesissa[2], Alessandra Piccirillo[2], Albino Gallina[1], Damiano Comin[1], Filippo Buniolo[1], Stefano Marangon[1], Lebana Bonfanti[1], [1]IZSVe, Legnaro (PD), Italy; [2]University of Padova, Legnaro (PD), Italy. Contact: gdimartino@izsvenezie.it

Purpose: Reg.852/2004/EC establishes requirements for livestock drinking water as “potable or clean” without specifying any qualitative limit. Groundwater is frequently used as a source of supply, but may be subjected to contaminant infiltration (inorganic substances and bacteria) and sometimes unsuitable as a mass medication vehicle (e.g. hardness higher than 200mg/L may interfere with tetracycline dissolution and adsorption). Limited data are available regarding the chemical-physical and microbiological quality of drinking water for turkeys in Italy. This study aimed at describing water quality in 14 turkey farms supplied with well water (WW) and 14 farms with aqueduct water (AW).

Methods: Salinity, hardness, pH, ammonia, sulfate, phosphate, nitrate, chromium, copper and iron were quantified in each sample. Total bacterial count at 22°C and 37°C, presence and enumeration of Enterococcus spp. and E. coli, and presence of Campylobacter spp. were evaluated. Water samples were collected in winter and in summer at 3 sites: at the water source (S), in the tank where drugs are mixed for medicated water preparation (T) and at the nipple line (N).

Results: Chemical-physical profile of WW and AW was mostly within the limit of tap water for human use (Counc.Dir.98/83/EC), despite hardness ranged between 80-500mg/L. Iron in WF had a maximum of 0.7mg/L at S and of 1.5mg/L at N. At S, microbiological quality of both WW and AW was mostly within the limit of tap water, while being poor at T and N (e.g. up to 4,400 CFU/100mL of E. coli in WW and 1,300 CFU/100mL in AW). C. jejuni and C. coli were isolated only once, in WW and AW respectively, both at T site. In winter the prevalence of real time PCR positivity exceeded 70% of both WF and AW farms; in summer it was 43% of WW farms and 71% of AW farms.

Conclusions: These preliminary findings indicate some criticisms in hardness and cleaning/disinfection procedures of pipeline.

Relevance: This is relevant for further studies aimed at determining the correct dosage of drugs delivered to livestock via medicated water, taking into account a decreased solubility/stability in water and the presence of pipeline microbiota. Project RC IZSVe 10/11.

P174

Farmers' perceptions and the human-animal relationship in Finnish sow herds

Paula S. Bergman[1], Tiina Kauppinen[2], Mari Heinonen[1], Anna-Maija Virtala[3], Anna Valros[2], [1]University of Helsinki, Faculty of Veterinary Medicine, Saarentaus, Finland; [2]University of Helsinki, Faculty of Veterinary Medicine, Helsinki, Finland; [3]University of Helsinki, Faculty of Veterinary Medicine, Helsinki, Finland. Contact: paula.bergman@helsinki.fi

Human characteristics determine our behavior towards animals. However, stockmanship is problematic to evaluate and improve, because of the diverse backgrounds, knowledge basis, moral values of stockpersons, and the influence of economic challenges. Farmers' attitudes and the human-animal relationship (HAR) need to be investigated in more depth.

Our aim was to study the attitudes of stockpersons in relation to animal welfare and production in 2014, and compare our data with those from an earlier survey in 2006. Moreover, we examined the associations between farmers' perceptions and HAR.

Altogether, 43 farms having 40-2100 sows were visited. Farmers' opinions were investigated using a Likert-scaled questionnaire (1=strongly agree/very likely/very much⋯7=totally disagree/very unlikely/not at all), and compared with the data of 296 farms from 2006. HAR was evaluated using the Fear of Human test modified from the Welfare Quality protocol.

The results from 2014 and 2006 were in close agreement. The most important means of improving welfare were maintaining animal health (2014:1.8/2006:1.9) and the farmers' own well-being (1.7/1.8). Yet, these were not perceived as easy to implement. The farmer's obligation to treat animals well continued to be valued (1.2/1.3). Among the future intentions, respondents in 2014 were more likely to intensify taking care of animal health and treating diseases (2.3/2.8). The opinions of 2014 and 2006 differed significantly with respect to agreement on the economic profitability of improving welfare (2.2/1.7). Greater agreement was reported for "Welfare should not cost too much" (2.1/2.6). This reflects the current financial challenges in pork production.

HAR varied little between farms. Over 70% of the animals behaved calmly, and the herds were put to two groups: ≥70% (CALM, n = 26) and <70% (LESS CALM, n = 17). Attitudes differed in the perceived easiness of arranging time to work unhurried. The CALM farms judged this to be more difficult. They might value spending time with the animals more highly, resulting in a greater work load. On LESS CALM farms work scheduling was assessed easier, possibly due to considering spending time with the animals as more trivial.

P175

Associations between average daily gain and calf health, feeding and management practices in preweaned dairy heifer calves in the US

Jason Lombard, Chelsey Shivley, Natalie Urie, Charles Fossler, USDA:APHIS:VS:Center for Epidemiology and Animal Health, Fort Collins, CO, Contact: jason.e.lombard@aphis.usda.gov

Purpose:
Preweaned dairy calves are traditionally fed lower amounts of milk compared to their beef counterparts. This practice is associated with lower average daily gains (ADG) and may also lead to increased morbidity and mortality. The objective of this study was to evaluate the effects of type and quantity of liquid diets, calf health, and management practices on ADG in heifer calves.

Methods:
This study was conducted as part of the National Animal Health Monitoring System's Dairy 2014 study and included 125 dairy operations in 13 states. This was a yearlong longitudinal study focused on dairy heifer calf health and management from birth to weaning. Liquid diets were categorized by type (i.e., milk replacer, waste/whole milk, or a combination) and by volume (i.e., > 4.9 kg/day or <= 4.9 kg/day). During the preweaned period, all health events were recorded and calf growth was assessed at 2 week intervals. Proc Mixed in SAS was used to determine which diet, health and management practices were significantly ($p<0.05$) associated with ADG. This interim analysis is based on 851 calves (approximately 25% of the expected total) from 92 operations.

Results:
The ADG was 0.7 kg/day with an average age at weaning of 58.8 days. Calves, on average, gained 41.2 kg during the preweaning period. The model, using initial results, included liquid diet, disease events, housing, and dehorning. Calves fed a combination diet had the highest ADG. Calves fed > 4.9 kg milk/day outgained calves fed milk replacer and calves fed <= to 4.9 kg milk/day. Calves without disease had a higher ADG than calves with one or more disease events. The ADG was higher for calves housed in groups than calves housed individually. Calves that were dehorned had a higher ADG than calves that were not dehorned during the preweaning period.

Conclusions:
Preliminary results show improved ADG and lower morbidity with increased milk volume fed. The relationship between ADG and morbidity and mortality will be further evaluated to try and elicit the causal relationship.

Relevance:
Improving nutrition to preweaned dairy heifer calves increases weight gain and decreases disease occurrence which improves animal welfare and decreases the use of antibiotics.

P176

Dairy cattle lying bout duration, frequency and total lying time in freestall herds as predicted by lameness and other animal and management related risk factors

Karin Orsel[1], Laura Solano[1], Herman Barkema[1], Clemence Nash[2], Derek Haley[2], Ed Pajor[1], Stephen LeBlanc[2], Jessica Zaffino Heyerhoff[2], Doris Pellerin[3], Jeff Rushen[4], Annemarie de Passille[4], Elsa Vasseur[5], [1]University of Calgary, Calgary, AB, Canada; [2]University of Guelph, Guelph, ON, Canada; [3]Universite Laval, Quebec, QC, Canada; [4]University of British Columbia, Agassiz, BC, Canada; [5]University of Guelph, Guelph, ON, Canada. Contact: karin.orsel@ucalgary.ca

Background: Lameness is a significant problem in the dairy industry. In addition to economic losses, it causes pain and reduces welfare. Detection of lameness and other risk factors that predict lying bout characteristics can help in optimizing lying behaviour in a cow comfortable environment. Objective: We investigated the association between lying behaviour and lameness to determine whether lying behaviour can be used for lameness detection. We identified the herd- and cow-level risk factors associated with lying bout characteristics (duration, frequency and total lying time). Methods: A total of 141 Canadian freestall dairy farms were enrolled. On each farm 40 lactating HF cows were fitted with accelerometers to measure lying behaviour. Information on the frequency and duration of lying bouts was monitored over a 4-day period. Cows were video-recorded to assess lameness prevalence and several scores were taken (e.g. BCS, injury score) when cows exited the parlor. Other management factors were captured during farm inspection and producer interviews. Associations between the outcome variable lying bouts characteristics and the predictor variables were assessed using univariate analyses. In the second step, predictors were screened in separate multilevel mixed logistic regression models (GLMMs). In this last step, all variables significant at $P \leq 0.10$ were combined and a backward elimination process was performed. Results: In a preliminary analysis, within-herd variation of lying bout characteristics predicted by presence of lameness was high. Correlations between bout duration, frequency and total lying times will be explored as well as other predicting risk factors for lying times in freestall dairies. Conclusions: Lying times are potential measures to evaluate dairy production in a cow comfortable environment. The association found with lameness helps to identify on-farm risk areas that can be improved to optimize cow comfort and productivity. Relevance: Optimized dairy production can be achieved if cows spend sufficient time ruminating when lying down. Sufficient lying bout characteristics can be identified using accelerometers, indicative of presence of lameness.

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Risk factors associated with leg disorders of gestating sows in 4 group-housing systems: a cross-sectional study in 108 farrow-to-finish French farms

Charlie Cador[1], Françoise Pol[2], Marion Hamoniaux[3], Virginie Dorenlor[1], Eric Eveno[1], Claudie Guyomarc'h[3], Nicolas Rose[1], [1]Anses, Ploufragan, France; [2]Anses, Ploufragan, France; [3]Cooperl Arc Atlantique, Lamballe, France. Contact: charlie.cador@anses.fr

Purpose:
Group-housing, instead of individual-housing systems, has been mandatory for gestating sows in the European Union (2008/120/EEC). However, leg problems (i.e. claw lesions and lameness) occur more frequently in group- rather than in individual-housing systems and these troubles are of welfare, health and economic concerns. A cross-sectional epidemiological study involving 108 farrow-to-finish French farms has been carried out to evaluate whether the type of the 4 main group-housing systems (large groups with electronic feeder station reared in stable or in dynamic groups, small groups in walk-in lock-in stalls or partial feeding stalls), the type of floor, and other husbandry practices, were associated with leg disorders.

Methods:
In each farm, a questionnaire on the herd management, observations and measurements of the climatic conditions in the sows breeding premises were performed. Sows were examined visually for claw lesions, scored for lameness and their breeding characteristics were recorded. A leg disorder score, specific to each farm and calculated from the frequency of lameness and the mean score for each claw lesion was created. Factors associated with the leg disorder score were identified using a multivariable logistic regression model.

Results:
Lameness was positively correlated with heel lesions and dewclaw lesions. Concrete slatted floor was a major risk factor (unadjusted relative risk RR = 9.9 [4.4; 34.5]) compared to straw bedding. From the multivariable model, housing sows in large groups (RR = 1.5; CI [1.1; 2.4]), on dirty floors (RR = 1.6; CI [1.0; 2.9]), exposed to a high level of ammonia (RR = 1.5; CI [1.1; 2.1]), with a strong feeding restriction in particular at the last stage of pregnancy (RR = 1.5; CI [1.0; 2.1]) and with a high number of sows per stockman (RR = 1.5; CI [1.0; 2.4]) significantly increased leg troubles on farms.

Conclusions:
Walk-in lock-in stalls was found to be the most protective system. Relative risk estimates were very close, highlighting the multifactorial origin of leg disorders.

Relevance:
A global approach including management of husbandry practices adapted to group size is needed to tackle leg troubles in breeding sow herds.

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Strengthening animal health service provider value chains to improve the healthcare available to working equids in low income countries

Polly Compston, Tamsin Hirson, Laura Skippen, The Brooke, London, United Kingdom. Contact: polly.compston@thebrooke.org

The Brooke is an international organisation working to improve welfare of working equids through strengthening health service provision among other activities. There are millions of working equids in low-income countries, who are essential in many rural and urban livelihoods. A range of service providers form a healthcare infrastructure around working equids. However, because they have low status at local and national levels there is often insufficient healthcare provision resulting in lost days of animal work and livelihood loss. Many development-orientated interventions in this sector focus on technical knowledge transfer and subsidised treatments, rather than providing support along the service provider value chain. This study explored current and potential strategies within The Brooke aiming to strengthen the service provider (SP) value chain.

A workshop discussing equine service provision value chains with senior vets from 7 country programmes was facilitated by 2 UK technical support team members. The value chain was described in 3 sections: inputs, service provision and business development. Current and potential programmatic activities in each of these 3 sections were systematically collated from all country programmes and discussed.

Forty-six percent (12/26) current interventions target improving technical capacity in SPs e.g. mentoring schemes, training courses, certification, peer-learning. Fewer interventions (27%; 7/26) aimed to strengthen inputs e.g. provision of starter kits and access to drug revolving funds - or business development (27%; 7/26) e.g. developing links with equid-owning communities.

Among potential reasons for these results are 1) strategies that strengthen inputs may be underdeveloped because animal health inputs are expensive; 2) business development activities may be hampered by difficulties inherent in working with communities with low financial literacy; 3) economic evaluation is complicated as many payments are made in kind and families often rely on multiple income streams. These findings support the need for an integrated approach from animal health economists and academics alongside agencies working directly with SPs.

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An economic analysis comparing small ruminant vaccination to the current brucellosis control policy in Egypt

Mieghan Bruce[1], Jonathan Rushton[1], Yamen Hegazy[2], Wael El-Tras[3], Mahmoud El Tholth[2], [1]Royal Veterinary College, London, United Kingdom; [2]Kafrelsheikh University, Kafrelsheikh, Egypt; [3]Auckland University of Technology, Auckland, New Zealand. Contact: mbruce@rvc.ac.uk

Purpose: Brucellosis is considered an economically and socially important disease in Egypt, especially for livestock farmers who suffer the double burden of zoonoses. Since 1981, the national control program for brucellosis involves test-and-slaughter of positive animals and voluntary vaccination of replacement animals. However, control efforts to date have been largely ineffective, despite the commitment of significant financial and human resources. Therefore, the aim of this study was to assess the net economic value of a change in disease control policy to mass vaccination of all small ruminants for two years followed by annual vaccination of replacement small ruminants

Methods: Disease transmission was simulated within and between ruminant populations and to humans to predict the effects of a change in control strategy over a ten-year period. The cost of the proposed strategy, cost of current control measures and the estimated change in disease frequency in livestock and people were used to calculate the net present value, benefit-cost ratio and cost per DALY-averted. The economic evaluation included human medical costs, income losses, and livestock productivity losses. Probability distributions were used for input parameters and the results expressed as median and 95% prediction intervals of 5,000 model iterations.

Results: The total cost of the proposed intervention was US$17.6 million for the ten-year period. The net present value was US$1.2 million (95% PI: 1.0m; 1.5m) and the median benefit-cost ratio 7.5. 300 DALYs would be saved with a cost-effectiveness of US$58,666 per DALY-averted. Sensitivity analysis indicated the economic benefits were most influenced by uncertainty in livestock productivity losses attributable to brucellosis and duration of human illness.

Conclusions: This study demonstrated small ruminant vaccination was economically efficient, however there was little improvement in human incidence. The high cost per DALY-averted means the One Health benefits must be promoted.

Relevance: The study results support a change in strategy for brucellosis in Egypt, although a vaccination strategy targeting cattle may be necessary to improve human health.

P180

Cost-benefit analysis of elk brucellosis prevalence reduction in the southern Greater Yellowstone Area

Kari Boroff[1], **Dannele Peck**[1], Mandy Kauffman[2], Brant Schumaker[3], [1]University of Wyoming, Laramie, WY, [2]Western EcoSystems Technology, Inc., Laramie, WY, [3]University of Wyoming, Laramie, WY, Contact: dpeck@uwyo.edu

Purpose: Recent cases of bovine brucellosis in U.S. cattle within the Greater Yellowstone Area (GYA) have been traced back to free-ranging elk. This raises questions about the most cost-effective means of reducing transmission risk from infected elk to cattle. Three elk management activities (elk test-and slaughter, low-density feeding at elk winter feedgrounds, elk vaccination with strain 19) attempt to reduce seroprevalence (a marker for prevalence) in elk. Yet it is difficult to determine the cost-effectiveness of reducing elk seroprevalence because we typically do not understand the extent to which it translates into fewer infected cattle herds. Recently, however, a stochastic risk model was developed that estimates the extent to which reduced seroprevalence in southern GYA elk would reduce the risk of cattle contracting brucellosis.

Methods: Using the risk model's results, we are able to estimate the expected economic benefits of reducing seroprevalence in elk. We then calculate the cost of reducing seroprevalence in elk using various management activities. Finally, we combine these expected benefit and cost estimates to determine circumstances in which individual management activities may be economically justifiable (i.e., generate positive expected net benefit).

Results: The three elk management activities we analyze each yield negative expected net benefits, ranging from a maximum of -$3000 USD per year for low-density feeding to a minimum of -$600,000 USD per year for test-and-slaughter.

Conclusions: Society's risk preference will determine whether strategies that generate small negative net benefit, such as low-density feeding, are worth considering. However, activities with large negative net benefits, such as test-and slaughter and strain 19 vaccination, are unlikely to be economically worthwhile.

Relevance: This study enables agencies responsible for managing bovine brucellosis in the southern GYA to identify disease management activities that are most likely to be economically worthwhile. Our methods can also be adapted for other locations facing similar wildlife-livestock disease transmission and management decisions.

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Center for Outcomes Research and Education - applied epidemiology and economics for quantifying the value of animal health initiatives.

David Renter, Natalia Cernicchiaro, Christy Hanthorn, Robert Larson, Brad White, Michael Sanderson, Kansas State University, Manhattan, KS, Contact: drenter@vet.ksu.edu

Although outcomes research, as a discipline, has been developed and broadly applied to human health initiatives, there has been little formal application of outcomes research to addressing contemporary animal health issues. Since outcomes research involves applying population-based research methods to optimize clinical and economic impacts of health care decisions, the principles and methods of both epidemiology and economics are critical. Our group in the new Center for Outcomes Research and Education is developing and enhancing interdisciplinary research and training programs focused on the application and extension of outcomes research in animal health from local through global perspectives. With a goal of improving effectiveness and efficiency in animal health care and its associated impacts on human health, our activities demonstrate the value of animal health interventions. Quantification of economic factors, comparative clinical effectiveness, risk analysis, willingness to pay, and health-related quality of life assessments are key areas of focus. Results of a recent literature review will be used to compare and contrast how outcomes research has been applied in the human health and animal health fields. In addition, specific examples will be used to illustrate the application of outcomes research to animal health issues, including 1) economic impacts of infectious disease management decisions, 2) quantification of potential value and costs associated with pre-harvest food safety interventions, and 3) risk management strategies for a common production-limiting disease in cattle. This information will be used to demonstrate opportunities for applying and enhancing approaches for outcomes research in animal health, as a new potential paradigm for generating, synthesizing, and utilizing evidence, including economic indexes, to advance health management decisions. By developing and advancing outcomes research methods, interdisciplinary collaborations and communications will strengthen, and there will be improved effectiveness and efficiency in animal health care as well as positive impacts on human health.

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A benefit-cost analysis decision framework for disease mitigation at the wildlife-livestock interface

Stephanie A. Shwiff[1], **Steven J. Sweeney**[2], Ryan S. Miller[2], Matthew L. Farnsworth[2], Pauline Nol[3], Steven S. Shwiff[4], Aaron M. Anderson[1], [1]U.S. Department of Agriculture, National Wildlife Research Center, Fort Collins, CO, [2]U.S. Department of Agriculture, Center for Epidemiology and Animal Health, Fort Collins, CO, [3]U.S. Department of Agriculture, Wildlife-Livestock Disease Investigations Team, Fort Collins, CO, [4]Texas A&M University-Commerce, Commerce, TX, Contact: steven.j.sweeney@aphis.usda.gov

Purpose: The economics of managing diseases at the wildlife-livestock interface have received heightened attention as agricultural and natural resource agencies grapple with emerging risks to animal health. In the fiscal landscape of increased scrutiny and shrinking budgets, resource managers seek to maximize the benefits and minimize the costs of disease mitigation efforts.
Methods: To address this issue, we used group ideation to develop an objective decision-making framework - based on benefit-cost analysis (BCA) - for weighing the economic efficiencies of various health management strategies at the wildlife-livestock interface. Within the context of this framework, we examined conclusions of a previously published benefit-cost analysis of vampire bat rabies control in Mexico.
Results: Our BCA decision framework fit well with the economic analysis and conclusions of the rabies control study, which found that vaccination of cattle against rabies was far more economically efficient than targeted control of vampire bat populations.
Conclusions: Benefit-cost analysis provides a structural framework that can be used to identify, assemble, and measure the components vital to the biological and economic efficiencies of animal disease mitigation efforts. The BCA framework allows for evaluation of management strategies across regions, diseases, types of livestock, and wildlife species, and can be applied to activities ranging from local interventions to broad programmatic actions. This framework can deliver quantitative or qualitative estimates based on user needs and data availability and can be adapted to situations other than diseases, for example, management of invasive species.
Relevance: Although we developed this BCA methodology to inform policy and program decisions in the United States Department of Agriculture, we believe it will be useful to the broader natural resource management community to maximize returns on financial and other resources invested in disease management programs.

P183

Economic evaluation of various copper sulphate footbath protocols in the prevention of digital dermatitis in Alberta dairy cattle.

Casey Jacobs, Karin Orsel, Herman W. Barkema, University of Calgary Faculty of Veterinary Medicine, Calgary, AB, Canada. Contact: jacobs.casey@gmail.com

Digital dermatitis (DD) is an infectious disease affecting the hooves of dairy cattle. It has implications on production as well as animal welfare as the lesions are painful and may lead to lameness. A common method to prevent DD is the use of footbaths to decrease the occurrence and severity of DD in the dairy herd. However, numerous products are used and result in immense variation of protocols with differing products, concentration, and frequencies. A cost-benefit economic decision model would be indispensible in the comparison of footbath protocols.

Purpose: To create an economic decision model to compare the net benefit of footbath protocols and to evaluate the cost-benefit to the farmer of three copper sulphate (CuSO4) footbath protocols in the prevention of DD. The three footbath protocols to be compared were 5% CuSO4 4 times weekly, 2% CuSO4 4 times weekly, and 5% CuSO4 4 times every other week. The net benefit of use of these protocols was calculated on a herd basis using costs and prevalence estimates from Alberta data where available.

Methods: A decision model was created to calculate the net benefit of each protocol. Net benefit was calculated as the revenues due to milk sales and slaughter value minus replacement costs, subsequent treatment costs, fertility losses, footbath costs and the cost to fill quota. Revenues were affected by the consequences of DD lesions on milk yield, fertility, and risk of culling.

Results:

Table 1. Incremental net benefit of CuSO4 footbath protocols

Protocol	Incremental Benefit
2% CuSO4 4 times weekly	$4 976
5% CuSO4 4 times every other week	$3 702
5% CuSO4 4 times weekly	$0

Conclusion: Footbath strategies for the prevention of DD lesions in dairy cattle in Alberta are cost effective (Table 1) with 2% CuSO4 4 times weekly resulting in the greatest net benefit to farmers over one lactation on a farm with 20% DD. Percentage of cows with DD and herd size were the main drivers of this model and results cannot be generalized to all dairy operations without incorporating these and other variables.

Relevance: An economic decision model calculating the net benefit of footbath protocols provides an additional method to compare potential footbath protocols.

P184

Economic impact of oestrosis in the Eastern region of Cuba

Pastor Alfonso[1], Vilmaris Matos[2], Paolo Calistri[3], Kleber Régis Santoro[4], Osvaldo Fonseca[1], Jesús G. Rodríguez-Diego[1], María A. Abeledo[1], **María I. Percedo**[1], [1]Centro Nacional de Sanidad Agropecuaria (CENSA), San José de las Lajas, Cuba; [2]Centro de Desarrollo de la Montaña (CDM), El Salvador, Guantánamo, Cuba; [3]Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, Teramo, Italy; [4]Universidade Federal Rural de Pernambuco (UFRPE), Garanhuns, Brazil. Contact: percedo@censa.edu.cu

Purpose:
Oestrus ovis L. is an important myiasis-producing agent of sheep and goats in diverse production environments that impairs the wellbeing and performance of their hosts. Despite of oestrosis importance, the disease is generally undervalued, perhaps by the limited existing studies upon its economic importance and, the benefit of control. The aim of this work was to assess the economic impact of oestrosis and expected benefit based on antiparasitic treatment in a region of Cuba where the disease is endemic.
Methods:
Based on a data set of oestrosis outbreaks during six years (2006-2011) a model was developed, using @Risk (Palisade Corporation) and Microsoft Excel 2007 and the simulation results were obtained after 1 000 interactions with Latin hypercube sampling. Sheep flocks were randomly pick up to estimate losses per year, according to probability distributions of risk for mortality, reduced daily weight effect and loss for capital immobilization. The average annual benefit per sheep was established based on a model developed by Stott & Gunn 2008 by foot and mouth disease, deriving probabilities to avoid losses across a range of expenditures on antiparasitic treatments.
Results:
the direct disease losses were near a million of the local currency (pesos) on a susceptible population of 139 536 sheep. In unitary form, the prevalence and lethality observed in the affected region, determined a loss of 6.91 pesos/sheep/year. The cost opportunity for fighting or either controlling oestrosis was considered beneficial; because of price of main antiparasitic was lowest concerning to 7 pesos/sheep as disease impact. The Cuban sheep raising is mainly for meat production, in which oestrosis cut, 472 Kg of sheep live weight each thousand susceptible animals.
Conclusion:
the probability to avoid disease losses through benefit function allow to established feasibility of treatment for reducing economic impact of oestrosis under the studied conditions.
Relevance:
the maximum average net benefit of disease control under studied epidemiological and farm business circumstances may help to persuade farmers to invest in oestrosis control.

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Evaluating economic optimal strategies for regional control of porcine reproductive and respiratory syndrome (PRRS): a collective choice problem approach

Pablo Valdes-Donoso[1,2], Andres Perez[1], Lovell S. Jarvis[2], [1]University of Minnesota, Minneapolis, MN, [2]University of California Davis, Davis, CA, Contact: pvaldesdonoso@ucdavis.edu

Purpose: Swine producers face incentives to control disease that largely depend on the type and expected severity of the disease, the feasibility and cost of containment and the expected economic impact on farm profits. Furthermore, system structure, knowledge about other producers, and government policy are likely to influence disease control. Although porcine reproductive and respiratory syndrome (PRRS) is a high-impact endemic disease affecting the swine industry in the U.S., there is no official program for its containment. However, some States have developed area regional voluntary control (ARC) programs.

Methods: This study aims to build a theoretical model of a regional PRRS voluntary control program to analyze the effects of varied individual and coordinated producer actions to control disease. A disease dynamics model, which assumes that disease spread between farms is related to farmers' individual and collective choice of production strategies, is used. We assume that disease risk is an endogenous factor that depends on factors such as health, production investments, and management decisions at production sites (e.g., vaccination, all in/all out, and unit size), system elements linking production sites (e.g., feed suppliers and animal transport modes), and the nature of firm agreements (e.g., sales contract incentives, system-based management).

Results: Several putative scenarios for collective action have been identified, and the resulting disease dynamics were compared and contrasted to identify economic impact.

Conclusions: A theoretical model to estimate optimal economic strategies for swine producers was created. Scenarios show that disease dynamics is tied to production preferences. To generate effective PRRS control actions, it is important to consider regional setting and interactions between producers and other suppliers.

Relevance: The proposed study will later utilize data from area regional control (ARC) programs such as the Minnesota Voluntary Regional PRRS Elimination Project (ARC N212) to test alternative approaches to PRRS regional control. This will provide a baseline for the assessment of state and federal control programs.

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Animal value chains shaping disease information networks: the case of HPAI in Vietnam and Thailand

Alexis Delabouglise[1], Guillaume Fournié[1], Raphael Duboz[2], Hiep Thi Dao[3], Thanh Tien Nguyen[4], Nicolas Antoine-Moussiaux[5], Vlasimir Grosbois[2], Aurélie Binot[2], Ton Dinh Vu[3], Khong Viet Nguyen[4], Suwicha Kasemsuwan[6], Dumaong Sakh Thatont[7], Gerard Salem[8], Marisa Peyre[2], [1]RVC, Hertfordshire, United Kingdom; [2]CIRAD, Montpellier, France; [3]Vietnam National University of Agriculture, Hanoi, Viet Nam; [4]National Institute of Veterinary Research, Hanoi, Viet Nam; [5]Liège University, Liège, Belgium; [6]Kasetsart University, Bangkok, Thailand; [7]Department of Livestock Development, Sukhothai, Thailand; [8]Paris Ouest University, Nanterre, France. Contact: alexis.delabouglise@gmail.com

Purpose:
The effectiveness of passive animal health surveillance system depends on its capacity to gather sanitary information from the animal production sector. We analyzed the flow of sanitary information related to Highly Pathogenic Avian Influenza (HPAI) suspicions in poultry.
Methods:
Two study areas with two different production sectors were targeted: commercial broiler chicken production in Northern Vietnam and backyard native chicken production in Northern Thailand. Poultry producers and other actors of the poultry sector were randomly selected in each study area. Data related to their ways of sharing HPAI suspicion information were collected in focus groups and individual interviews. These data were used to build a network of information-sharing between these actors.
Results:
First, matrix logistic regression was used to assess the influence of several link attributes on the probability of information transmission. In both study areas, actors living in the same village were more likely to share information. Secondly, the influence of several poultry farming attributes on a measure of actors' centrality - Bonacich's alpha centrality - was assessed using linear regressions with permutation tests. According to the production sector, specific types of actors had better access to HPAI suspicion information. In Vietnam commercial broiler sector feed sellers, who provide veterinary support to their customers had the highest centrality. In Thailand native chicken farming sector, cock fighting practitioners were the most central in the information network.
Conclusions:
The results show that the structure of the network of information sharing vary according to the production sector.
Relevance:
This result has strong implication on the types of actors who should be targeted to enhance passive surveillance systems to improve data collection and early warning.

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Applied animal health economics for foot-and-mouth disease control in Cambodia

James Young[1], Sothoeun Suon[2], Russell Bush[1], **Peter Windsor**[1], [1]University of Sydney, Camden, Australia; [2]Ministry of Agriculture, Forestry and Fisheries, Phnom Penh, Cambodia. Contact: peter.windsor@sydney.edu.au

Foot-and-mouth disease (FMD) is endemic in Cambodia with significant but poorly described impacts on smallholder farmer livelihoods. Since 2008, a team from the University of Sydney has been conducting research in collaboration with the Cambodian Department of Animal Health and Production, to identify improved methods for FMD control (funding mainly by the Australian Centre for International Agricultural Research). The aim was to improve understanding of the socioeconomic impacts of FMD on smallholder farmers to guide investments in FMD control. Data from longitudinal large ruminant production studies, trader and disease impact surveys, was applied to partial budget for farmer FMD vaccine use. Further, a benefit-cost analysis (BCA) for a 5-year national vaccination campaign using Monte Carlo simulation to account for variation in incidence was determined. Partial budget analysis identified a strongly positive incentive for farmers to vaccinate their cattle biannually, providing a benefit of USD 31.48 per animal for each animal owned. In the national BCA, using a predicted cost of USD 6.3 an animal per year, a benefit-cost ratio of 1.40 (95% CI 0.96-2.20) was identified when accounting for recent prices of cattle and buffalo in Cambodia and based on an expected annual incidence of 0.2 (assuming one major epizootic in the 5-year vaccination program). As the majority of the large ruminants are owned by smallholders, and mostly the poor are involved in agricultural employment, the successful implementation of an FMD control program would be expected to avoid estimated annual losses of USD 135 million; equivalent to 10.6% of the 2010 farm-gate value. These studies provide some of the first published evidence describing the impact of FMD on smallholder farmers, and indicate the net benefit for FMD control in Cambodia. The studies are relevant to the OIE's regional SEACFMD campaign, and timely given that in 2014 there were 58 outbreaks reported including re-emergence of Type A virus. Financial impacts and economic justification for disease control activities is essential in developing countries where resources are severely limited and appropriation of public funds is highly competitive.

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Economic implications of the predicted effects of climate change on tick fever of cattle in the highlands of the Neotropic

Efrain Benavides[1], Natalia Polanco[2], Jaime R. Romero[3], [1]Universidad de La Salle, Bogota, Colombia; [2]Universidade Estadual de Campinas., Campinas., Brazil; [3]Instituto Interamericano de Cooperación para la Agricultura, Lima, Peru. Contact: efbenavides@unisalle.edu.co

Purpose: In the Neotropic the tick Rhipicephalus (Boophilus) microplus transmits the agents of tick fever of cattle, anaplasmosis and babesiosis. Traditionally it is known that the tick survive in the ground until altitudes of about 2,200 m.a.s.l.; distribution determined by the preferendum of temperature of the parasite that inhibits oviposition at constant temperatures of the ground below 18 °C. Appropriate information on ecology of the tick regarding altitude is scarce. In lowlands the tick and hemoparasites occur as classic "enzootic stability" where animals develop co-infectious immunity and are healthy carriers, requiring resistant individuals and breeds. In highlands exits areas totally free of ticks or areas of enzootic instability, with the occasional presence of the tick that causes occasionally outbreaks of tick fever when the vector is introduced

Methods: Climate change or the adaptation of ticks may modify this epidemiologic condition generating disease problems in dairy production systems with highly susceptible animals located in highlands. The potential economic impact of these changes were estimating by scenario analysis based on biological and ecological information of the vector, formulating risk maps of occurrence.

Results: It was found that a change of one degree of temperature is associated with an increased risk of colonization of ticks to new areas and therefore negative effects on dairy systems represented in direct losses by deaths, treatments and decreased production. Additionally harmful effects are discussed in terms of safety and quality of milk by the use of parasiticides, making it imperative to develop control strategies with non-chemical methods such as vaccines against hemoparasites and ticks

Conclusions:

It is necessary to generate epidemiological information coupled with economic analysis in the search of alternative integrated control measures, based in local information, to guide appropriate decision making procedures that contributes to the viability and profitability of the dairy production system under these new scenarios.

Relevance: Climatic change could render unfeasible intensive dairy production in the tropic´s highlands

P189

Farmers' perceptions and intention of implementing foot and mouth disease control in Ethiopia

Wudu T. Jemberu[1,2], Monique C. M. Mourits[1], Henk Hogeveen[1], [1]Wageningen University, Wageningen, Netherlands; [2]University of Gondar, Gondar, Ethiopia. Contact: temesgenha@yahoo.com

Purpose: Foot and mouth disease (FMD) is endemic in Ethiopia, affecting the cattle production. The objective of this study was to explore cattle farmers' intentions to implement FMD control, and to identify perceptions that significantly influence these intentions using the Health Belief Model (HBM) framework.

Methods:Data were collected by face to face interview from 293 farmers in the pastoral, crop-livestock mixed (CLM) and market oriented cattle production systems. The influence of the HBM perception constructs (viz. perceived susceptibility, perceived severity, perceived benefits and perceived barriers) on the intention to implement control measures was analyzed using multivariable binary logistic regression. In a subsequent step the effect of socio-demographic and husbandry variables on the constructs that significantly influenced intentions were analyzed using multivariable ordinal logistic regression.

Results: Farmers' intention to implement vaccination free of charge was very high (>97%) while this intention decreased if vaccination would be given at own cost, especially in the CLM system where it decreased to 30%. The intentions to implement herd isolation and movement restriction were low, especially for subsistence production systems. Perceived barrier (costs of vaccination) was the only HBM construct that significantly influenced the intention to implement vaccination. Perceived susceptibility (frequency of outbreak), perceived benefits (effectiveness of measures) and perceived barriers (difficulty to implement measures) were the significant predictors of the intention for herd isolation and animal movement restriction measure. The type of production system and age of farmers were the most important factors that significantly modified the relevant perceptions for intention to implement the various FMD control measures.

Conclusions: The results of this study suggest that promotion campaigns designed to increase farmers' participation in FMD control by vaccination and movement control should give more attention to the perceived barriers of the control measures and should account for the difference in perceptions among the production systems.

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Epidemiologic and economic impacts of applying alternative control strategies for FMD in cattle feedlot operations

Amy Delgado, Amy Hagerman, Melissa Schoenbaum, USDA-APHIS-VS-STAS, Fort Collins, CO, Contact: amy.h.delgado@aphis.usda.gov

Purpose
Emergency response exercises have recognized issues associated with a traditional stamping out (S-O) response to FMD in large feedlots. Alternative methods are needed for minimizing disease spread while allowing animals to reach their intended purpose.
Methods
The spread and control of FMD within a 7 state region of the US was modeled for 3 strategies: S-O with ring vaccination (baseline strategy), modified S-O with ring vaccination but with no depopulation of feedlots; modified S-O with ring vaccination with no depopulation or vaccination of feedlots. Effects of strategy and start location on outbreak characteristics were explored using K-Wallis comparisons and logistic regression. Epidemiologic results were fed into an economic modeling framework to estimate national economic impacts for each strategy. A break-even marketed beef price for feedlot operations was determined for which each strategy became viable.
Results
Alternative strategies did not increase the number of infected herds or animals ($p>0.05$ for all comparisons), while the alternatives resulted in a 98% reduction in the median number of depopulated animals compared to the baseline ($p<0.004$). The baseline strategy resulted in shorter outbreaks (36 vs 43 median days for other strategies; $p<0.004$). Controlling for number of infected feedlots, time to first detection, and wait time for depopulation, the odds of having an outbreak that lasts longer than 50 days (the 75th percentile of outbreak duration) were 8 times greater under the alternatives ($p<0.000$).
Conclusions & Relevance
Declines in national fed cattle prices were largely driven by trade assumptions. Analysis of impacts on individual feedlot operations concluded that alternative strategies resulted in reduced response costs to government, while feedlots could still profit on controlled slaughter cattle, even under post-disease market conditions. Allowing feedlot cattle to recover and enter market channels post-outbreak does not appear to have serious epidemiologic consequences. Economic viability of alternative strategies must balance tradeoffs in response cost savings, controlled slaughter capacity, and market response.

P191

Economic assessment of alternative eradication strategies against foot-and-mouth disease in New Zealand

Masako Wada[1], Tim Carpenter[1], Naomi Cogger[1], Mark Stevenson[2], [1]Massey University, Palmerston North, New Zealand; [2]The University of Melbourne, Melbourne, Australia. Contact: M.Wada@massey.ac.nz

Purpose:
There has been a recent shift in the international attitudes toward use of emergency vaccination, especially vaccinate-to-live policies, although stamping-out only has historically been the primary strategy for control and eradication of foot-and-mouth disease (FMD) in the majority of FMD-free countries. The objective of this study was to assess relative benefits of alternative emergency vaccination policies in New Zealand.

Methods:
Using a pre-developed stochastic disease simulation model for FMD, the net present value (NPV) of vaccinate-to-die and vaccinate-to-live policies in comparison with a stamping-out policy for an epidemic randomly seeded in two regions was quantified, and linear regression models were fitted.

Results:
The density of susceptible populations in the outbreak region, the incidence rate and the incidence rate ratio during the first 2 - 3 weeks of an epidemic significantly increased the NPV. In addition, the NPV of vaccinate-to-die was greater than vaccinate-to-live by USD 3.5 billion (95% CI: 3.3 - 3.6 billion) under the current international standard. If the OIE's ruling on the waiting period for vaccinate-to-live policies were shortened to 3 months then the NPV for the vaccinate-to-live was greater than vaccinate-to-die by USD 0.77 billion (95% CI: 0.59 - 0.95 billion).

Conclusions:
A vaccinate-to-die policy would minimise the total cost of an epidemic for a rapidly spreading epidemic, while stamping-out alone would be preferred for a slow spreading epidemic under the current international standard in a New Zealand context. Vaccinate-to-live policy would be potentially advantageous if the waiting period were aligned with other policies.

Relevance:
The results of the study can inform policy makers regarding control of FMD in New Zealand, and may provide implications for other FMD-free countries similar to New Zealand.

P192

Assessment of herd immunity generated by FMD vaccination in Argentina

Facundo J. Linares[1], Andres Perez[2], Maria F. Dotta[1], Bernardo Cosentino[1], [1]Servicio Nacional de Sanidad y Calidad Agroalimentaria (SENASA), Buenos Aires, Argentina; [2]University of Minessota, Minessota, MN, Contact: flinares@senasa.gov.ar

Purpose: Foot and mouth disease (FMD) is caused by a virus of the genus Aphthovirus, family Picornaviridae that infect cloven- hoofed animals. In Argentina the last outbreak was in 2006 and currently the country has two zones with vaccination and three zones without vaccination recognized by the Word Organization for Animal Health (OIE). The FMD vaccine currently used in Argentina is oil-adjuvated and tetravalent, including the A24/Cruzeiro, A/Argentina/2001, O1/Campos, and C3/Indaial strains. In Argentina, vaccination is performed twice a year in most of the country and only cattle are vaccinated. Annually, the National Service for Agrifood Health and Quality (SENASA) performs different serological surveillance strategies in all the country to demonstrate the situation of FMD and the efficiency of the vaccination.The objective of this study was to evaluate the effectiveness of systematic FMD mass vaccination campaigns in Argentina during 2013, by estimating immunity generated by vaccine in cattle

Methods:A three stage random sampling design was used to estimate the proportion of cattle protected against FMDV. Ten blood samples were collected per farm during the first vaccination campaign of the year from animals 6 to 12 months old cattle (category 1) and three samples from 12 to 24 months old (category 2). Serum samples were analyzed using the liquid-phase blocking (LP) ELISA, to determine the level of antibody titer against FMDV O1/Campos and A24/Cruzeiro strains in the Central Laboratory of SENASA. The analytical method used was based on the estimation of the proportion of protected animals and protected farms in vaccinated populations, as reflected by levels of antibodies measured by LP ELISA.

Results:In total 35,910 animals from 2,764 farms were analyzed.

Conclusions: Results indicated an adequate immunization coverage and no significant differences were observed in the levels of antibodies in the two strains.

Relevance:The results presented in this study represent a good method to evaluate the coverage of the FMD vaccination campaign in Argentina and will have impact on the implementation of new strategies of vaccination campaigns in the country.

P193

Assessment of a pilot surveillance program for foot and mouth disease in swine, Puerto Rico

Karyn A. Havas[1], Sally Ann Iverson[1], Fred Soltero[2], [1]United States Department of Agriculture, Veterinary Services, Greenport, NY, [2]United States Department of Agriculture, Veterinary Services, Hato Rey, PR, Contact: karyn.a.havas@aphis.usda.gov

Purpose: The Comprehensive and Integrated Surveillance (CIS) for swine is a pilot active surveillance system designed for early detection of Foot and Mouth Disease (FMD) in targeted swine populations using a real-time polymerase chain reaction diagnostic test. FMD is absent from Puerto Rico. This study evaluates the positive predictive value for the CIS active surveillance program.
Methods: Positive predictive value is defined as the proportion of test positive animals that were truly diseased and is a measure that is highly affected by the disease prevalence. Predictive values were calculated using a deterministic Bayesian approach with known validation data and a range of prevalence estimates.
Results: The positive predictive value equal to 50.5% was calculated at a prevalence of 0.1%. One log difference in the prevalence from 0.1% to 0.01% decreases the positive predictive value proportion from 50.5% to 9.2%. At this point, greater than 90% of the positive test results were false positives. For infected animals that appear clinically normal, the 50% positive predictive value was found to be between 0.1% and 1% prevalence. To detect one case in a population of 50,000 hogs, 45,849 hogs would have to be sampled; of the positive results from this sample, one would be a true positive and 41 would be false positives.
Conclusions: Positive predictive values must be considered as a part of resource management. If having a positive test results in a resource intensive response, the cost of the program must be considered. For potential cases of a foreign animal disease in the United States and its territories, costs could include confirmatory testing, additional sampling, chartered flights to rapidly move samples to national reference laboratories, and approval of resources to complete testing, including the use of overtime compensation. Potentially, all of this could be done in response to a false positive test result.
Relevance: If the surveillance results in a larger market share, then the surveillance system may be justified. Yet, the depletion of resources to manage the false positives associated with low predictive values must be considered when establishing such a program.

P194

Bio-economic analysis of foot-and-mouth disease transmission between wildlife and livestock populations in Limpopo Province, South Africa.

Ndiadivha Sikhweni, Tshwane University of Technology, Pretoria, South Africa. Contact: ndiadivha@yahoo.com

Livestock plays a crucial role in sustaining the livelihood of people living in rural areas. Nevertheless, the inability of small-scale farmers to extract maximum profits from their livestock assets, especially when dealing with outbreaks of animal diseases such as foot-and-mouth disease (FMD) hamper their ability to extract maximum benefits.

The study utilized a bio-economic model to assess the trade-offs between wildlife conservation and the livelihood objectives of the small-scale farmers faced with FMD transmission (negative externality) from buffalo to cattle populations in Limpopo Province, South Africa. The model was solved theoretically under three scenarios; (1) a conservation scenario with no unified resource management policy, (2) a social planner scenario and (3) a no-disease scenario.

Results of the sensitivity analyses of the bio-economic model indicate that overall, higher benefits are achieved when intervention measures contributing to a reduction in the proportion of buffalo that escape from the park and a reduction in cattle-to-cattle transmission are introduced simultaneously (9% increase). However, comparing the two measures, investing more in preventing infection among cattle populations through quarantine and vaccination programmes would yield higher benefits to the farmers (5% increase) compared to decreasing FMD transmission from buffalo to cattle populations through culling of buffalos and/or increased investment in maintenance of the fence (1% increase).

Improved management of cattle-to-cattle transmission can improve the livelihood of small-scale farmers while preserving the wildlife heritage in Limpopo Province. Management solutions and policy measures for balancing the trade-off between environmental and economic benefits of keeping wildlife and the livelihood objectives of small-scale farmers living adjacent to conservation areas can be evaluated though the use of bio-economic models. Such approaches should be implemented more widely to inform policy interventions.

P195

A quantitative risk assessment for the risk of human exposure to ESBL-producing *E. coli* via the milk chain

Alex Berriman, Luke Randall, Emma Snary, **Robin Simons**, Animal and Plant Health Agency, Addlestone, United Kingdom. Contact: robin.simons@apha.gsi.gov.uk

Antibiotic resistant strains of bacteria are a concern, rendering an increasing number of current treatments for both humans and animals ineffective. *E. coli* is recognised as a commensal bacterium in the UK cattle population, but some strains can also be associated with disease such as enteritis. Extended spectrum *β*-lactamase-producing (ESBL) *E. coli* are resistant to 3rd and 4th generation cephalosporins and have been isolated from dairy cattle. Thus, the milk chain is one potential route of human exposure, in particular the consumption of raw milk products, which do not have the safeguard of a pasteurisation step. In this study we developed a quantitative stochastic farm-to-consumption exposure assessment to estimate the levels of both ESBL *E. coli* and antibiotic residues in four dairy products (raw milk, pasteurised milk, and hard and soft cheese made from raw milk) and hence the resultant level of human exposure. Antibiotic residues in milk are in practice subject to stringent controls; the model is used to explore their influence were such controls not in place.

The model consisted of two main sections; on-farm and post-farm. The on-farm module simulated transmission within the dairy herd and the corresponding levels of ESBL *E. coli* and antibiotic residues in the bulk tank. The post-farm module focused on the processes after the milk leaves the bulk tank; simulating the growth and/or decay of ESBL *E. coli* in dairy products during each stage of the process.

The model results suggested soft cheese presented the highest risk for human exposure to ESBL *E. coli*, due to short maturation times. A sensitivity analysis suggested that ineffective bulk tank cleaning and national delivery of raw milk products, in the absence of a suitable cold chain, could substantially increase the risk of human exposure to ESBL *E. coli*.

This risk assessment provides a quantitative estimate of the level of ESBL *E. coli* at human exposure, but it does not provide further insight into the consequences of this. While the introduction of resistant commensal *E. coli* to the human gut is unlikely to be a direct threat to human health, they could pass resistance on to other bacteria, which could potentially have public health relevance.

P196

Assessment of the probability of introduction of bovine tuberculosis to Danish cattle farms

Alessandro Foddai[1], Liza Rosenbaum Nielsen[2], Kaspar Krogh[3], Lis Alban[1], [1]Danish Agriculture & Food Council, Copenhagen, Denmark; [2]University of Copenhagen, Copenhagen, Denmark; [3]Knowledge Centre for Agriculture, Aarhus, Denmark. Contact: afo@lf.dk

Denmark is recognized as officially free (OTF) from bovine tuberculosis (bTB) and keeping this status is a priority.
The objective was to estimate the annual probability (PIntro) of introducing *Mycobacterium bovis* into the Danish cattle population through (a) imports of cattle or (b) foreign personnel coming from countries with high incidence of tuberculosis in humans and working in Danish cattle herds. Potential risk mitigation measures were also assessed.
Data from 2000-2013 with date, number and origin of imported cattle were obtained from the Danish Cattle Federation. Information on immigrant workers in Danish cattle herds was obtained through a questionnaire sent by email to 460 Danish cattle farmers. Inputs obtained by data analysis, the questionnaire and literature were fed into three stochastic scenario tree models, which were used to simulate the effect of import trade patterns, and contact between immigrant workers and cattle. Moreover, we investigated the opportunity of testing imported animals as an industry-driven initiative.
Results showed that the risk depends mainly by the importation of cattle. Immigrant workers represented only 0.2% of the annual risk. The combined median annual probability of introducing *M. bovis* into the Danish cattle population by either imported cattle or infectious immigrant workers, ranged from 0.3% in 2001 to 4.9% in 2009. The median of the median PIntro estimates from the 14 years was 0.7%. Hence, on average, approximately one introduction each 100 years could be expected, if the annual number and origin of imported animals do not change remarkably in the future.
If the number of imported animals increases, additional testing of imported cattle might be considered. For instance, in 2009, PIntro would have been reduced to 0.8% if animals from OTF countries had been tested by tuberculin skin test and animals from non-OTF countries had been tested using the interferon-γ test.
Testing immigrant workers did not seem to be necessary, although there was some uncertainty on the number of immigrant workers.
Our model could be used easily in other countries with similar bTB status as Denmark, where imported cattle represent the main pathway of bTB introduction.

P197

Quantitative microbiology risk assessment: assessing the effects of contagious distributions of Salmonella cells in dry sausage on the risk of salmonellosis.

Luis G. Corbellini[1], Ana Sofia Ribeiro Duarte[2], Luis E. da Silva[3], Eduardo F. Costa[1], Marisa Cardoso[1], Maarten J. Nauta[2], [1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil; [2]National Food Institute, Søborg, Denmark; [3]Ministério da Agricultura, Rio de Janeiro, Brazil. Contact: luis.corbellini@ufrgs.br

Purpose: Dry-fermented sausages (salami) are a ready to eat product that contains 60 to 80% of pork meat. Transmission of the pathogens through the manufacture process is complex; contagious distribution of Salmonella cells can occur due to incomplete mixing of contaminated chopped pork. The objective of this study was to assess the impact of the clustering of Salmonella cells on the risk of salmonellosis in southern Brazil.
Methods: A description of food pathway from prechill carcasses up to the finished product was made, followed by the definition of the Modular Process Risk Model (MPRM) structure, which covers processing steps and describe the changes in both the number of pathogen and the prevalence per unit of product. The processes used were: i) partitioning (cutting room); ii) mixing (grinding meat and mixing ingredients); iii) survival (Bigelow model, maturation process); and iv) partitioning (stuffing). The units used were: i) carcass (16,500 cm^2) and shoulder surface area (2,300 cm^2); ii) weight of shoulder (5 Kg) and mixed meat batch/day (1,000 Kg); iv) unit of salami (0.25 Kg); and v) servings (20g). The distribution of Salmonella concentration in pork carcasses was estimated using a Complete Likelihood Method [Normal(-1.89, 1) log CFU/mL] and the prevalence of contaminated carcasses between days of slaughter was given by a Beta(0.41,1.05) distribution. A betabinomial distribution was applied to test different scenarios of Salmonella cells distribution in units of salamis from 'perfect' homogeneity to heterogeneous (contagious) varying the 'clustering' parameter (b>0) of the distribution. The concentration of Salmonella in a given portion of contaminated salami was estimated and used in the exposure assessment.
Results: A more homogeneous distribution of cells in the mixed meat resulted in a higher prevalence before the maturation, while the opposite was observed after maturation (i.e. higher prevalence when more heterogeneous), subsequently resulting in higher number of cases.
Conclusion: This fact demonstrates the importance of including the uncertainty about the heterogeneity in the distribution of pathogens in future risk assessment.

P198

Assessing the emergence of porcine diseases associated with biosecurity practices in Canada using a Bayesian Belief Network

Ruth Cox, Crawford Revie, Javier Sanchez, University of Prince Edward Island, Charlottetown, PE, Canada. Contact: rucox@upei.ca

Purpose

Quantification of pathogen threats is a priority for the Canadian swine industry so that resources to prevent the introduction and spread of disease can be focused where they will have the most impact. Based on information collected from commercial swine farms across Canada, we created a model to explore the effectiveness of various biosecurity practices in preventing the emergence of four diseases on Canadian swine farms: Porcine Reproductive and Respiratory Syndrome (PRRS), (a highly prevalent endemic aerosol pathogen), Swine influenza (a potential zoonosis), *Mycoplasma pneumonia* (an endemic respiratory disease spread by close contact) and Swine dysentery (an enteric disease which is re-emerging in Canada).

Method

We used data about the biosecurity practices on 218 farms, as well as data regarding the health status and disease outbreaks on more than 90 of those farms to build a naïve Bayesian Belief Network (BBN). The BBN models the interaction between biosecurity practices and the relative risk of disease. We used expert opinion to select 15 biosecurity practices that might be considered the most important in preventing disease emergence on a farm. These included: proximity to other livestock holdings, the health status of purchased stock, waste disposal methods, as well as the procedures for admitting vehicles and staff.

Results and Conclusion

Sensitivity testing showed how the relative risk of disease varied according to various combinations of these practices. For example, outbreaks of Swine influenza or Swine dysentery were associated with an increased proximity of other livestock holdings. The probability of Swine dysentery decreased when the health status of purchased stock was known, while the probability of other diseases did not change considerably with variation in this biosecurity practice.

Relevance

The particular advantage of this novel approach is that it allows the user to explore the complex interaction of the various risk factors on the probability of disease outbreak.

P199

Integrated tick management to mitigate the impact of Rhipicephalus microplus, bovine anaplasmosis, and bovine babesiosis in livestock farming systems of Puerto Rico

Jose H. Urdaz-Rodriguez[1], Robert J. Miller[2], Pete D. Teel[3], Ivan Castro-Arellano[4], Felix D. Guerrero[5], Mathew T. Messenger[6], Fred V. Soltero[1], Carmen Oliver-Canabal[7], Myrna Comas-Pagan[7], Adalberto Perez de Leon[5], [1]United States Department of Agriculture - Animal and Plant Health Inspection Service, Hato Rey, PR, [2]United States Department of Agriculture - Agricultural Research Service, Edinburg, TX, [3]Texas A&M University, College Station, TX, [4]Texas State University, San Marcos, TX, [5]United States Department of Agriculture - Agricultural Research Service, Kerrville, TX, [6]United States Department of Agriculture - Animal and Plant Health Inspection Service, Riverdale, MD, [7]Puerto Rico Department of Agriculture, San Juan, PR, Contact: jose.h.urdaz@aphis.usda.gov

Ticks and tick-borne diseases (T&TBD) are detrimental to livestock farming systems in several world regions, including the Caribbean. The southern cattle fever tick (SCFT), *Rhipicephalus (Boophilus) microplus*, is considered the most economically impactful livestock ectoparasite worldwide, and it is a known vector of the infectious agents that cause bovine anaplasmosis (BA) and bovine babesiosis (BB). This T&TBD complex impedes the full productivity potential of livestock farming systems in the island of Puerto Rico (PR). Studies conducted in PR between 2005 and 2006 determined risk factors and the prevalence of SCFT (16%), BA (27%), and BB (26%). This information established the critical need for improved SCFT control while addressing endemic instability of BA and BB. A partnership involving the local livestock industry, PR Department of Agriculture, Texas A&M University, Texas State University, and the USDA was established in 2014 to conduct foundational research for an integrated SCFT control program in PR.

These aspects of the research project will be addressed during the presentation: 1) re-assessment of current epidemiological status of SCFT, BA, and BB using more specific and sensitive laboratory diagnostic tests, 2) evaluation of small Asian mongoose, *Herpestes javanicus,* as a potential reservoir of SCFT in livestock farms, 3) development of spatially explicit, individual-/agent-based, stochastic model to simulate spatial-temporal SCFT dynamics and economic effects in response to changes in climatic conditions, landscape structure, host community composition, and current management systems practices, 4) development of T&TBD module as part of computerized dairy herd management system to enhance cow health, and milk production. Project Phase 1 results will be presented. An update on Phase 2 efforts to implement integrated treatment protocols involving the use of technologies such as an anti-tick vaccine, essential-oil based product, endectocide, tick growth regulator, and biocontrol agent will be discussed.

P200

Assessing engagement of sentinel farmers in syndromic surveillance reporting

Caitlin N. Pfeiffer[1], Angus J. D. Campbell[1], **Simon M. Firestone**[2], Mark A. Stevenson[2], John W. A. Larsen[1], [1]The University of Melbourne, Werribee, Australia; [2]The University of Melbourne, Parkville, Australia. Contact: simon.firestone@unimelb.edu.au

Purpose: Surveillance for livestock disease is important for regulatory purposes, market assurance, animal welfare and detection of emerging disease syndromes. However, surveillance data collection from extensive sheep and beef enterprises in Australia is limited, due to minimal regular veterinary contact and high tolerance for common disease events that do not trigger veterinary involvement. Farm workers frequently observe animal health issues, but these observations are not presently captured by existing surveillance systems.

Methods: This project engages sentinel farmers in providing regular syndromic reports of the disease events they observe on-farm, with a 6 month pilot completed in March 2015. Assessment of participant engagement is a crucial component of such a system, to understand motivators and barriers to reporting. By evaluating participation and compliance, the system can be modified to maintain or improve data quality and completeness.

Results: Periodic surveillance system evaluation is often limited to assessment of data and compliance rather than deeper investigation of the behaviours and motivators of participants. During the pilot phase, data reporting the incidence of 10 syndromes were requested from 35 farms monthly for 6 months. Monthly response rates ranged between 83% to 97% and complete records were provided by 19 farms. Sheep-only, cattle-only and mixed farms (sheep and cattle) were included, with farms located in six distinct geographic regions of Victoria in southern Australia (3 to 8 farms per group). Further engagement data will be presented and the role of these data in the development of focus group discussions to detect barriers to compliance will be described.

Conclusions: Through a better understanding of their motivation to initiate and maintain participation in data exchange for surveillance purposes, farmers' valuable daily observations can form an important part of broader surveillance strategy.

R**elevance:**

Engagement of farmers from extensive production systems in traditional surveillance reporting can prove challenging, especially when good-will between producers and government is strained.

P201

The integrated management system for the Salmonella control programs in Italy

Patrizia Colangeli[1], Elio Malizia[1], Simona Iannetti[1], Anna Sorgente[2], [1]Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise- Teramo, Teramo, Italy; [2]Ministry of Health, Rome, Italy. Contact: p.colangeli@izs.it

Purpose:
Salmonella infections are the main cause of food-borne outbreaks in Italy as well as in other industrialized countries: food of poultry origin is the main source of infection. The EU legislation (White Paper, Commission Regulation (EC) No. 178/2002) identifies in the control of the food chain the more effective approach to ensure food safety, indicating in the primary production a pivotal point for control of Salmonella infections. In 2003, the EU set for Member States the objective of reducing the prevalence of Salmonella on the basis of specific control programs approved by the Commission (Commission Regulation (EC) No. 2160/2003): eradication programs, control and monitoring of salmonellosis (serotypes relevant to public health) in breeding flocks of Gallus gallus, laying hens, broilers, turkeys were approved. With the subsequent Regulation (EC) No. 1003/2005, the requirement for farmers to implement an industry sampling program was also introduced, thus contributing to the achievement of the Community objective of reducing the prevalence of infection.

Methods:
An information system, named SISalm, was implemented in Italy to collect and manage information and data derived from the application of the national Salmonella Control programs, to standardize data collection and information flows, thus avoiding redundancy and errors.

Results:
SISalm, collects detailed data both on official and on industry sampling. SISalm is also integrated with other information systems, such as the National register for animals and holdings (BDN) and the Italian Information System for the notification of outbreaks of animal diseases (SIMAN) for the automatic notification of the suspected outbreak.

Conclusions:
This integration allows a comprehensive reporting with the fulfilment of the information debts towards the European Commission, the EFSA and the OIE. The data collected also allows the programming of activities, their periodic verification and risk analysis.

Relevance:
Data entered in SISalm is aggregated and reported to the EFSA, according to EFSA's technical specifications, for the evaluation of the reduction target by the Commission.

P202

SurVet: An open-source, web-based tool for designing and analysing complex epidemiological questionnaire surveys

Peter A. Durr[1], Kerryne Graham[1], Wiryadi Sastraningrat[2], [1]AAHL-CSIRO, Geelong, Australia; [2]UrRemote, Denpasar, Indonesia. Contact: peter.durr@csiro.au

Purpose:
Although there exist a large number of survey design software applications, currently there is none which is suitable for complex epidemiological questionnaires. Here we describe development of a web-based application ("*SurVet*") filling this need.
Methods:
SurVet began development in 2011, for a complex survey of poultry farms in west Java, Indonesia. Since them *SurVet* has been used, *inter alia*, for a large One Health sero-survey in Laos, and for the design of farm-level validation of an avian influenza DIVA test.
We are currently rebuilding *SurVet* (version 3) to incorporate many of "Web 2.0" features - particularly those which enable a "rich user experience", comparable in their interactivity to a desktop application. *SurVet 3.0* is also built with open-source development tools: the *Ruby-on-Rails* framework, the *Postgres* database system and the *D3* charting JavaScript library. It is intended that *SurVet* will be released to the community via the *GitHub* repository and thus be freely available to install.
Results:
SurVet consists of 4 modules. Module 1 allows users to design questions varying from simple, open ones to extremely complex one involving multiple sub-questions with different data types. The 2nd module allows users to translate and format the questionnaire for printing and the 3rd module allows data entry. The 4th module provides for visual summaries of the data, and the capability to export the data for further analysis. Guidance and tutorials in the use of *SurVet* is available through an accompanying *MediaWiki* application.
Conclusions:
SurVet fulfils a need when epidemiologists (and other field scientists) need to undertake complex questionnaire type surveys, those for which existing tools like *EpiCollect* and *Epi Info* are not suitable.
Relevance:
SurVet 3.0 represents the maturing of the *SurVet* "project", and will provide an advanced design and analysis tool for the veterinary epidemiology community needing to undertake the design and analysis of complex questionnaire surveys.

P203

Assessment the cut-off in function of population size to declare a herd as infected by bovine brucellosis.

Andres Gil[1], José Piaggio[1,2], Bruno Lanfranco[3], Alicia von Gehlen[1], Federico Fernandez[4], [1]Universidad de la Republica, Montevideo, Uruguay; [2]Ministerio de Ganadería Agricultura y Pesca, Montevideo, Uruguay; [3]Instituto Nacional de Investigación Agropecuaria, Montevideo, Uruguay; [4]Ministerio de Ganaderia Agricultura y Pesca, Montevideo, Uruguay. Contact: adgr@adinet.com.uy

Bovine brucellosis program in Uruguay is based on the principle of test and remove. Approximately the number of susceptible cattle to brucellosis is 6 million and perform serology for surveillance 1.5 million a year. By law all farm with a serum positive cattle is declared infected and goes into quarantine at least for 1 year with the consequent economic damage for the farmer. Prevalence estimated in cattle is 0.2% and in farms 0.8%. Several farms with large populations were quarantined with a single seropositive animal without any other evidence of disease. This situation questioned if it is sufficient a serum positive to declare an infected farm. The objective is to determine what would be the cut-off (number of seropositive animals) which is considered enough evidence to declare a farm as infected.
We stratified the farms population according to the susceptible population to analyze potential scenarios. Herd specificity (HSp) was estimated for each scenario and different cut-off with the binomial distribution for an individual specificity of 0.999 to compare the HSp values. Herd sensitivity was also calculate for the same scenarios using the hypergeometric distribution with an individual sensitivity of 0.95 and an intra-herd prevalence that ranged from 6% to 1%. A cut-off of 1 will ensure the maximum HSe, but the HSp goes down with the population sizes increase, with the consequent high proportion of false positives. In the Uruguayans' conditions, we recommended a cut-off of 1 in farms of up to 300 susceptible cattle (94-95% HSe and 82-95% HSp); a cut-off of 2 for farms between 301 and 500 (HSe > 99% and 90-99% HSp), and a cut-off of 4 in farms with more than 500 susceptible animals (96-100% HSe and HSp>99.8%). We should not ignore farms with any serological evidence of brucellosis, they must be investigated to confirm or rule out the presence of infection. In conclusion, in farms with large populations a single serum positive is not enough to confirm it as infected without any other evidence of infection. Legislation and eradication strategy should update with this information.

P204

The contribution of epidemiological studies to assess the efficacy of bovine brucellosis control policies in Minas Gerais, Brazil.

Vitor S. P. Gonçalves[1], Luciana F. Oliveira[2], Andrey P. Lage[2], Ana Lourdes A. A. Mota[1], José S. Ferreira Neto[3], Fernando Ferreira[3], Ricardo Dias[3], José Henrique H. Grisi Filho[3], Marcos Amaku[3], Evelise O. Telles[3], [1]Universidade de Brasília, Brasília, Brazil; [2]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil; [3]Universidade de São Paulo, São Paulo, Brazil. Contact: vitorspg@unb.br

Bovine brucellosis is a widespread zoonosis that also entails significant losses to the value of livestock production. The state of Minas Gerais holds a bovine population of just under 21 million animals, kept in approximately 340,000 herds, is one of the most important beef production states and is first in the national rank of dairy production. In the early eighties, the state veterinary administration (SVA) carried out a sample survey that estimated the herd prevalence at 20.5% and animal level prevalence at 6.6%. This epidemiological situation led the SVA to implement the compulsory vaccination of heifers. The federal legislation followed suit and, in 2001, a new national programme was launched that also comprised accreditation of free herds. As part of this new effort, it was conducted a new sample survey in 2002 that made it possible to assess the progress of the on-going policy. Twenty years later, the herd prevalence was 6.04% (95% CI: 4.98 - 7.1) and animal prevalence went down to 1.09% (95% CI: 0.78 - 1.41), no doubt a clear sign that the vaccination policy had been effective. The present study was the latest of a series of major surveys, conducted in 2012, with the aim of assessing the evolution of the programme, ten years after the inception of the new federal regulations. Overall, 2,185 herds were random sampled and 18,990 adult cows were serologically tested. The apparent seroprevalence went down again: 3.60% (95% CI: 2.76 - 4.42) for herds and 0.80% (95% CI: 0.51 - 1.1) for animals. At the time of testing it was applied a questionnaire. The herd-level multivariable logistic model revealed that the odds of being positive increased markedly with the number of females in the herd and was significantly different amongst regions. It can be concluded that the vaccination strategy seems have worked out over the last two decades, but the efficacy is variable throughout the state. More intensive surveillance strategies are necessary to ensure continuous progress, a more challenging task at lower prevalence levels. Those should be targeted at geographical areas and production systems that proved to be at higher risk.

P205

Insight into epidemiology of swine dysentery by using analysis of treatment records and simulation modelling

Krysia Walczak[1], **Zvonimir Poljak**[1], Robert Friendship[1], Amy Greer[1], Alfons Weersink[2], [1]University of Guelph, Guelph, ON, Canada; [2]University of Guelph, Guelph, ON, Canada. Contact: zpoljak@uoguelph.ca

Purpose:
Swine dysentery (SD) is characterized by mucohemorhagic diarrhea in finisher pigs. Once thought to be controlled by good husbandry practices, the disease has started to re-emerge in some swine populations. Because of the potentially severe nature of the disease, its detection is accompanied by rapid implementation of control strategies which ultimately have impact on circulation of the pathogen. This is one of the reasons why observational studies of SD at the individual level are rare. In this study we used treatment records from a herd with SD. The objectives were to; estimate parameters of importance for circulation of SD in a finisher herd, apply modelling to understand disease patterns, and evaluate efficacy of different control strategies using a simulation approach.
Methods:
The study herd was a 3-barn finisher site with ~1500 animals per barn. Herd records from 19 cohorts on treatment with injectible tiamulin and lincomycin were used as indication of morbidity due to SD, and to extract parameters important for disease transmission. Then, a stochastic difference equation SIRS model was constructed.
Results:
Analysis of treatment records indicated that winter was the season with the highest rate of i/m lincomycin usage ($p<0.01$). The stochastic model consistently reproduced the rate of i/m application of lincomycin. Nonetheless, the treatment rates could only be reproduced by the model if a considerable proportion of animals was assumed to be subclinical. With an assumption that 25% of infected animals become clinical and with no effective intervention, the model predicted mortality that was close to historical reports. Intramuscular application of effective antimicrobials dramatically reduced mortality and we are currently investigating efficacy and cost-effectiveness under simulation conditions.
Conclusions:
Model results suggest that buildup of clinical cases in the grower-finisher stage is due to high frequency of infectious animals in this stage of production.
Relevance: The study indicates how syndromic data and simulation modelling could be used to understand circulation of disease under field conditions.

P206

Is participation in the Alberta Johne's Disease Initiative associated with Mycobacterium avium subspecies paratuberculosis herd-level prevalence or herd size?

Caroline Ritter[1], Robert Wolf[1], Charlotte Pickel[1], Mike Slomp[2], Jodi Flaig[2], Steve Mason[1], Cindy L. Adams[1], David F. Kelton[3], Joalnda Jansen[4], Karin Orsel[1], Jeroen De Buck[1], Herman W. Barkema[1], [1]University of Calgary, Calgary, AB, Canada; [2]Alberta Milk, Edmonton, AB, Canada; [3]University of Guelph, Guelph, ON, Canada; [4]St. Anna Advies, Nijmegen, Netherlands. Contact: cmnritte@ucalgary.ca

Introduction/Purpose: The voluntary Alberta Johne's Disease Initiative (AJDI) aims to reduce transmission of Mycobacterium avium subsp. paratuberculosis (MAP) on and between farms through farm-specific risk assessments and management plans. Approximately 60% of Alberta dairy farmers participated in the program in 2012. The objective of this study was to assess whether MAP prevalence or herd size is associated with AJDI participation.
Methods: On 271 AJDI participating farms as well as on 65 farms not enrolled in the AJDI environmental samples were collected. Six samples of each farm, collected from 3 different locations, were taken from September 2012 until July 2013 and analysed for MAP. Samples were processed using a standardized 3-day decontamination protocol that was followed by 48 days of culture using a TREK ESP culture protocol. All culture products were then analysed with conventional IS900 PCR. Information on herd size was collected at a farm visit using a standardized questionnaire.
Results: The apparent MAP herd-level prevalence on AJDI participating Alberta dairy farms was 54% (95% CI: 47-60%), whereas the apparent MAP herd-level prevalence for non-participating farms was 51% (95% CI: 40-61%) and hence not significantly different ($p=0.34$). The median number of lactating cows on participating farms and non-participating farms was 102 and 90, respectively ($p<0.01$).
Conclusion/Relevance: Participation in the AJDI is associated with herd size but not with MAP herd-level prevalence. However, it cannot be excluded that management changes elicited by the AJDI have already had some impact on the MAP prevalence. Results of this study provide an important basis to monitor changes in MAP prevalence on Alberta dairy farms.

P207

Design of surveillance plans for Rift Valley fever in southern Africa

Hendrik Camphor, **Peter Thompson**, University of Pretoria, Pretoria, South Africa. Contact: peter.thompson@up.ac.za

Purpose:
Rift Valley fever (RVF) is a mosquito-borne transboundary livestock disease characterized by irregular epidemics occurring under favourable environmental conditions. A prominent feature of RVF is the occurrence of large abortion storms and neonatal mortality in ruminants, with human illness in high risk groups in contact with affected livestock. RVF virus has in recent decades spread beyond its historical distribution in southern and East Africa to trigger epidemics in livestock and humans further afield and is now considered a major veterinary public health, food security and bioterrorism threat.
The epidemiology of RVF is complex, shaped by macro-scale climatic events and location-specific environmental, vector and vertebrate host variables. RVF ecology varies greatly between regions within southern Africa, complicating the timely identification of viral activity and delaying the implementation of risk mitigation measures. In southern Africa there is a lack of detailed knowledge of the epidemiology of RVF and a lack of well-designed surveillance plans, tailored to regions. This constrains the development of locally relevant risk models which may inform the implementation of timely, cost-effective risk mitigation measures in the region.
Methods:
Results:
This paper describes the development of active, hazard-specific surveillance plans for RVF focused on the risk-based sampling of sentinel livestock and vectors at sentinel sites in two ecological zones: the tropical coastal plain of central Mozambique where RVF is endemic and the arid central interior plateau of South Africa where occasional large RVF epidemics occur. The surveillance is designed to detect viral activity and facilitate collection of data to elucidate local virus ecology in different ecological zones with different patterns of virus circulation and inter-epidemic maintenance.
Conclusions:
Relevance:
The proposed plans could facilitate the development of an integrated surveillance system to support the timely, cost-effective implementation of risk mitigation measures, and to contribute to the development of predictive risk models for each ecological zone.

P208

IGOR-P: A framework to facilitate the use of available data sources to improve pig health and welfare surveillance in Great Britain

Sue C. Tongue[1], Carla Correia-Gomes[1], Madeleine K. Henry[1], Jude I. Eze[1], Susanna Williamson[2], R. P. Smith[3], [1]SRUC, Inverness, United Kingdom; [2]APHA Bury, Bury St Edmunds, United Kingdom; [3]APHA Weybridge, Addlestone, United Kingdom. Contact: sue.tongue@sruc.ac.uk

Monitoring health and welfare can benefit the pig industry by measuring the effectiveness of control and improvement initiatives, assessing change over time and helping to recognise emerging issues or threats. In England, substantial amounts of pig health and welfare data are collected by a large number of government agencies and industry bodies. The challenge is to optimise the use of available data sources to augment existing surveillance systems; especially when data capture, for these sources, has not been designed with such use in mind.

Our objective was to develop a conceptual framework to facilitate the integration of such data sources. The requirements were to: include an inventory and summarised evaluations of each data source; identify existing and potential analytical linkages both generically and within the specific context; be dynamic and adaptable over time, and have potential to include additional information (e.g. outputs and progress reports) at a later date.

A multi-dimensional integrated framework (IGOR-P) was developed. Thirteen data sources were evaluated using the SERVAL standardised evaluation process for animal health surveillance systems (http://www.rvc.ac.uk/VEPH/SERVAL.cfm). Existing baseline estimates were noted and the suitability of different methods of statistical analysis for utilising multiple data sources was assessed on a subset of data. Where estimates did not exist, ways of deriving them (or appropriate proxies) from the data sources were identified.

We concluded IGOR-P could be implemented with sufficient will from the industry and data owners. Its development identified how limitations, imposed by a range of data issues, might be addressed and what core data are required for a data source to be useful for monitoring purposes.

IGOR-P has provided background information for a number of surveillance initiatives; been adapted for the Scottish pig industry; modified to inform monitoring of the implementation of slaughterhouse legislation, plus there is scope for extension to other species and contexts. IGOR-P turns data into information and information into knowledge, providing intelligence for health and welfare surveillance purposes.

P209

Contingency planning for disease outbreaks at the science-policy interface

Lisa Boden[1], Harriet Auty[2], George Gunn[2], Nia Ball[3], Jared Stewart[3], Colin Macaldowie[3], Dominic J. Mellor[1], [1]University of Glasgow, Glasgow, United Kingdom; [2]SRUC Epidemiology Research Unit, Inverness, United Kingdom; [3]Animal, Health and Welfare Division, Scottish Government, Edinburgh, United Kingdom. Contact: lisa.boden@glasgow.ac.uk

Purpose: An explicit role for knowledge brokers is recognised and included within the EPIC consortium, the Scottish Government's Centre for Expertise on Animal Disease Outbreaks. This virtual centre brings together scientific experts to provide Government policymakers with access to high-quality, multidisciplinary advice and analyses to best prepare Scotland for any major animal disease incursion. Knowledge brokers coordinate and communicate information exchange and translation across the science-policy interface in an efficient and streamlined way.

Methods: EPIC has participated in Scottish and GB-level disease exercises (on FMD, avian influenza and classical swine fever), as well as in a bespoke disease exercise designed to test relationships between EPIC, Scottish Government (SG), and its partners and stakeholders.

Results: Disease exercises have tested the resilience and coordination of EPIC's outbreak response structures and highlighted opportunities and challenges involved in the demand and supply of scientific evidence during an outbreak. Exercises have highlighted areas where EPIC capacity can be made available to provide appropriate and up-to-date disease simulation models, rapid risk assessments, economic analyses, post-outbreak surveillance strategies and analysis of sequence data to provide SG with useful and timely evidence to inform decisions being taken within short timescales. The benefits of this preparedness were borne out in the most recent avian influenza outbreak in GB in 2014.

Conclusion: Efficient communication and timely responses to SG requests during disease outbreaks are possible because of the development of trusted relationships between EPIC and SG. In large part, this has been achieved through the routine presence and work of EPIC knowledge brokers in Scottish Government offices and at national stakeholder meetings during 'peace time'.
Relevance: Knowledge brokering activities have promoted greater inclusiveness and proximity of EPIC scientists to policy makers and have made it possible to respond quickly with a relevant scientific evidence base to inform specific policy questions that arise at different stages of an outbreak.

P210

New protocols of communication between Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) and the public services using mobile solutions.

Grazia Manca[1], Michele Brichese[2], Stefano Marangon[1], [1]Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro - PD, Italy; [2]Regione Veneto - Veterinary Department, Venezia, Italy. Contact: gmanca@izsvenezie.it

Purpose: In accordance with broad guidelines drawn up at Community level, Member States should establish national control plans, on the basis of shared and documented procedures involving both official authorities and laboratories. Data gathering standardisation and documents dematerialization play a key role to establish coherent and fast protocols of communication, to set traceability systems and epidemiological networks, required by legislation in force. For the management of public health and food hygiene controls in Northern Italy, an Information System has been developing, involving both veterinarian and nutritionist components of Local Public Health Units (LPHUs). From 2014 a new project has been launched for the integrated management of official controls. The aim of this paper is to highlight the innovative solutions adopted, like mobile assets and electronic signature *in field* for document dematerialization.
Methods: The entire architectural infrastructure of the procedure is based on Internet technologies (HTTP, SOAP, XML, Web Services) with a strong logic of integration (common master data). The internet application is implemented in Delphi 2010 (object-oriented language). The Web Server used is Apache 2.2 (Apache © Software Foundation), which manages client requests and the execution of webservices. E-signature has been introduced, and the possible use of graphometric system has been evaluated.
Results: The project allows two different ways for data registration: a “traditional working station” (TWS, through desktop) and a “mobile working station” (MWS, through tablet), to ensure maximum flexibility. The web e-signature of the accompanying form of samples collected has been developed.
Conclusions/Relevance: the project optimizes the way of communication, using modern solution applicable to the field. The dematerialization allows reducing costs and enhances official data availability. The Graphometric signature could allow people (e.g. farmers) not equipped for the smart card to sign electronic documents.

P211

A systematic review of genetically modified feed effects in production animals and a value chain analysis for future surveillance opportunities within the European Union .

Louise C. Vince[1], Kaloyan Kostov[2], Ralf Einspanier[3], Paul Biker[4], Dirk Pfeiffer[1], Javier Guitian[1], [1]The Royal Veterinary College,, London, United Kingdom; [2]AgroBioInstitute, Sofia,, Bulgaria; [3]Freie Universität, Berlin, Germany; [4]Wageningen UR, Wageningen,, Netherlands. Contact: lvince@rvc.ac.uk

Purpose: To inform future policy on Animal Health Surveillance in the context of genetically modified feed. To contribute to the development of new methods for the monitoring of animal health syndromes potentially affected by genetically modified (GM) feed.
Methods:A systematic literature review to evaluate feeding studies on production animal populations. Inclusion criteria was through a key word search including all strains of GM feed, variants and production animals. Inclusion in the database was based on a 3 stage selection criteria. An In-depth Value Chain Analysis, including both feed chain analysis and livestock monitoring was performed. All sources of data containing feed chain information, animal tracking and animal health monitoring were compiled and evaluated for possible analysis.
Results:47 studies were included in a database and data extracted for future analysis. There was no consistent evidence for adverse effects associated with genetically modified feed. http://ipafeed.eu Livestock chain analysis showed great variability across European countries, production types and population groups. There is no current legislation to ensure labelling of strain type or percentage concentration in of GM varieties within animal feed, as such monitoring of GM feed at an epidemiological level is not possible at present.
Conclusions: Absence of evidence is not sufficient to conclude all genetically modified feedstuffs are safe. Monitoring to ensure detection occurs is recommended. Current feed and animal health monitoring systems are insufficient to be able to attribute potential adverse effects to genetically modified feed. The capacity of current systems can be strengthened to incorporate genetically modified feed monitoring parameters both through improved understanding of current surveillance systems and feed labelling.
Relevance:GM feed consumption in livestock has increased exponentially over the last 20 years. Due to market pressures this trend is likely to continue. Future monitoring of animal health effects will prove a challenge and understanding of new methodologies for monitoring the effects of emerging technologies at a population level is ongoing.

P212

Using spatial tools for high impact zoonotic agents' surveillance design in backyard production systems from central Chile.

Raúl A. Alegría-Morán, Nicolas Bravo, Francisca Di Pillo, Andres Lazo, Santiago Urcelay, Christopher Hamilton-West, University of Chile, Santiago, Chile. Contact: ralegria@veterinaria.uchile.cl

Purpose:
Specific location of backyard production systems (BPS) in Chile remains unclear; becoming a risk and a difficulty to design a surveillance system for early detection of high impact zoonotic agents like avian influenza and Salmonella spp. This study aims to prove the use of a spatial tools into the surveillance design such as ArcGis 10®, Google Earth® and Google Maps® in backyard production systems from central Chile.

Methods:
Considering a stratified and proportional random sampling among all 15 provinces of Valparaiso, Libertador General Bernardo O'Higgins and Metropolitana de Santiago regions, assuming a 50% of prevalence of a high impact zoonotic agent (e.g. avian influenza, Salmonella spp.) and adjusting for the population size, result in 329 BPS to sample. Using ArcGis 10® 329 random sample points were allocated within the study area, searching for BPS with poultry or swine breeding. On a second stage random points were validated using GoogleEarth® searching for points allocated within agricultural land use and point allocated over hills or water sources (lakes or rivers) using a 5 kilometer radius criteria. On a third stage, BPS were identified with field work, using Google Maps® for field work planning and radius criteria checking.

Results:
From the total of the random sampling points, over 70% were correctly allocated (sample points allocated on feasible sampling sites). On the provinces of Cachapoal, Chacabuco, Petorca and San Felipe, less than 50% of the points were allocated on feasible sampling areas. From the total BPS sampled, more than 90% met de 5 kilometer radius criteria, the provinces of Talagante, Valparaiso and Cordillera present more than 20% of the sampling points that not met de radius criteria.

Conclusions:
This approach allows increasing the efficiency of sampling and field activities, decreasing time and logistic used to locate sampling point, but would be much useful to generate maps with the locations of all BPS from Chile.

Relevance:
Given the lack of knowledge about the specific location of SPT, identification represents a high cost in surveillance of pathogens. The use of spatial tools is positioned as a support to healthcare management.

P213

Assessing impact for behaviour change interventions: a case-study of British dairy farms.

William Gilbert[1], Jenny Gibbons[2], Claire Wathes[3], Jonathan Rushton[1], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]DairyCo, Kenilworth, United Kingdom; [3]Royal Veterinary College, Hatfield, United Kingdom. Contact: wgilbert@rvc.ac.uk

Purpose:
To assess the impact of a knowledge transfer initiative on dairy farmers' biosecurity practices and management of calves up to 42 days of age.
Methods:
A mixed methods approach based on a new theoretical framework is applied to investigate the impact of knowledge transfer on biosecurity and hygiene practices in the management of dairy calves up to 42 days of age. The study consists of two stages. A survey of current calf management practices on dairy farms in Great Britain by means of a postal survey administered to 1200 dairy farms is to be conducted during April 2015. Analysis of the survey data will assess clustering amongst respondents. Survey respondents matched using the clusters will be allocated to treatment or control groups. Treatment groups will be exposed to knowledge transfer material recommending new hygiene practices. Intention to adopt recommendations will be assessed using semi-structured face-to-face interviews to allow exploration of underlying influential factors across each cluster.
Results:
Baseline data describing the management of calves up to 42 days of age will be collected through the postal survey, and a qualitative exposition of farmers' perceptions of the intervention will be drawn from interview.
Conclusions:
The study's conclusions should support the development of future interventions targeting behaviour change and begin the process of validation for the framework used.
Relevance:
This is the first use of a newly developed framework for evaluating interventions requiring behaviour change, based on an extension of Ajzen's theory of planned behaviour (TPB). While this theory provides a solid basis for investigating behaviour, risk, uncertainty and externalities complicate decision making in the context of disease control. The framework is therefore tailored specifically to account for these factors, with antecedents to TPB variables capturing past experience, trust in risk communication, perceived risk of disease and the costs and benefits of the intervention. Specific to this case study, enteritis and pneumonia are significant causes of losses in dairy calves; good hygiene and management are critical in mitigating the risk of these diseases.

P214

Surveillance for avian influenza and Newcastle disease in Brazil

Mariana Ramos Queiroz[1], Bruno Pessamilio[2], José Henrique de Hildebrand e Grisi Filho[1], Ricardo Dias[1], José Soares Ferreira Neto[1], **Vitor Salvador Picão Gonçalves**[3], Fernando Ferreira[1], [1]Faculty of Veterinary Medicine and Animal Science, University of São Paulo, São Paulo, Brazil; [2]Ministry of Agriculture, Livestock and Food Supply, Brasília, Brazil; [3]Faculty of Agronomy and Veterinary Medicine, University of Brasilia, Brasília, Brazil. Contact: vitorspg@unb.br

From 2003 to March 3, 2015, the World Health Organization (WHO) reported 784 cases and 429 deaths in humans due to avian influenza (AI). The World Health Organization for Animal Health (OIE) reported for the period 2005-2014 a total of 2.974 and 40.434 outbreaks of AI and ND, respectively. Given the paramount importance of these diseases there is a case for evaluating the avian surveillance system in Brazil. The Brazilian surveillance system for AI and ND is coordinated by the Ministry of Agriculture, Livestock and Supply (MAPA), which is now working with the Laboratory of Epidemiology and Biostatistics (LEB) to identify ways of improving the on-going surveillance for AI and ND. The present study is following the Guidelines for Evaluating Public Health Surveillance Systems of the Centers for Disease Control and Prevention (CDC). The avian surveillance has six components. One is passive surveillance, within which any citizen can warn the veterinary administration about any suspicious birds by phone, email or personally. Active surveillance happens when the official veterinarians of each state take, on a monthly basis, a sample of breeding and laying hens at the end of their productive life or go to the farms to register, certify or inspect poultry establishments. Every year, on the sites of migratory birds, resident birds are sampled after the wintering period when migratory birds passed through Brazil. Another component is the federal inspection at poultry slaughterhouses, where the lot is inspected *ante* and *post mortem*. The last component is the International Agricultural Monitoring System (VIGIAGRO), the authority responsible for checking people entering the country and for the oversight and monitoring of all imports.

P215

Rift Valley fever in ruminants in Mayotte from 2010 to 2013: comparison of passive and active surveillance results and performances

Lisa Cavalerie[1,2], Laure Dommergues[3,4], Philippe Mérot[5], **Harena Rasamoelina**[6], Catherine Cêtre-Sossah[1,2], Eric Cardinale[1,7], [1]CIRAD, Sainte Clotilde, Réunion; [2]INRA, Montpellier, France; [3]CIRAD, Mamoudzou, Mayotte; [4]COOPADEM, Coconi, Mayotte; [5]DAAF 976, Mamoudzou, Mayotte; [6]Indian Ocean Commission, Ebene, Mauritius; [7]INRA, Montpellier, France. Contact: harena.rasamoelina@coi-ioc.org

Purpose

Rift Valley fever (RVF) is a zoonotic vector-borne disease causing abortion storms in cattle and human epidemics. RVF circulation was detected in Mayotte from 2008 to 2011 and thought to have become endemic there. Our aim was to study the results and performances (data quality, timeliness, sensibility, cost-efficiency) of 2 surveillance systems implemented in Mayotte (active and passive).

Methods

Blood samples were performed in sentinel herds and tested for antibodies against RVF 5 times between 2010 and 2013. At each abortion notification, samples were taken for RVF detection by PCR. Abortion declaration rate was approached by a questionnaire to the sentinel herds. Direct costs of the surveillance systems were calculated by a simple budget method. An alternative scenario was studied to optimize surveillance costs.

Results

The passive surveillance system led to 47 abortion notification, none positive for RVF. Active surveillance results are still being processed. Mean delay between sample and analysis results was 63 and 444 days for active and passive surveillance respectively. Total costs to implement the active surveillance were 10 times higher than for passive. Sensitivity is currently being assessed.

Conclusions

Implementing an efficient surveillance system in a remote island is uneasy. Timeliness should be urgently improved. Passive surveillance seems insensitive in this endemic context and with extensive farming practices. Active surveillance is costly but could be optimized by delegating more work to private vets. Pursuing surveillance of RVF in Mayotte remains essential to maintain actors and farmers awareness in case of re-emergence.

Relevance

Following-up the situation was critical and a unique opportunity for science. Detecting the impact of RVF as well as comparing cost-efficiency of active and passive was critical for sound policy making.

P216

Surveillance of Escherichia coli antimicrobial resistance from laying farms within the main Cuban poultry-producing region

Michel Baez, Ivette Espinosa, A. Duque, Siomara Martínez, **María I. Percedo**, Pastor Alfonso, Centro Nacional de Sanidad Agropecuaria (CENSA), San José de las Lajas, Cuba. Contact: percedo@censa.edu.cu

Purpose: Escherichia coli is a major pathogen of widespread importance in commercially produced poultry and, concurrently, an important commensal bacteria that inhabits the gastrointestinal tracts of humans and animals. The aim was to determine antimicrobial susceptibility profiles of E. coli from laying hens.
Methods: five representative poultry farms within the main poultry-producing region were selected to test susceptibility to antimicrobial agents (AMA). Laying hens showing gastroenteric disorders were sampled by pooled cloacal swaps in each farm. Susceptibility to nine different AMA was assessed by the agar-disc diffusion technique. The frequencies of susceptibility to AMA were modelled by beta distribution after 1000 iteractions with Latin hypercube sampling, using @Risk (Palisade Corporation) and Microsoft® Excel 2007.
Results: resistence to tetracycline had a probability of 0.69 with CI 95% 0.50-0.88. Fluoroquinolones as second choice AMA had a lowest but noteworthy, level of resistence (0,54; CI 95% 0.40-0.68) with major differences across poultry flocks. Among evaluated AMA, those belong to polypeptide and nitrofuran class showed the highest evidences of terapeutic efectiveness with probabilities of resistence of 0.28, CI 95% 0.10-0.46 and 0.20, CI 95% 0.07-0.33 respectively. Aminoglycosides showed intermediate levels. The probabilities to found multi-drug-resistant isolates ranged from 0.41 to 0.50, in some cases including second and third generation cephalosporins of exclusive use in human.
Conclusions: resistance showed the highest levels to most commonly used antimicrobials in poultry, whereas polypeptides and nitrofurans were particularly noteworthy as terapeutic alternative strategies.
Relevance: the study provides support in favor of an evidence-based approach to antimicrobial treatment providing opportunities for reducing unnecessary use of less effective antimicrobials that may strengthen evolution of antimicrobial resistance even with potential negative impact on public health. Alertness was made according to detected levels of resistance, including cephalosporins of exclusive use in human.

P217

NORA - a rapid risk assessment tool for qualitative release risk assessment

Jonna Kyyrö, Leena Sahlström, Tapani Lyytikäinen, Finnish Food Safety Authority Evira, Helsinki, Finland.
Contact: jonna.kyyro@evira.fi

The NORA rapid risk assessment tool was developed for situations of change in the disease status of easily transmissible animal diseases in neighbouring countries or in countries with noticeable interactions with Finland. The goal was to develop a tool that is fast and robust and will provide acceptable repeatability and reliability in order to support risk management decisions related to rapid changes in disease risks. The model contains 63 questions which define the potential for spread into the country by nine different routes. 23 claims define the magnitude of consequences. The weight of different routes is defined according to the properties of the assessed disease. The model was built as an EXCEL-spreadsheet and its use does not require advanced computer skills.
As an outcome, the model gives the possible routes of disease entry into the country, an overall estimate for the likelihood of entry, an overall estimate for the consequences and a combined risk estimate (probability*magnitude of consequences). Different scenarios can easily be compared and constructed to take the uncertainty of the situation being assessed into account. Model repeatability and reliability will be assessed by an expert panel.

P218

Tilapia production and the associated sanitary risks in public reservoirs: a challenge to aquatic health services

Geórgia D. Roriz[1], Marina Karina V. C. Delphino[2], Vitor Salvador P. Gonçalves[1], [1]University of Brasília, Brasília, Brazil; [2]Ministry of Fisheries and Aquaculture, Brasília, Brazil. Contact: georgiaroriz@gmail.com

Brazil is a country of important aquaculture potential, though it still ranks 14th in the ranking of the world's aquaculture production. Fish production in public waters, in large reservoirs, is one of the activities that have growing in Brazil, mostly carried out by small-holder fish farmers. However, the production systems and its main sanitary problems are not well described, constraining the planning of health and extension services. The present project will provide a knowledge base for the development of effective surveillance and control measures that may underpin fish production in such environments. It is planned as a pilot study conducted in the reservoir of Três Marias, Minas Gerais, Brazil. The reservoir covers an area of 202.500 m³, where, as of December 2014, 76 small tilapia farmers were operating. Amongst the main constraints faced by producers are the difficulty in obtaining environmental licenses, the current low level of water in the reservoir due to prolonged drought, the limited number of fish processing units, the scarcity of technical assistance, the high price of feed and the uncertainty about sanitary issues. Farmers report varying mortality rates over the year, with the largest losses concentrated in the summer, as well as losses due to low quality fingerlings and the presence of pathogens such as Streptococcus spp. and Francisella spp. There are challenges related to the design of epidemiological studies for aquatic animals raised in public waters, notably the definition of the epidemiological units, the problems arising from temperature fluctuations, water level and other natural phenomena and the lack of data needed to assist the development of methodologies for mitigating the identified risk factors and to ensure sanitary certification of production. This project combines a cross-sectional survey aimed at characterizing the local production systems, including the producers' perceptions and attitudes towards health risks, with a longitudinal study to identify the dynamic of the key disease risks that hamper productivity, in order to define biosecurity strategies such as risk-based surveillance and propose effective extension services.

P219

Spatial analysis of Classical Swine Fever outbreaks in Pinar del Río province, Cuba.

Osvaldo Fonseca[1], Kleber Régis Santoro[2], Pastor Alfonso Zamora[1], Edyniesky Ferrer[1], María Antonia Abeledo[1], Octavio Fernández[1], Miriam Blanco[3], Yobani Rabelo[3], **María Irian Percedo**[1], [1]Centro Nacional de Sanidad Agropecuaria (CENSA), San José de las Lajas, Cuba; [2]Universidade Federal Rural de Pernambuco (UFRPE), Garanhuns, Brazil; [3]Instituto de Medicina Veterinaria, Pinar del Río, Cuba.
Contact: percedo@censa.edu.cu

Purpose:
Classical Swine Fever (CSF) can cause high morbidity and mortality in susceptible hosts, depending on the virus strain, immune status of the herd and age of the pigs. It is one of the most highly contagious animal diseases and it is considered a devastating disease for the pig industry throughout the world, concerning both economic and sanitary issues. In Cuba, CSF is an endemic disease and it is under control through vaccination programs among other sanitary measures. The Cuban Veterinary Medicine Institute (IMV) has planned a campaign for CSF eradication by zones. Therefore, identifying high risk areas for outbreak occurrences should be very useful for implementing a most efficient control measures as well as understanding CSF distribution in specific regions. The aim of this study was to identify high risk areas for CSF outbreak occurrences in Pinar del Río province, which is one of the provinces selected for starting the eradication campaign.

Methods:
Information from the provincial census and records of CSF outbreaks in the province during four-year-period (2009 - 2012) were recorded. A risk map was created using the Indicator Kriging method. Scan statistic (SaTScan 9.3) method was used for detecting clusters using purely spatial analysis and the probabilistic Poisson model. Maps were made using ArcGIS 9.3.1.

Results:
A high rate cluster (RR: 3.058; $p<0.039$) was detected, high risk areas involve municipalities from south and north coasts but relatively near to the border of Artemisa province. This province has the worst epidemiological situation if it is compared to our scenario. CSF spread by illegal pig movements between private producers could play an important role, because the introduction of pigs from other provinces was forbidden fallowing the strategy implemented by the Veterinary Medicine Institute (IMV).

Conclusions:
High risk areas and clusters were identified. Those results can contribute to improve CSF control program in this province selected.

Relevance:
A more extensive study should be made at national level; it will support the strategies in the control and eradication campaign against CSF in Cuba.

P220

Spatial and temporal analysis of cattle movements in Argentina

Facundo J. Linares[1], Andres Perez[2], Gustavo Rodriguez Vazquez[1], Bernardo Cosentino[1], [1]Servicio Nacional de Sanidad y Calidad Agroalimentaria (SENASA), Buenos Aires, Argentina; [2]University of Minessota, Minessota, MN, Contact: flinares@senasa.gov.ar

Purpose:
Cattle movements are regarded as the main route of transmission of infectious diseases. As a consequence, the evaluation of animal movements' networks is of key importance for predicting and controlling the spread of infection diseases. The characterization of such movements is important to establish areas and periods of high risk of introduction and potential spread of disease, as well as new measures to establish surveillance systems and identify risk farms.This study aims at temporal-spatial characterization of cattle movements in Argentina during 2012.
Methods:
A detailed description of the origin and destination movements from Provinces and Departments in terms of frequency number of animals, distance, types of movement, date performed, among others, were obtained from data supplied by the Integrated Management System for Animal Health (SIGSA) of the National Service for Agrifood Health and Quality (SENASA).The description and analysis of direct movements and spatiotemporal patterns was performed using the methodology of network analysis algorithms and graph theory by R Language v2.10.1 with igraph library. The space-time permutation scan statistic was used to identify clusters of high risk operations for animal movement. The descriptive analysis was performed using graphs with Excel (12.0) and the maps were created by software ArcGIS version 9.3 (ESRI).
Results:
The results obtained in this study identified areas and times of the year at high risk for the potential introduction and spread of cattle diseases in Argentina.
Conclusions:
This may provide support to SENASA to design risk-based surveillance strategies and contingency planning, in addition, this methodology is particularly interesting in those cattle diseases where animal movements are the primary means of entry of the disease onto farms, and where movement databases are available and updated periodically, as in Argentina.
Relevance:
It also offers essential information to include in computer models to simulate the potential disease spread and epidemic size of potential epidemics in the country.

P221

Assessing probable spatial and temporal clusters of *Salmonella sp.* isolates from commercial layer flocks in Iran

Saied Bokaie[1], Fereshteh Ansari[1], Seyed Mostafa Peighambari[1], Mahmood Mahmoudi[1], Mohammad Hossein Fallah[2], Farshad Tehrani[3], Abolfazl Rajab[3], Seyed Ali Ghafouri[3], Seyed Mehdi Tabatabaei[3], Maryam Shabani[3], **Kayhan Ilbeigi**[4], [1]University of Tehran, Tehran, Iran, Islamic Republic of; [2]Space Transportation Research Institute, Iranian Research Center, Tehran, Iran, Islamic Republic of; [3]Iranian Veterinary Organization, Tehran, Iran, Islamic Republic of; [4]Islamic Azad University of Garmsar, Garmsar, Iran, Islamic Republic of. Contact: Keyhan.ilbeigi@gmail.com

Purpose: The aim of this study was to identify prevalence and probable spatial and temporal clustering of Salmonella infection in laying farms in Iran.

Methods: A total of 187 holdings were selected from 882 layer flocks at random using simple random sampling, stratified by active layer flocks in the province. Two 150 g composite fecal samples were obtained from each flock. Fecal samples were transferred to the laboratory to undergo bacteriological and serological tests. The information of all the sampled farms were recorded and maps were created using GIS arc map. We designed to determine the high risk foci of the disease by using Getis Ord's Gi* test and optimized hot spot analysis and distinguish temporal clustering by Scan test.

Results: During the study period, 4 of 187 layer flocks were identified as Salmonella positive (2.1%). Spatial clustering techniques could not be performed due to low number of positive layer holdings. The infection had one peak in September of 2013. This peak was belonged to the two positive samples of Yazd province but there was no detectable temporal cluster.

Conclusions: Based on this study results, the prevalence of Salmonella in laying farms of Iran is low and the Salmonella infection is randomly distributed in space and time.
Relevance: This was one of the widest studies to determine the overall prevalence of Salmonella and its distribution in Iran. This study was conducted synchronously in a wide territory and according systematic sampling methods. The result of this study would assist decision makers to establish a more effective control program against salmonella infection in laying farms.

P222

Studying the association between poultry density and salmonella infection in commercial laying flocks in Iran using a kernel density function

Fereshteh Ansari[1], Saied Bokaie[1], Seyed Mostafa Peighambari[1], Mahmood Mahmoudi[1], Mohammad Hossein Fallah[2], Farshad Tehrani[3], Abolfazl Rajab[3], Seyed Ali Ghafouri[3], Seyed mehdi Tabatabaei[3], Maryam Shabani[3], **Kayhan Ilbeigi**[4], [1]University of Tehran, Tehran, Iran, Islamic Republic of; [2]Space Transportation Research Institute, Iranian Research Center, Tehran, Iran, Islamic Republic of; [3]Iranian Veterinary Organization, Tehran, Iran, Islamic Republic of; [4]Islamic Azad University of Garmsar, Garmsar, Iran, Islamic Republic of. Contact: Keyhan.ilbeigi@gmail.com

Purpose: Salmonellosis in laying flocks is one of the major health concerns all over the world and the size of flock have been introduced as an important risk factor associated with increased risk of salmonella. The aim of this study was to evaluate the association between poultry density and salmonella contamination in layer flocks.

Methods: A total of 113 holdings were selected using simple random sampling stratified by active layer holdings in each province of Iran. Two fecal sample were obtained from each flock of holding and information of sampled holdings were acquired from GIS system.

Results: The prevalence of Salmonella contamination in laying hen holdings was 3.5% and the risk of Salmonella contamination was associated with the size of the poultry-holding (OR = 5.6; CI 95% = 1.35, 23.57; p = 0.018). None of the positive farms were located in high density surface at farm level. Two of the positive farms were at the density surface of more than 13 flocks per square kilometer and all the positive farms were in the regions with poultry density of more than 319,000 per square kilometer.

Conclusions: According statistical and spatial analysis keeping large number of poultries in a certain area is an important risk factor for salmonella contamination while increasing the density of farms in the unit of area can modify the effect of poultry density.

Relevance: Salmonella; Layer hens; spatial analysis; kernel density

P223

Spatial epidemiology of Angiostrongylus vasorum in the United Kingdom

Georgina Limon[1], Kim B. Stevens[1], Patricio Artigas[2], Laura Kirk[1], Carlos Hermosilla[3], Javier Guitian[1], Mark T. Fox[1], [1]Royal Veterinary College, Hatfield, United Kingdom; [2]Universidad de Valencia, Valencia, Spain; [3]Liebig University, Giessen, Germany. Contact: glimon@rvc.ac.uk

A. vasorum is a parasitic nematode that may cause cardiopulmonary disease, neurological signs and/or coagulopathies in dogs. It was first reported in England in 1980 and has emerged as cause of infection in the dog population in recent years. No studies have described the spatial distribution of the parasite or identified risk factors associated with its distribution.

Purpose: The aim was to describe the spatial distribution of *A. vasorum* in the UK together with any clusters of canine infection and to identify risk factors.

Methods: A postal questionnaire was sent to all registered small animal practices in the UK (n=3950) to determine the prevalence of practices that reported seeing at least 1 confirmed case of *A. vasorum* in the previous 12 months. Spatial scan statistic was used to identify significant clusters of practices with a high probability of seeing at least 1 confirmed case. A boosted regression tree model was used to identify risk factors associated with distribution of canine infection from a range of key environmental, host and bioclimatic factors.

Results: Of the 1419 practices that replied, 21% reported seeing at least 1 confirmed case while 4% reported at least 6 confirmed cases. The parasite was distributed throughout the UK - two clusters of practices with a significantly (p=0.001) higher risk of seeing at least one confirmed case were identified; one located in south-eastern England (RR=4.4; radius102 km) and the second in Wales(RR=4.9; radius 36 km). Dog density accounted for 30% of the variation in *A. vasorum* distribution with risk of infection increasing rapidly with increasing dog density, before plateauing above 400 dogs/km^2. Vegetation index (in December) and land cover accounted for 17 and 12% respectively of the variation in infection distribution with highest probability occurring between an NDVI of 4000-8000 and in areas of grassland.

Conclusions: *A. vasorum* infection is widespread in the UK with two high-risk clusters of infection, and that variation in distribution is driven by dog density, vegetation index and the presence of grassland. Relevance: Maps showing areas of high risk can be used to alert local practitioners of the risk of *A. vasorum* infection in their area.

P224

Performance of FAMACHA scores for detecting anemia in sheep

Kathleen Barton[1], Jeff D. Ondrak[2], Karen Shuck[2], David R. Smith[1], [1]Mississippi State University, Mississippi State, MS, [2]University of Nebraska-Lincoln, Clay Center, NE, Contact: kbarton@cvm.msstate.edu

Purpose

The FAMACHA scoring system is used to identify sheep or goats clinically affected by internal parasites. Although FAMACHA is commonly perceived to be highly correlated with anemia, the diagnostic performance of FAMACHA to predict anemia as measured by packed cell volume (PCV) has not been well characterized. The objective of this study was to evaluate the diagnostic performance of FAMACHA scores in sheep for identification of anemia.

Methods

From 2011 to 2014, 279 rams were scored using the FAMACHA system, and concurrent blood samples were taken to determine PCV. Anemia was defined as a PCV of <27%. The FAMACHA scores were evaluated for sensitivity, specificity, likelihood ratios, and predictive values.

Results

No sheep scored above 4. The majority of sheep classified as anemic at any FAMACHA cut-off value had PCV ≥27%. FAMACHA scores <4 did not differentiate anemic from non-anemic sheep. At a cut-off value of FAMACHA score 4, sensitivity to detect anemia was 0.70 (95% CI = 0.93, 0.35); specificity was 0.94 (95% CI= 0.97, .91). The likelihood ratio for a score of 4 was 12.6. At a cut-off value of FAMACHA score ≥3, sensitivity was 0.80 (95% CI = 0.97, 0.44) and specificity was 0.74 (95% CI = 0.79, 0.69). The likelihood ratio for a score of 3 was 0.50. At a cut-off value of FAMACHA score ≥2, sensitivity was 1.0 (95%CI = 1.0, 0.69); specificity was 0.23% (95% CI = 0.29, 0.18). The likelihood ratio for a score of 2 was 0.34. At a cut-off value of FAMACHA score ≥1, sensitivity was 1.0 (95% CI = 1.0, 0.31) and specificity was 0.0 (95% CI = 0.0, 0.01). The likelihood ratio for a score of 1 was 0. Negative predictive value of scores of 3 or 4 exceeded 90% in populations with less than 20% prevalence of anemia. Positive predictive value of scores of 4, 3, and 2 exceeded 90% in populations with 50%, 80%, and 90% or greater prevalence of anemia, respectively. A score of 4 classified the greatest percentage of sheep correctly until anemia prevalence reached 0.7; then lower scores classified more sheep correctly.

Conclusions

A FAMACHA score of 4 had the greatest diagnostic usefulness.

Relevance

A FAMACHA score of 4 might enable modest sorting of anemic from non-anemic sheep except in flocks with high prevalence of anemia.

P225

Standardization of SYBR Green qPCR for diagnosis of leptospirosis in domestic animals from Nicaragua

Byron Flores[1], Hector Fuertes[2], Jessica Sheleby-Elias[1], José Luis Muzquiz[3], William Jirón[1], Tania Pérez-Sánchez[3], Ana Muniesa[3], Christiane Düttmann[1], **Ignacio de Blas**[3], Nabil Halaihel[2], [1]Universidad Nacional Autónoma de Nicaragua, León, Nicaragua; [2]Universidad de Zaragoza/ ALQUIZVETEK SL, Zaragoza, Spain; [3]Universidad de Zaragoza, Zaragoza, Spain. Contact: deblas@unizar.es

Purpose: In Nicaragua and other countries of the world, the Microscopic Agglutination Test (MAT) is the gold standard for the diagnosis of leptospirosis, but MAT is laborious and needs to maintain viable the bacteria. The qPCR is a technique known to be highly specific, sensitive and quantitative, compared to direct isolation and serology. The aim of this study was to design a SYBR green qPCR for the diagnosis of pathogenic Leptospira in domestic animals.

Methods: Forward and reverse primers were obtained using Prime 3 application, targeting conserved region of to LipL32 gene from twelve different sequences obtained from NCBI gen collection, after sequence alignment using MEGA 6 application. CFX CONNECT Real Time System of BIO-RAD was used. The detection limit was determined using pure DNA of L. interrogans, Pomona strain, quantified by spectrophotometry in BioDrop (Cambridge, UK). Eight logarithmic serial dilutions for determining a standard curve were made. Twenty seven reference strains representing seven pathogenic species of Leptospira were used as positive controls. DNA from 26 different bacteria, including non pathogenic Leptospira species Patoc I, were probed for specificity. A total of 77 urine samples of domestic animals from an endemic region were collected. These samples were processed and data results from MAT, the newly designed qPCR and the qPCR described by Levett et al. (2005) were compared.

Results: The detection limit of the new qPCR was 1.59 x 101 genome equivalent per reaction. An efficiency rate of 99.50% (R2=0.99) was obtained. A diagnostic sensitivity of 93.75 (CI95% = 78.76, 100) with a 100% (CI95% = 98.08, 100) specificity. The Youden's J was 93.75% (CI95% = 81.89, 100). The assay was able to detect Nicaragua and Shermani serovars, that were not detected by qPCR described by Levett et al. (2005). The kappa coefficient compared to MAT was 0.200 ($p<0.001$), whereas for the qPCR described by Levett it was 0.788 ($p<0.001$).

Conclusions:

This LipL32 qPCR should be considered as a valuable tool in diagnostic and monitoring cases of leptospirosis in Nicaragua.

Relevance: Potential false negatives in samples from Nicaragua could be avoided with this new technique.

P226

Sensitivity and specificity of IFAT and skin LnPCR techniques for detection of L. infantum in wild lagomorphs estimated using a Bayesian approach.

María Luisa de la Cruz[1], Andrés Pérez[2], Mercedes Domínguez[3], Inmaculada Moreno[3], Nerea García[1], Lucas Domínguez[1], Julio Álvarez[2], [1]VISAVET Health Surveillance Centre, Madrid, Spain; [2]University of Minnesota, Saint Paul, MN, [3]Instituto de Salud Carlos III, Majadahonda, Madrid, Spain. Contact: m.cruz@visavet.es

Purpose

Leishmaniasis, caused by *L. infantum,* is a vector-borne zoonotic disease that is endemic to the Mediterranean basin. Recently, a leishmaniasis outbreak in the province of Madrid (Spain), the largest outbreak registered in Europe, triggered the question of whether rabbits and hares may act as competent reservoirs for *L. infantum*. Given the lack of standardized diagnostic tests for leishmaniasis in these species, a Bayesian approach was used here to estimate the sensitivity and specificity of the immunofluorescence antibody test (IFAT) and the *Leishmania* nested PCR analysis (LnPCR) of skin samples for the detection of *L. infantum*.

Methods

A latent class model was applied to the diagnostic results obtained from 217 rabbit and 70 hare samples from two different populations in the region of Madrid. Both diagnostic tests were assumed to be conditionally independent, and two alternative cut-off values were assumed for the interpretations of the IFAT results. Prior distributions were fitted based on information available from the peer-reviewed scientific literature. Analyses were implemented in WinBugs 1.4.3.

Results

Posterior estimates for the sensitivity of the LnPCR were below 30% regardless of the IFAT interpretation used (28.9% and 21.3%, for the conservative and sensitive interpretation, respectively), although the 95% CI of the estimate suggested a large uncertainty, particularly when the conservative interpretation was assumed (19.2-70.8). In contrast, this technique was estimated to be highly specific (96% for both interpretations). Sensitivity and specificity posterior estimates of the IFAT showed a large overlapping with the prior values used (sensitivity above 70% and specificity slightly below 85%, regardless the interpretation).

Conclusions

Limited sensitivity of the LnPCR using ear skin may have been related to low parasitic load or poor analytic sensitivity of this technique. Results suggest that the IFAT may be a useful screening tool in lagomorphs' populations.

Relevance

These results will help to the design and eventual implementation of effective programs for *Leishmania* prevention and control in infected regions.

P227

Bounds of dependency in the combined use of diagnostic tests in different scenarios.

Jose Piaggio[1], Joaquin Baruch[1], Federico Fernandez[2], Alicia von Gehlen[1], Alvaro Nuñez[1], **Andres Gil**[1], [1]Universidad de la Republica, Montevideo, Uruguay; [2]Ministerio de Ganadería Agricultura y Pesca, Montevideo, Uruguay. Contact: adgr@adinet.com.uy

Diagnostic schemes constituted by more than one test are widely used in control programs of diseases. The dependency between tests can alter the combined results. To study these conditional probabilities in known populations of infected and not infected is difficult and complicated to implement. Sensitivity (Se) and Specificity (Sp) estimations of tests, and the prevalence object of the control program are the generally available information. The conditional probabilities are delimited by the values Sp and Se of the tests, which enables to model the final results of the diagnostic scheme.
Bounds of conditional probabilities was determined according to the infectious status in a scheme of parallel and serial tests. The bound values were confirmed by an electronic worksheet.
In serial tests, in infected animals, the positive proportion at test 1 that keep positive in test 2 has a maximum =Se2/Se1, whereas the minimum is 0 if Se2+Se1≤1 or [(Se2+Se1)-1]/Se1 if Se2+Se>1. In healthy animals proportion of positive at test 1 which become negative at test 2 has a maximum =Sp2/(1-Sp1), while the minimum is 0 if Sp1≥Sp2 or (Sp2-Sp1)/(1-Sp1) if Sp1<Sp2.
In parallel tests, in infected animals, negative proportion at test 1 which turn positive at 2 has a maximum = Se2/(1-Se1), whereas the minimum is 0 if Se1≥Se2 or (Se2-Se1)/(1-Se1) if Se1<Se2. In healthy animals the proportion of nevatives at test 1 that keeps negative at test 2 has a maximun=Sp2/Sp1, while the minimun is 0 if Sp2+Sp11.
In order to determine the best diagnostic strategy to implement in the control/eradication programs, it should be considered the lack of independency of combined diagnostic tests. The dependency between tests resulted in changes in Se and Sp of the proposed diagnostic schemes. We can obtain better results as supposing independency of tests if they are supplementary.

P228

Evaluation of a PCR test for Coxiella burnetii detection in dust samples in dairy cattle farms using latent class analysis

Aurelien Madouasse, Simon Nusinovici, **Thierry Hoch**, Raphael Guatteo, Francois Beaudeau, INRA - ONIRIS (Nantes-Atlantic National College of Veterinary Medicine), Nantes, France. Contact: thierry.hoch@oniris-nantes.fr

Purpose: Different tests performed on bulk tank milk samples (BTM) are available to determine the C. burnetii (causative agent of Q fever) status of herds. However, these tests, which are based on the detection of either antibodies directed against C. burnetii (ELISA) or bacterial DNA (PCR), have limitations. A currently disease-free herd infected in the past may continue to test positive with ELISA due to the persistence of antibodies in animals that were infected and that subsequently cleared the infection. Infectious herds can also be misclassified using PCR due to absence of bacteria in the BTM when the test is performed. Recently, PCR has been used for bacterial DNA detection in the farm environment, which constitutes the main reservoir of C. burnetii. The objectives of this study were to (i) assess and compare the sensitivities and specificities of one commonly used PCR test in BTM and of a PCR applied to environmental samples in dairy cattle farms, and (ii) infer the relevance of these tests to detect farms where C. burnetii is present (referred to as 'infectious farms').

Methods: BTM and dust samples (using environmental swabs) were collected at the same time in 95 herds. Test performance was assessed using latent class analysis and parameters estimated. within a Bayesian framework.

Results: PCR applied to dust samples had a slightly higher sensitivity than PCR applied to BTM (0.72 versus 0.68). Moreover, when responses from both PCR tests using a parallel reading were considered, 91% of infectious farms were detected.

Conclusions: The test based on the detection of C. burnetii DNA in dust samples had good test performance in order to assess the status of ruminant farms towards Q fever.

Relevance: Therefore this test could be used in surveillance programs of Q fever, alone or in combination with a PCR applied to BTM, to assess the risk of C. burnetii transmission between ruminant farms, together with the zoonotic risk.

P229

Evaluation of the performance of five diagnostic tests for Fasciola hepatica infection in naturally infected cattle using a Bayesian no gold standard approach.

Stella Mazeri[1], Ian Handel[2], Mark Bronsvoort[1], Neil Sargison[2], [1]The Roslin Institute, Edinburgh, United Kingdom; [2]Royal (Dick) School of Veterinary Studies, Edinburgh, United Kingdom. Contact: stella.mazeri@roslin.ed.ac.uk

Purpose: To improve our knowledge on the performance of tests available for the diagnosis of F. hepatica infection in cattle.
Methods:A Bayesian no gold standard approach was used to estimate the diagnostic characteristics of 5 diagnostic tests; detailed liver necropsy, faecal egg counting, a commercially available copro-antigen ELISA, an in-house serum excretory/secretory antibody ELISA and abattoir liver inspection. In total 619 cattle slaughtered at one of Scotland's biggest abattoirs were sampled, during 3 different sampling periods; summer 2013, winter 2014 and autumn 2014. Sensitivities and specificities of the tests were estimated. These were allowed to vary between seasons if tests were a priori believed to perform differently for any reason. Additionally, correlation coefficients between parasite burden, liver fibrosis scores and the continuous measures from the ELISA based tests and FECs were estimated.
Results: The results of this analysis provide novel information on the performance of these tests in a naturally infected cattle population and at different times of the year where different levels of acute versus chronic infection are expected. Furthermore, there is evidence to suggest that the copro-antigen ELISA does not cross-react with Calicophoron daubneyi parasites, while the serum antibody ELISA does. Finally, good correlations of FEC and copro-antigen ELISA with parasite burden show that these tests might be used to estimate infection levels, while the serum antibody ELISA could be used to estimate extent of fibrosis, which in turn could be a measure of the infection's effect on production.
Conclusions:
Establishing good estimates on diagnostic tests quantitative and qualitative characteristics can aid the liver fluke management on farm. Similarly, routine abattoir liver inspection can be used as a tool for monitoring the epidemiology of F. hepatica as well as evaluating herd health planning.
Relevance: Tests available for the diagnosis of F. hepatica infection in cattle are far from perfect. The evaluation of diagnostic tests has mainly been carried out using gold standard approaches or under experimental settings, the limitations of which are well known.

P230

Assessing the validity of an ELISA test for the serological diagnosis of equine viral arteritis

Marina Pavlak[1], Marinela Tadić[2], Vlado Stevanović[3], Ivana Lohman Janković[4], Ljupka Maltar[4], Tomislav Kiš[4], Ivica Sučec[4], Ljubo Barbić[5], [1]Faculty of Veterinary Medicine , University of Zagreb, Zagreb,, Croatia; [2]Veterinary Clinics Mario Veterina d.o.o., Sisak, Croatia; [3]Faculty of Veterinary Medicine , University of Zagreb, Zagreb,, Croatia; [4]Ministry of Agriculture, Zagreb,, Croatia; [5]Faculty of Veterinary Medicine , University of Zagreb, Zagreb,, Croatia. Contact: marina.pavlak@vef.hr

Purpose: The aim of this study was to evaluate the diagnostic performance of ELISA based on the virus neutralisation (VN) test which is recommended by the World Organization for Animal Health (OIE) as "gold standard" for the detection of the antibodies to equine arteritis virus as well as to evaluate its application as screening test in a routine laboratory diagnostics.

Methods: The study was carried out as a part of monitoring equine viral arteritis in Croatia. We analyzed data for 118 sera from the territory of the Republic of Croatia. The samples were taken during the year 2010 and delivered to the Virology Laboratory of Faculty of Veterinary Medicine University of Zagreb. All sera samples were tested by commercial ELISA kit (ELISA ID.VET, Montpellier, Francuska) and VN-test. A kappa statistic was used to measure the agreement between obtained results (kappa values at 95% confidence interval).
Results: Out of 118 sera subjected to ELISA and VN-test, 81 sera were positive and 15 were negative in both tests; 3 samples tested negative by ELISA but positive by VN-test and 19 were positive by ELISA and negative by VN-test. The sensitivity and specificity of ELISA were 96,43 (CI 95% from 92,45 to 100,00%) and 44.12 % (CI 95 % from 27,43 % to 60,81 %), respectively, with VN-test as gold standard. The percentage agreement between ELISA and VN-test was 47 % Kappa (CI 95% from 27% to 67%). A moderate correlation was found between ELISA and VN-test ($r = 0,65$, $P<0,05$). The true prevalence of equine viral arteritis was 71,18% (CI 95% from 63,02% to 79,36) with apparent prevalence of 84,75% (CI 95% from 78,26% to 91,23%) by the VN-test and ELISA, respectively.

Conclusion: The ELISA showed high sensivity and low specificity and had a moderate agreement with VN-test. Therefore, 13,56% of positive samples by ELISA were false positive as well as 2,54% of negative samples by ELISA were thrue positive.

Relevance: Because ELISA is the diagnostic test that have adequate sensitivity it can be recommended to use as a screening test for equine viral arteritis diagnostic but because of false negative result it can be not good for conformation of the disease free status as well as for the determination of the infection in single animal.

P231

Factors affecting culture and PCR test performance for *Tritrichomonas foetus*

Carla L. Huston, Jennifer Cain, Frank W. Austin, Terry Doler, Alejandro Banda, Lanny W. Pace, Kevin Walters, R. Hartford Bailey, **David R. Smith**, Mississippi State University College of Veterinary Medicine, Mississippi State, MS, Contact: dsmith@cvm.msstate.edu

Purpose:
Trichomoniasis is a costly venereal disease of cattle worldwide and the target of many US state and international import regulations. Current diagnostic methods may be ineffective in detecting the protozoan organism *Tritrichomonas foetus* and thus ineffective in preventing the spread of the disease. The objective of these studies was to evaluate factors affecting *T. foetus* diagnostic test performance.
Methods:
For the first study, 600 pouches of selective enrichment media were inoculated with preputial bacteria from four healthy, *T. foetus* negative bulls. Three hundred pouches were randomly chosen to be inoculated with 30 *T. foetus* organisms each. Pouches were then randomly assigned to 20C pre-incubation treatments of 0, 2 and 4 days. Samples were incubated 37C after the holding period, and cultures were examined microscopically (100x) on days 1, 3, and 5. For the second study, 40 pouches were randomly assigned to 4 levels of *T. foetus* inoculation (67, 670, 6,700, or 67,000 organisms/pouch) and 2 levels of bacteria (inoculated with bacteria or not). Pouches were incubated at 37C and examined microscopically daily for 7 days. In the third study, 4 10-fold dilutions of *T. foetus* were incubated 37C for 7 days and examined microscopically daily.
Results:
PCR testing was more sensitive than culture, with sensitivity and specificity decreasing with increased holding times. Sensitivity was affected by the presence of bacteria ($p<0.0001$). All pouches inoculated with bacteria were culture negative; however, *T. foetus* was detected at least once from all pouches without bacteria. For those pouches, sensitivity increased daily (OR= 4.5, $p = 0.02$). In the third study, the lower inoculums peaked in concentration later.
Conclusions:
These results demonstrate that increased holding time and bacterial contamination may adversely affect test sensitivity, and that PCR may have advantages over culture when bacterial contamination exists.
Relevance:
Standardized sample handling and diagnostic testing procedures are needed in order to design effective control programs against trichomoniasis in cattle.

P232

Estimating the effectiveness of vaccination against infectious diseases in food animal populations: A Bayesian modeling and simulation approach

Zhao Lu, **Yrjo Grohn**, Cornell University, Ithaca, NY, Contact: ytg1@cornell.edu

The objective of this study was to propose a Bayesian modeling and simulation approach to estimate the direct, indirect, total and overall effectiveness of vaccination against infectious diseases in food animal populations.

Control of infectious disease spreading in farm animals is important to improve and promote both animal and human health as well as to reduce the economic burden. Vaccination has been used in farm animals as one of various control strategies. To assess the effectiveness of a vaccination program with no biases from herd management, clinical trials with both vaccinated and control cohorts are typically established within the same herd. However, this study design inevitably introduces difficulties in estimating the indirect, total and overall effectiveness of vaccination, because of the herd immunity and no control herd available with exactly the same herd management.

To solve this problem, we present a 3-step framework of a Bayesian modeling and simulation approach. The first step is to build an infectious disease transmission model with vaccination based on the available knowledge of the pathogen and vaccine of interest. The second is to estimate a few key epidemiological parameters in the vaccination model using the approximate Bayesian computation techniques, using longitudinal prevalence data collected from vaccinated and control cohorts from the same herd. The last is to generate a simulated control herd with the same herd management by running the model with parameters estimated from the second step.

To illustrate this Bayesian modeling and simulation approach, we performed a simulated case study of proof of concept for a killed whole-cell vaccine against paratuberculosis in dairy herds. Using simulated longitudinal prevalence data from control and vaccinated cohorts, we estimated the direct, indirect, total, and overall effectiveness of vaccination as a function of the proportion of vaccinated incoming calves into a herd and time since vaccination. This study is particularly useful for evaluating the effectiveness of vaccination in farm animal populations, which clinical trials of studies are not able to achieve without biases due to herd management.

P233

The utilisation of qualitative research methods in UK veterinary research

Marnie L. Brennan[1], Pru Hobson-West[1], Stephanie Mabey[2], Martin J. Downes[1], [1]University of Nottingham, Loughborough, United Kingdom; [2]Ashfield House Veterinary Hospital, Long Eaton, Nottingham, United Kingdom. Contact: marnie.brennan@nottingham.ac.uk

Qualitative research can be defined as research that interprets the views and experiences of individuals. The benefits and criticisms of conducting qualitative research are cited in the literature. Qualitative research methods are increasingly being successfully used in the medical field, but it is unknown how these methods are being used in veterinary research.

The aim of the study was to determine to what extent qualitative research methods have been used in published veterinary literature in the UK, and the opinions held on qualitative research and the methods employed by academics carrying out research in UK veterinary schools.

An objective review of the qualitative research methods used by authors in 3 species-specific veterinary journals was carried out. Additionally, a questionnaire was sent to academics in UK veterinary schools asking questions about the use of, and experience with, qualitative research methods. Questions were also asked about the advantages and disadvantages of using such methods, and what areas of veterinary science qualitative research methods could be applied to.

Of the 1684 primary research papers published in the 3 journals over a 10 year period, 19 were found to have used qualitative research methods. The journal focusing on cattle production had the largest number of papers utilising these methods compared with the other species. Of the 279 survey respondents, approximately one third (34%) of participants had previously used qualitative research methods. Advantages cited were the ability to collect rich, broad data that generated new research hypotheses. The main disadvantages cited were the subjectivity of the data, but also that qualitative research was often not taken seriously, particularly in relation to publication of research and research funding.

Veterinary researchers appear to have an appreciation of the benefits of using qualitative research methods, but have experienced barriers associated with the publication of research which may explain why these methods have not been utilised substantially in the published literature. Further work with a broader range of journals and other researchers is required to fully explore this finding.

P234

Evaluation of ELISA by Bayesian latent class analysis and quantitative misclassification bias analysis for effect of T.gondii exposure on abortion in New Zealand red deer

Kandarp K. Patel[1], Peter R. Wilson[2], Cord H. Heuer[3], Laryssa J. Howe[4], Geoffrey W. Asher[5], [1]Massey University, Palmerston North, New Zealand; [2]Massey University, Palmerston North, New Zealand; [3]Massey University, Palmerston North, New Zealand; [4]Massey University, Palmerston North, New Zealand; [5]AgResearch, Invermay, New Zealand. Contact: k.k.patel@massey.ac.nz

Background: Abortion due to *Toxoplasma gondii* infections during pregnancy was suspected to reduce reproductive performance in New Zealand red deer.
Purpose: 1. to validate a commercial *T.gondii* ELISA for deer by Bayesian latent class approach and by comparing it to western blot (WB), gold standard, and a commercially available latex agglutination test (LAT). 2. Using validated ELISA in a larger population, adjust the odds ratio (OR) for the effect of *T.gondii* exposure on abortion for misclassification bias.

Methods: 1. Sera from randomly selected hinds from pilot abortion study were tested for *T.gondii* antibodies on LAT, ELISA and WB. Sensitivity (Se) and specificity (Sp) values of LAT and ELISA were obtained using WB as a gold standard, or latently, in the absence of a gold standard, using Bayesian latent class statistics. 2. Sera from aborted (cases) and randomly selected non-aborted (control) hinds from a bigger two-year deer abortion study were tested on validated ELISA. A quantitative bias analysis was done to adjust for the *T. gondii* exposure misclassification by ELISA in cases and control hinds.

Results: 1.Bayesian analysis estimated the Se and Sp to be 0.89 and 0.74, respectively, for LAT, 0.96 and 0.94, respectively, for WB, and 0.97 and 0.95, respectively, for ELISA at an optimised cut-off. Using WB as a gold standard, the Se and Sp for ELISA, at manufacturer's cut-off SP% of 30 were 0.79, 0.97, respectively, whereas for LAT (cut-off of 1:32) it remained 0.83 and 0.73, respectively. 2. The sero-prevelence of *T.gondii* using ELISA test (cut-off SP% of 18.3) in hinds with (n=270) and without (n=432) abortions were 31% and 22%, respectively. Adjusting the odds-ratio (OR) for *T.gondii* exposure on abortion for misclassification by ELISA revealed -9% bias. The OR increased from 1.65 (crude) to 1.81 and both were significant (p=0.004).

Conclusions and relevance: Reducing the ELISA cutoff increased sensitivity. The performance of LAT was poorer than ELISA and WB. Misclassification bias only had a small impact on the OR. Sero-prevalence study using validated ELISA suggests that *T.gondii* may be a cause of abortions in NZ farmed deer.

P235

Bayesian estimation of true prevalence, sensitivity and specificity of three diagnostic tests for detection of Escherichia coli O157 in cattle feces

Pius S. Ekong, Michael W. Sanderson, Lance W. Noll, Natalia Cernicchiaro, David G. Renter, T. G. Nagaraja, Kansas State University, Manhattan, KS, Contact: pekong@k-state.edu

Purpose
E. coli O157 is a foodborne pathogen that colonizes the hindgut of cattle and is shed in feces. *E. coli* O157 in feces contaminates hides and is eventually transferred onto carcasses at slaughter. Detection in cattle feces has used culture and PCR-based methods. The aim of this study was to estimate true prevalence in cattle feces and evaluate diagnostic performance of culture, conventional PCR (cPCR), and multiplex quantitative PCR (mqPCR) tests using a Bayesian latent class model.
Methods
A total of 576 fecal samples collected during summer 2013 from cattle in a commercial feedlot were used. The enriched fecal suspensions were subjected to three detection methods: cPCR, mqPCR, and culture (immunomagnetic separation and plating on selective media). We implemented a three-test one-population model, assuming conditional dependence of the two PCR tests. Priors were formulated for the sensitivity and specificity of the three tests based on literature estimates.
Results
The true prevalence was estimated as 87.9% (95% credibility interval [CI]: 77.9-94.3%). Forty-three percent (247/576), 54.7% (315/576), and 89.8% (517/576) of enriched samples were positive by culture, cPCR, and mqPCR, respectively. The sensitivities of culture, cPCR, and mqPCR were 48.9% (95% CI: 43.5-55.8%), 58.1% (95% CI: 52.9-63.6%), and 93.2% (95% CI: 89.9-95.7%), respectively. The Specificities were 99.8% (95% CI: 98.9-99.9%), 76.8% (95% CI: 59.8-89.7%), and 52.8% (95% CI: 33.6-74.3%), respectively. Conditional covariance (sensitivity & specificity) between cPCR and mqPCR were 0.034 (95% CI: 0.017 to 0.052), and 0.065 (95% CI: -0.028 to 0.167), respectively.
Conclusions and Relevance
The results indicate that true prevalence of *E. coli* O157 was high in this population of cattle. PCR-based tests, especially mqPCR, were the most sensitive for detection in feces of naturally-infected cattle. mqPCR was less specific compared to cPCR and culture. PCR-based methods offer a higher throughput and sensitivity of detection in feces but at the cost of decreased specificity. This data provides important estimates of test performance for calculating true prevalence and adjusting for test bias in risk modeling.

P236

Episensr: an R package for deterministic and probabilistic bias analysis of epidemiologic data

Denis Haine, Université de Montréal, St-Hyacinthe, QC, Canada. Contact: denis.haine@gmail.com

Purpose:
Random and systematic errors are present in any observational studies. If random error can be reduced by increasing the sample size, systematic error (also referred to bias) is due to issues with study design or the methods used to obtain the study data and is not influenced by sample size. Bias can result from classification errors, selection bias, and unmeasured or unknown confounders. Assessment of bias is seldom realized due in part to the lack of appropriate and easy-to-use tools.

Methods:
The R package episensr is a tool allowing to perform a quantitative bias analysis, adjusting the relative risk for selection bias, unmeasured confounding, and uni- or multi-dimensional misclassification of the exposure, outcome, or covariates. Both deterministic and probabilistic sensitivity analyses are implemented, with a choice of probability distributions for the bias parameters.

Relevance:
By investigating the exposure-outcome relationship under various conditions of systematic errors, reseachers can assess the impact of bias on their study results. The implementation of qualitative bias analysis within R, a free, open-source, statistical software, make this appraisal easy, transparent, and accessible to any investigators.

P237

Novel method for quantification of bovine colostrum immunoglobulin G using infrared spectroscopy and multivariate data analysis

Ibrahim Elsohaby[1], J. T. McClure[1], Christopher Riley[2], Anthony Shaw[3], Gregory Keefe[1], [1]Atlantic Veterinary College, Charlottetown, PE, Canada; [2]Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand; [3]National Research Council of Canada, Medical Devices Portfolio, Winnipeg, MB, Canada. Contact: ielsohaby@upei.ca

Colostrum is the initial secretion from the mammary gland after parturition, and is an important source of immunity and nutrition for newborn calves. Colostrum contains a high concentration of immunoglobulins which are passively transferred to newborn calves. Colostrum varies considerably in IgG content; therefore, it is beneficial for producers to test colostrum quality before feeding it. The radial immunodiffusion assay (RID) is acknowledged as the reference standard test for the quantification of IgG in bovine colostrum, but it has significant drawbacks as it take 18-24 hours to obtain the results, utilizes reagents and is expensive. Infrared (IR) spectroscopy in combination with partial least squares (PLS) regression was used for prediction of IgG content of bovine colostrum. Colostrum samples (n = 250) were collected from 7 commercial dairy farms and tested simultaneously by the reference RID assay and IR spectroscopy. The colostral IgG concentrations obtained by RID assay were linked to the spectra and divided into two sets: calibration set and test set. Partial least squares (PLS) regression was applied to the calibration set (n = 167) and calibration models were developed. The best calibration model has 13 PLS factors, lowest root mean squared error for the Monte Carlo cross validation value (RMMCCV = 16 g/L) and highest correlation coefficient (r = 0.91). The test set (n = 83) was used to assess the predictive ability of the calibration model. The Pearson and concordance correlations between IgG predicted by IR assay and measured by the RID assay for the test set were 0.91. Bland-Altman analysis did not show any systematic bias between IR and RID methods. The IR assay showed relatively lower precision than the RID method with a coefficient of variation of 8.9%. The Se, Sp and accuracy of the IR assay to differentiate between poor and good quality colostrum were 90%, 92% and 90%, respectively. The PLS calibration model, in combination with IR spectroscopy, is an effective method for rapid quantification of bovine colostral IgG concentration and for assessment of colostrum quality.

P238

Canine visceral leishmaniasis in an endemic rural area of central-western Brazil: considerations about diagnostic methods

Juliana Arena Galhardo[1], Roberta Vieria de Moraes Bronzoni[2], David José Ferreira da Silva[2], Eriana Serpa Barreto[2], Alessandra Kataoka[2], Elaine Dione Vênega da Conceição[2], Artur Kanadani Campos[3], Tatiana Elias Colombo[4], Maurício Lacerda Nogueira[4], Janaína Olher Martins Montanha[4], Tânia Cristina Higino Estécio[4], [1]Universidade Federal de Mato Grosso do Sul, Campo Grande-MS, Brazil; [2]Universidade Federal de Mato Grosso, Sinop-MT, Brazil; [3]Universidade Federal de Viçosa, Viçosa-MG, Brazil; [4]Faculdade de Medicina de São José do Rio Preto, São José do Rio Preto-SP, Brazil. Contact: juliana.galhardo@ufms.br

Purpose: In Brazil, Visceral Leishmaniasis (VL) is a vector borne disease caused by *Leishmania infantum* and transmitted by sandflies from genus *Lutzomyia*. Dogs are considered the main domestic reservoirs in the zoonotic transmission cycle, with prevalence ranging from 63% to 80% in endemic areas. Brazilian Ministry of Health recommends canine serological survey followed by culling of seropositive dogs to control the incidence of human VL. Although thousands of serological positive dogs have been sacrificed annually, the incidence of human VL has not been reduced.

Methods: For diagnosis of VL were taken conjunctival swab, whole blood and serum samples from 105 domestic dogs living in endemic rural areas of Sinop municipality, Mato Grosso state, Brazil. Conjunctival swab and whole blood were analyzed by PCR using primers targeting the *L. infantum* kinetoplast minicircle DNA. Serum samples were tested by serological assays recommended by Brazilian Ministry of Health (Indirect Immunofluorescence Assay, ELISA, and Immunochromatographic test).

Results: DNA was detected at least in one clinical sample of 47/105 (45%) dogs. Among these PCR-positive dogs, only 10.6% displayed symptoms compatible with VL. The remaining animals, including PCR-negative dogs were asymptomatic. Using blood samples, the PCR was able to detect parasite DNA in 28/105 dogs (26.7%), and in 29/105 dogs using the conjunctival swab (27.6%). There was no agreement between results obtained when PCR was carried out using blood or swab conjunctival. Of 105 serum samples, only six (5.7%) were positive in serological assays.

Conclusions: Neither conjunctival swab nor whole blood may be used as unique methods for LV diagnosis. Diagnostic methods used in surveillance studies in Brazil do not have the appropriate clinical sensitivity required to detect early or asymptomatic infections.
Relevance: Asymptomatic dogs can remain infected without displaying apparent clinical signs for years, even for their entire life, and would be able to infect sandflies. In this way, accurate diagnosis is essential to detect the asymptomatic dogs to avoid disease transmission to human and dog population.

P239

Methods for the evaluation of binary logistic regression predictions

Caroline Fenlon[1], Luke O'Grady[2], John Dunnion[1], [1]University College Dublin, Dublin 4, Ireland; [2]University College Dublin, Dublin 4, Ireland. Contact: caroline.fenlon@ucdconnect.ie

Purpose:
Logistic regression is a statistical modelling technique that is widely used for the analysis of binary events in epidemiology. Similar to some forms of linear regression, logistic regression works by using Maximum Likelihood estimation to determine a function mapping one or more independent variables to a binary outcome. All major statistical software packages allow such models to be built with relative ease, but evaluation of the resultant predictions is not widely documented. Existing software facilitates the use of tests for determining overall goodness of fit (e.g. the likelihood ratio test for comparisons with the null model), but there is little focus on predictive capability.

Methods:
This study describes the application of visual and statistical methods for the evaluation of logistic regression, including models with random effects, using the statistical programming language R. The usage and suitability of each method for binomial and binary data is examined by application to dairy cattle conception risk.

Results:
Pearson residuals help to identify outlying records which are predicted poorly by the model. Calibration plots can be used for broad evaluation of grouped predictions, to identify overall bias or error. The Hosmer-Lemeshow test also groups predicted probabilities and uses a chi-square test to determine if the group predictions are statistically different from the real outcomes. Evaluation of predictions for discretised independent variables highlights error in a more fine-grained manner.

Conclusions:
In-depth analysis of individual predictor variable responses is useful for checking the suitability of the model for prediction at a more granular level.

Relevance:
The evaluation methods most prevalent in literature are those suitable for binomial data (where the outcome is coded as the proportion of events occurring within a group with identical values in each predictor variable), but which do not apply to binary data, where records may be impossible to group due to continuous independent variables (i.e. outcome is 1 or 0 for a single record). The methods described here are applicable to both binomial and binary data.

P240

Evaluation of a smartphone app to improve disease diagnosis, surveillance and treatment of cattle in rural Ethiopia

Tariku Jibat[1], Sami Ibrahim[2], Ashenafi Feyisa[1], Takele Beyene[1], Crawford W. Revie[3], [1]Addis ababa University, Bishoftu/Debre zeit, Ethiopia; [2]Cojengo Ltd, Glasgow, United Kingdom; [3]University of Prince Edward Island, Charlottetown, PE, Canada. Contact: jibattariku@gmail.com

Ethiopia has one of the largest livestock populations in Africa, with cattle representing the largest segment, at around 50 million animals. Despite this the country has yet to fulfil its potential in this sector, with productivity currently among the lowest in Africa. A key limiting factor is lack of access to experienced veterinary services, and consequently the mis-diagnosis and incorrect treatment of common endemic cattle diseases. In this context we are evaluating a smartphone app, VetAfrica-Ethiopia, to assess whether it can improve diagnostic performance and become an integral part of animal health management in a limited resource setting.

The methods used included eliciting veterinary expert opinion on the most important livestock diseases and their clinical signs in three agro-ecologies of Ethiopia. Once the diseases had been identified and characterised according to their respective clinical signs, the knowledge was embedded in a Bayesian inference engine as part of the smartphone app, developed by the commercial project partner, Cojengo, who also manage the Cloud-based data sets. Fifteen final-year DVM students from the College of Veterinary Medicine and Agriculture in Addis Ababa University were assigned across the three regions to carry out clinical diagnoses on cattle with the aid of the VetAfrica app. Sample material (faecal, blood, tissue or serum) was collected from case animals and submitted to a laboratory to provide a ‘gold standard’ against which to compare student and app-based diagnostic performance.
The level of match between the students and the app varied from around 33% to over 90% of cases, depending on disease. We also found a high degree of between-student variation in terms of agreement with the diagnoses suggested by the app. Factors involved in these variations and the associations to lab-based results are explored through multinomial regression.

Such studies also offers an assessment of public-private collaboration in terms of utilizing Cloud-based data management and making mobile-based software available to public veterinary services; resulting in solutions with a longer 'shelf life' than the duration of the project itself.

P241

Adaption and Bayesian validation of a human immunofluorescence assay for detecting antibodies to Coxiella burnetii in small ruminants

Michael Muleme[1], John Stenos[2], Stephen Graves[2], Joanne M. Devlin[1], Angus Campbell[3], Alexander Cameron[4], Colin R. Wilks[1], Mark Stevenson[1], **Simon Firestone**[1], [1]University of Melbourne, Parkville, Australia; [2]Australian Rickettsial Reference Laboratory, Geelong, Australia; [3]University of Melbourne, Werribee, Australia; [4]University of Melbourne, Parkville, Australia. Contact: simon.firestone@unimelb.edu.au

In ruminants, infection with *Coxiella burnetii* may cause infertility and decrease milk production. Ruminants are also the main source of Q fever infections in humans. *C. burnetii* serological diagnosis in livestock is still nascent with the Complement Fixation Test (CFT) widely used for detecting past exposure despite known low diagnostic sensitivity (DSe). Several studies have reported agreement statistics on the indirect immuno-fluorescence assay (IFA) that indicate it is more sensitive in detecting antibodies to *C. burnetii* in ruminants than the CFT, and of similar DSe and diagnostic specificity (DSp) to available Enzyme Linked Immunosorbent Assays (ELISAs). The IFA also provides greater differentiation of recent versus past infections. However, there are currently no published DSe or DSp estimates for this test.

Purpose: Our study aimed to develop and optimise a new IFA protocol adapted from a human sero-assay to characterise this new test's performance in the absence of a 'gold standard' for detection of antibodies to *C. burnetii* in ruminants.

Methods: After optimising the new IFA on 12 negative samples (from *Coxiella*-free New Zealand), we tested these and an additional 84 samples from an infected goat farm in parallel with the IFA, CFT and ELISA. We applied Bayesian latent class modelling to estimate DSe and DSp at different cut-offs titres of the IFA in comparison with the other two tests. We also calculated the repeatability and inter-observer agreement of the IFA readings using the kappa statistic (*K*).

Results: At the optimal IFA cut-off dilution (1:160), the IFA's DSe was estimated to be 94.9% (95% Probability Interval, PI: 81.5, 99.6%) for the detection of IgG antibodies against *C. burnetii* compared to the CFT 43.2% (95% PI: 25.4, 69.3%) and ELISA 79.1% (95% PI: 61.9, 94.5%). All three tests were highly specific with posterior median DSp estimates of 95.1, 95.4 and 97.6% for the IFA, ELISA and CFT, respectively. Repeatability and inter-observer agreement between IFA readings were almost perfect (*K* >0.80).

Conclusion: These results demonstrate the suitability of the IFA over the CFT and ELISA for epidemiological studies of *C. burnetii* in ruminant populations.

P242

An online calculator for assisting in the design of herd-level prevalence surveys whilst taking into account test imperfections.

Andrew J. Duncan[1], **Harriet Auty**[2], Roger W. Humphry[2], [1]UHI, Inverness, United Kingdom; [2]SRUC, Inverness, United Kingdom. Contact: harriet.auty@sruc.ac.uk

Background: Most practitioners in epidemiology will be familiar with the fact that calculating sample sizes for surveys is often an iterative process due to there being more than one adjustable variable. This is especially so in veterinary epidemiology of livestock because we may have more than one stratum at which to sample - namely animals within herds and sampling the herds themselves.

Purpose: Our online calculator adopts a relatively simple method (Humphry et al. 2004) for the question of determining the number of animals and the number of herds to test in order to achieve a desired confidence about a measured herd level prevalence.

Methods: For this calculation there is a trade-off between the number of animals in the herd and the number of herds to be tested. This trade-off is hard to explore without testing various different scenarios. Our calculator presents a suite of scenarios via simple 2-D graphs so as to assist the practitioner in “exploring the options” more holistically than is done using the more conventional style of calculator which gives a single result for a single scenario.

Result/Conclusions: Our poster briefly describes the method in the black box alongside screen shots of the calculator with accompanying interpretation in order to demonstrate its utility.
A Beta version is available on: https://aj2duncan.shinyapps.io/Two-stageSampleSizeCalculator/

Relevance: this should be useful to any practitioner seeking to make an informed decision on sample sizes within and between flocks/herds when designing a herd prevalence survey using an imperfect test.
Reference: Humphry et al. 2004. P.V.M. 65: 173-188

P243

An online calculator for assisting in the design of herd-level prevalence surveys whilst taking into account test imperfections.

Hector Fuertes[1], Byron Flores[2], Tania Pérez-Sánchez[3], José Luis Muzquiz[3], Imanol Ruiz-Zarzuela[3], Ana Muniesa[3], **Ignacio de Blas[3]**, Nabil Halaihel[1], 1Universidad de Zaragoza/ ALQUIZVETEK SL, Zaragoza, Spain; 2Universidad Nacional Autónoma de Nicaragua, León, Nicaragua; [3]Universidad de Zaragoza, Zaragoza, Spain. Contact: deblas@unizar.es

Purpose: Canine parvovirus type 2 (CPV-2) was described in the 1970s, as causative of serious cases of gastroenteritis in pups worldwide. Since then three variants are differenciated based on VP2 sequence CPV-2a, CPV-2b and CPV-2c. The genome of CPV-2 is a single stranded DNA virus with two open reading frames, one coding in capsid proteins VP1-VP2 and the other for the nonstructural proteins NS1-NS2. Also, it harbours VP3 capsid protein. The aim of the study was to determine the circulating virulent genotype from symptomatic dogs.
Methods: A total of 70 fecal samples were collected from clinic animals of Spain (n=70). Viral DNA was extracted by PowerFecal® DNA Isolation kit. Real-time PCR gave 24 positive samples with different loads of viral DNA/mg faeces.
We only chose samples with very high load (>109 DNA copies/mg faeces) for subsequent characterization. A conventional PCR was performed to amplify around 583 bp of VP2 from these samples. We used MEGA 6 application and applied the ClustalW algorithm of different CPVs types from GenBanK database along with these seven isolates. Based on codon position 426 of VP2 types were assigned as CPV-2a (426-Asn), CPV-2b (426-Asp) and CPV-2c (426-Glu). However, a more detailed comparison through distant Estimates of Evolutionary Divergence between Sequences revealed other discrepancies.
Results: The results of the sequence analysis were characterized as CPV-2a (n=1), CPV-2b (n=5) and CPV-2c (n=1). We observed a single amino acid sustitution Ile418Thr, that has not been described in any database, indicating this isolates would be a new variant of CPV-2a. Another isolate had an amino acid Ala505Thr substitution that was discribed in China (2009). These new variants are described for the first time in Spain
Conclusions: Parvovirus DNA isolation followed by VP2 sequencing of infected animals with an elevated load of viral DNA, helps detecting relevant circulating CPV variants.
Relevance: An epidemiological survey from highly replicating CPV and determining their genotype proximity would help to detemine the new genotypes that are to be included in the elaboration of future vaccines.

P244

Preliminary use of run charts as predictor tool for outbreaks of Blue Tongue in Spain

Ignacio Ruiz Arrondo[1], Rosa Estrada[1], Ana Muniesa[1], Ignacio de Blas[1], Sarah Delacour Estrella[1], Miguel Ángel Miranda[2], Javier Lucientes Curdi[1], [1]Facultad de Veterinaria, Zaragoza, Spain; [2]Universidad de Islas Baleares, Mallorca, Spain. Contact: ignacioruizarr@yahoo.es

Purpose: Blue Tongue (BT) is a vector borne disease caused by an Orbivirus that can replicate in all species of ruminants.
The large BT epidemic began in 1998 (ongoing in many areas) through Europe. In Spain, several BT outbreaks caused by different BTV serotypes have occurred since 2000.
Culicoides biting midges (Diptera: Ceratopogonidae) are the main vectors implicated in the transmission of bluetongue virus (BTV). Specifically *Culicoides imicola* Kieffer is the species that is thought to have been the main vector in recent BTV epizootics in the southern Europe and Mediterranean area.
Methods: Based on run charts methodology with a mobile median and comparing periods biweekly and monthly, we have designed a preliminary predictor tool. Culicoides and BTV outbreaks data were from 2004 to 2014 and they were provided by the Spanish Bluetongue National Surveillance Program and Veterinary Health Warning Network (RASVE) both supported by the Spanish Ministry of Agriculture, Food and Environment.
Results: Classical correlation models did not provided significant results in this kind of disease so, different approaches base on run charts were carried out to analyze potential relationship between the evolution of the abundance of main vectors of BTV and the outbreaks. A qualitative interpretation of run charts offers a interesting information of the risky periods for BT, but objective criteria should be proposed in order to standardized this technique.
Conclusions: This new methodology could be a very interesting tool in order to improve the early detection of the BT outbreaks.
Relevance: A new predictor tool for outbreaks of Blue Tongue like that can be a useful method to support other classical strategies providing additional information to the surveillance program of BT.

P245

A proposed strategy for the global eradication of peste des petits ruminants

Jeffrey C. Mariner[1], Bryony A. Jones[2], Karl M. Rich[3], Samuel Thevasagayam[4], John Anderson[5], Martyn Jeggo[6], Yi Cai[4], Andrew R. Peters[7], Peter L. Roeder[8], [1]Tufts Cummings School of Veterinary Medicine, N. Grafton, MA, [2]Royal Veterinary College, University of London, Hatfield, United Kingdom; [3]Lab 863 Ltd, Edgware, United Kingdom; [4]Bill and Melinda Gates Foundation, Seattle, WA, [5]The Nelson Mandela African Institute of Science and Technology, Arusha, Tanzania, United Republic of; [6]Geelong Centre for Emerging Infectious Disease, Medical Faculty, Deakin University, Geelong, Australia; [7]Scotland's Rural College, Edinburgh, United Kingdom; [8]Taurus Animal Health, Headley Down, Hampshire, United Kingdom. Contact: jeffrey.mariner@tufts.edu

Purpose and Relevance

Peste des petits ruminants (PPR) is caused by a morbillivirus that affects small ruminants and is closely related to rinderpest (RP), the second disease to be globally eradicated in 2011. As small ruminants are key to the livelihoods of the poor, PPR can have significant negative impacts on rural communities. This paper outlines a strategy that continues the tradition of innovation that led to the success of RP eradication. A benefit-cost analysis of the strategy is presented in a companion paper.

Methods

The success of RP eradication depended on accurate epidemiologic intelligence to target vaccination to critical points in the virus' ecology. Complications to PPR eradication include larger small ruminant populations, faster reproduction, lower value per animal, and easier marketing to meet short-term cash needs than cattle. Unlike cattle, it is very difficult to progressively build up herd immunity levels over time. Hence, a PPR eradication program requires dynamic, targeted actions capable of interrupting virus transmission that are focused on specific populations with time windows defined in months rather than years.

Results and Conclusion

We propose a 12-year program with preparatory, eradication and validation phases. The preparatory phase consists of epidemiological and socio-economic assessments to inform the strategy and strengthen risk-based surveillance and service delivery. Delivery strategies should be based upon an understanding of the socio-economic incentives that drive stakeholder participation. Transmission rates should be measured to establish immunity targets. In the eradication phase, 2-3 vaccination campaigns in rapid succession with less than 50% national herd coverage could interrupt transmission if they are well targeted. In the validation phase, an evidence-based assessment would be carried out to confirm eradication.

The eradication program should be coordinated nationally, regionally and globally, but implemented as national small ruminant health initiatives at a pace consistent with the local context. Global coordination should be independent and inclusive, working closely with relevant international agencies.

P246

Development of individual animal and herd-level parameters for use in epidemic simulation models of classical swine fever in domestic swine

Timothy Boyer[1], Michelle Meyer[2], [1]University of Minnesota, Saint Paul, MN, [2]University of Minnesota, Minneapolis, MN, Contact: boye0087@umn.edu

Purpose: Classical swine fever (CSF) outbreaks can cause serious animal health and economic consequences. Significant changes have occurred in the United States swine industry since CSF was eliminated there in 1978, complicating efforts to plan for a potential CSF outbreak. Epidemic simulation models can be used to determine the scope and impact of a potential outbreak, as well as to evaluate control and response measures; however, past efforts to model CSF in North America have been limited. The purpose of this study was to develop individual animal and herd-level disease state parameters for CSF for use in epidemiologic simulation models.
Methods: A review of published studies on experimental infection of CSF in domestic swine was performed. Data on disease progression in individual animals exposed to CSF virus through contact with experimentally infected animals were extracted to create a dataset containing the durations of latent, subclinical infectious and clinical infectious disease states for both highly and moderately virulent CSF strains. Probability density functions were fit to the dataset to create individual animal disease state parameters that reflected natural variation. To create herd-level disease state parameters, the individual-level parameters were used to simulate within-herd disease spread for highly and moderately virulent CSF in 11 production types representing different stages of swine production and herd size.
Results: Fifteen studies met the inclusion criteria resulting in a dataset of 307 individual animals. Median herd-level latent, subclinical infectious, and clinical infectious disease state durations were 3-6 days, 0-6 days, and 34-103 days, respectively. Both the animal-level and herd-level disease state durations varied by virulence category. The herd-level disease state durations also varied by production type category.
Conclusions and Relevance: The parameters developed for this study provide needed inputs for epidemiologic simulation models that will inform future efforts to simulate between-herd CSF transmission.

P247

Indicators for the quantification of human and veterinary antimicrobial consumption: a review

Lucie Collineau[1], Catherine Belloc[2], Katharina D.C. Stärk[1], Anne Hémonic[3], Merel Postma[4], Jeroen Dewulf[4], Claire Chauvin[5], [1]SAFOSO AG, Bern Liebefeld, Switzerland; [2]Oniris, INRA, LUNAM, Nantes, France; [3]IFIP – French Institute for pig and pork industry, Le Rheu, France; [4]Ghent University, Faculty of Veterinary Medicine, Ghent, Belgium; [5]Anses-French Agency for Food, Environmental and Occupational Health and Safety, Ploufragan, France. Contact: lucie.collineau@safoso.ch

Purpose: An increasing number of indicators of antimicrobial usage has become available with no consensus on the appropriate indicators. Therefore, the objective of this review was to provide suggestions to select the most suitable indicators of human and veterinary antimicrobial usage in accordance with the study objective.

• Method: Four main possible objectives for quantifying usage were identified; they resulted in different requirements (e.g. resolution) on the way antimicrobial usage should be quantified. Available indicators were then described, focusing on 24 indicators calculated from antimicrobial sales, prescriptions and reimbursements (n=134 articles). By combining the requirements of the study objective with the available indicators, we finally provided suggestions on the most suitable indicators for each study objective.

• Results: Standardization is critical for studies aiming at comparing antimicrobial usage between different populations and can be achieved by selecting the same indicators and parameters to compute them. Important progress has been realized in this direction in human medicine, but standardization in veterinary medicine is still work in progress. However, standardization implies a less accurate description of the exposure to antimicrobials, which may be an issue especially for studies aiming at analyzing the link between antimicrobial usage and resistance. In that case, quantification should better rely on actual treatment parameters; this approach has mostly been developed in veterinary medicine.

• Conclusions: Human and veterinary medicine share common difficulties to quantify antimicrobial usage and could benefit from the experience gained in the other discipline to improve their own approach and to move towards a common approach to measure antimicrobial usage in human and animals.

• Relevance: This study provided a rationale for the selection of indicators to be considered for future antimicrobial usage studies. Major data gaps were also identified and included among others the absence of a gold standard for evaluating indicators and the lack of a scientific basis for the quantification of antimicrobial selection pressure.

P248

Is it feasible to test if liver fluke (Fasciola hepatica) is associated with increased risk of verocytotoxin producing Escherichia coli O157 from an existing study protocol?

Graeme L. Hickey[1], Peter J. Diggle[2], Tom N. McNeilly[3], **Sue C. Tongue[4]**, Margo E. Chase-Topping[5], Diana J. L. Williams[6], [1]University of Liverpool, Liverpool, United Kingdom; [2]University of Liverpool, Liverpool, United Kingdom; [3]Moredun Research Institute, Penicuik, Nr Edinburgh, United Kingdom; [4]SRUC, Inverness, United Kingdom; [5]University of Edinburgh, Edinburgh, United Kingdom; [6]University of Liverpool, Liverpool, United Kingdom. Contact: sue.tongue@sruc.ac.uk

Purpose: The liver fluke parasite, Fasciola hepatica, is a major cause of economic loss to cattle industries worldwide. Cattle are also the principle reservoir of Verocytotoxigenic Escherichia coli O157 (VTEC O157), an important cause of disease in humans. It is hypothesised that F. hepatica, which is known to suppress type 1 immune responses and induce an anti-inflammatory or regulatory immune environment in the host, may promote colonisation of the bovine intestine with VTEC O157. However, there has been little empirical research on the interaction between F. hepatica and VTEC O157 and the collection of suitable samples from representative field surveys is expensive.
We assessed whether it would be statistically feasible to augment a planned study - to quantify the prevalence of VTEC O157 in cattle in Great Britain - with additional testing of samples for liver fluke, as a pilot study to test this hypothesis.
Methods: We simulate data that conforms to known individual-level and farm-level prevalence on average under a mixed-effects logistic regression model framework. We use Monte Carlo sampling to empirically calculate the power to detect an association effect size (odds ratio) of 2. In order to reduce the resources required for such a study, we exploit the fact that the test results for VTEC O157 will be known in advance of testing for F. hepatica by restricting analysis to farms with a VTEC O157 sample prevalence of >0% and <100%.
Results: From a total of 270 farms (mean 27 cows per farm) that will be tested for VTEC O157, power of 87% can be achieved, whereby testing of F. hepatica would only be necessary for an expected 50 farms, thus considerably reducing costs.
Conclusion: It is feasible to use the planned VTEC study samples to test whether there is an association with liver fluke status, at an animal-level.
Relevance: Pre-study sample size calculations are an important part of any study design. The framework developed might be applicable to the study of other co-infections.

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Estimating African buffalo and cattle contact as a proxy for foot-and-mouth disease transmission risk at the Kruger National Park, South Africa

Louis van Schalkwyk[1], Eva M. De Clercq[2], Claudia De Pus[3], Darryn L. Knobel[4], Guy Hendrickx[5], [1]Government of South Africa, Skukuza, South Africa; [2]Université catholique de Louvain, Louvain-la-Neuve, Belgium; [3]Institute for Tropical Medicine, Antwerpen, Belgium; [4]University of Pretoria, Pretoria, South Africa; [5]Avia-GIS, Zoersel, Belgium. Contact: lvs@vodamail.co.za

Relevance: Most African buffaloes in the Kruger National Park in South Africa are persistently infected with foot-and-mouth disease (FMD) virus, posing a risk of spreading FMD to livestock in adjacent communal and small holder farming areas. FMD transmission from buffaloes to cattle is still poorly understood, although it is accepted that the two species need to be in close contact for it to occur.
Purpose: The aim of this work was to estimate the relative probability of contact between these species as a proxy for FMD transmission risk.
Methods: Data on cattle movement as well as records of buffaloes straying from the FMD infected zone were used in a maximum entropy approach to construct habitat suitability (HS) layers for cattle as well as stray buffaloes to assess potential overlap. Cattle density was incorporated into cattle HS layers to estimate cattle abundance (CA). Furthermore, permeability of the FMD fence was estimated and translated into a cost surface to simulate stray buffalo movement from the FMD infected zone to livestock areas along a least cost path (LCP).
Results: The HS approach estimated the highest risk of buffalo-cattle contact during the cool dry season, when cattle dispersal was greatest, and stray buffalo dispersal most constricted. To the contrary, CA switched the probability of buffalo-cattle contact to being highest in the warm wet season, mainly due to the concentration of high cattle numbers in preferred grazing areas and wider dispersal of stray buffaloes during this season. The LCP approximations, in combination with cattle abundance, provided useful insight into possible 'hotspots' for buffalo-cattle contact. Model outputs were tested against past FMD outbreaks. HS and CA type risk models could distinguish most outbreak areas as being more prone to FMD transmission. LCP was only able to estimate higher contact risk in outbreak areas versus non-outbreak areas in two cases.
Conclusions: The three methods proposed here can be applied practically to delineate disease control zones, set up strategic vaccination programs as well as to identify potential corridors frequently used by stray buffaloes to direct fence maintenance priorities.